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ALIGNMENTS 3 AV42855 standard; protein; 49 AA. AV42855; 3-JAN-2000 (first entry) JAN-2000 (first en	ALIGNMENTS MAY 2855 standard; protein; 49 AA. AV42855. AV42855. 3-JAN-2000 (first entry) Aman growth hormone (hGH) N-terminal fragment #1. COUCTION: pield; DOCTION: yield; DOCTION: Yiel	255	98			ABG94895	an growth
ALIGNMENTS MY2855 standard; protein: 49 AA. MY2855: MY42855. MY42855: M	ALIGNMENTS MY42855 standard; protein; 49 AA. MY42855; 9-JAN-2000 (first entry) man growth hormore (hGH) N-terminal fragment #1. rowth hormore; chaperone; intramolecular; itsulin; precursor; siding; conformation; chimeric protein; clearable; recombinant; roduction; yield. DWG-1999. 1-MAR-1998; 98WG-CN00052. 1-MAR-1998; 98WG-CN00052. POGT-1999. 1-MAR-1998; 98WG-CN00052. POGT-1999. 1-MAR-1998; 98WG-CN00052.						
AY42855 standard; protein: 49 AA. AY42855. 3-JAN-2000 (first entry) Man growth hormone (hGH) N terminal fragment #1. Towth hormone; chaperone; intramolecular; i.sulin: precursor; Miding: conformation; chimeric pritein; cleavable; recombinant roduction; yield. D9950302-A1. 1-MAR-1999. 1-MAR-1998; 98WO CN00052. 1-MAR-1998; 98WO CN00052. 1-MAR-1998; 98WO CN00052. PTONG-) TONGHUA GANTECH BIOTECHNOCOGY LID. PT. 1999-610839/52.	AY42855 standard; protein; 49 AA. AY42855; 3-JAN-2000 (first entry) Luman growth hormone (hGH) N-terminal fragment M1. Cowth hormone; chaperone; intramolecular; itsulin; precursor; siding; conformation; chimer:c protein; cleavable; recombinant; roduction; yield. DMO Sapiens. 1-MAR-1998; 98WC-CN00052. 1-MAR-1998; 98WC-CN00052. POCT-1999. 1-1999-610839/52.						
irst entry) rmore (hGH) Niterminal fragment #1. chaperone; intramolecular; insuiin; precursor; mation; chimeric protein; cleavable; recombinantid. 98WO-CN00052. GANTECH BIOTECHNOLOGY LID.	irst entry) rmore (hGH) N terminal fragment #1. chaperone: intramolecular; i.sulin; precursor; mation; chimeric protein; cleavable; recombinant; 1d. 98WO-CNO0052. GANTECH BIOTECHNOLOGY LID.	55	7			•	
irst entry) rmore (hGH) N-terminal fragment #1. chaperone; intramolecular; i.sulin; precursor; mation; chimeric protein; clouvable; recombinant id. 98WO-CN00052. GANTECH BIOTECHNOLOGY LID.	irst entry) rmone (hGH) N terminal fragment #1. chaperone; intramolecular; i.sulin; precursor; mation; chimeric protein; cleavable; recombinant; id. 98WO-CNO0052. GANTECH BIOTECHNOLOGY LID.	**************************************	1010		=		
irst entry) rmore (hGH) Niterminal fragment #1. chaperone; intramolecular; issuin; precursor; mation; chimeric protein; choavable; recombinant ld. 98WO-CN00052. GANTECH BIOTECHNOLOGY LID. 9/52.	irst entry) rmore (hGH) N-terminal fragment #1. chaperone; intramolecular; issuin; precursor; mation; chimeric protein; clearable; recombinant; id. 98WO-CN00052. GANTECH BIOTECHNOLOGY LID.	AY42855					
rmone (hGH) Niterminal fragment #1. chaperone; intramolecular; insulin; precursor; mation; chimeric protein; choavable; recombinant ld. 98WO-CN00052. GANTECH BIOTECHNOLOGY LID.	chapterone; intramolecular; issuin; precursor; mation; chimer; c protein; cleavable; recombinant; id. 98WO-CNOO052. GANTECH BIOTECHNOLOGY LID.	0	÷	5	- >		
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Growth hormone; chaperone; intramolecular; insulin: precursor; folding: conformation; chimeric pratels; clearable; recombinant production; yield. Homo sapiens. W0995u302-Al. 07-OCT-1999. 31-MAR-1998; 98WG-CN00052. 31-MAR-1998; 98WG-CN00052. GTONG-) TONGHUA GANTECH BIOTECHNOLOGY LTD. Gan 2; WPI; 1999-610839/52.	Growth hormone; chaperone; intramolecular; itsulin; precursor; folding; conformation; chimeric protein; clearable; recombinant; production; yield. Homo sapiens. W09950302-Al. 07-OCT-1999. 31-MAR-1998; 98WG-CN00052. 31-MAR-1998; 98WG-CN00052. (TONG-) TONGHUA GANTECH BIOTECHNOLOGY LID. Gan 2. WPI: 1999-610839/52.	Human grow	od 1			terminal tragment #	
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M09950302-A1, 07-OCT-1999, 31-MAR-1998, 98MG-CN00052, 31-MAR-1998, 98MG CN00052, (TONG-) TONGHUA GANTECH BIOTECHNOLOGY LT Gan 2, WPI: 1999-610839/52.	M09950302-A1. 07-0CT-1999. 31-MAR-1998; 98WG-CN00052. 31-MAR-1998; 98WC-CN00052. (TONG-) TONGHUA GANTECH BIOTECHNOLOGY LID. Gan 2. WPI: 1999-610839/52.	Homo sapiens					
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31-MAR-1998; 98WG-CN00052. 31-MAR-1998; 98WG-CN00052. (TONG-) TONGHUA GANTECH BIOTECHNOLOGY LTGan 2; WPI: 1999-610839/52.	31-MAR-1998; 98WG-CN00052. 31-MAR-1998; 98WG-CN00052. (TONG-) TONGHUA GANTECH BIOTECHNOLOGY LID. Gan 2; WPI: 1999-610839/52.	07 - 007 - 1944					
31-MAR-1998; 98WG-CN00052. 31-MAR-1998; 98WG-CN00052. (TONG-) TONGHUA GANTECH BIOTECHNOLOGY LIGAN 2; WPI: 1999-610839/52.	31-MAR-1998; 98WG-CN00052. 31-MAR-1998; 98WG-CN00052. (TONG-) TONGHUA GANTECH BIOTECHNOLOGY LID. Gan 2. WPI: 1999-610839/52.						
31-MAR-1998; 98MO CN00052. (TONG-) TONGHUA GANTECH BIOTECHNOLOGY LTGan 2; WPI: 1999-610839/52.	31-MAR-1998, 98WO CN00052. (TONG-) TONGHUA GANTECH BIOTECHNOLOGY LID. Gan 2. WPI: 1999-610839/52.	31-MAR-1998	J.	BWO - CNOC	~		
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Gan 2) WPI; 1999-610839/5	Gan 2; WPI; 1999-610839/52.	(TONG-)			вю	드	
WPI; 1999-610839/5	WPI; 1999-610839/52.	C					
WPI; 1999-610839/5	WPI; 1999-610839/52.	7 1100					
		19-6661 ;	8	2			

Claim 4; Page 28; 46pp; English.

provide human insulin with correctly linked cysteine bridges with fewer necessary procedural steps, and hence resulting in a higher yield of human insulin. The IMC sequences not only protect insulin sequences from intracellular degradation by a microorganism host, but also promote the folding of the fused insulin precursor, facilitate the solubility of the fusion protein and decrease the internal cular interactions among the fusion proteins, thus allowing folding of the fused insulin precursor cyanogen tromide cleavage, oxidative sulphitolysis and rejated purification sieps can thus be eliminated adona with the use of high purifications of mercaptian or the use of hydrognostic absorbent resins. hormone (hGH) which is a component of a chimeric protein, hGH-mini-proinsulin (AAY42860). The hGH portion of the chimeric protein acts as an intramolecular chaperone (IMC) for the insulin precursor, enabling it to fold correctly. A cleavable peptide linker with a C-terminal Arg residue (AAY4887) enables the hGH portion of the chimeric protein to be removed after folding has taken place. Production of recombinant human insulin via an hGH-proinsulin chimeric protein can represents an N-terminal fragment of human growth

49 AA; Sequence

·: 0 Gaps .. O DB 20; Length 49; Indels 100.0%; Score 260; DB 20; 100.0%; Pred. No. 2.Ne-25; Live 0; Mismatches 0; 49: Conservative Best Local Similarity Matches 49; Conserv Query Match

1 MFPTIPLSKLFDNAMLRAHRLHQLAFDTYQEFELAYIPKEQKYSFLCNP 49

ò qa

RESULT 2 AAY42856

AAY42856 standard; protein; 92 AA

19-JAN-2000 (first entry)

Human growth hormone (hGH) N-terminal fragment #2.

Growth hormone; chaperone; intramclecular; instin; precursor; folding; conformation; chimeric protein; chavable; recombinant; production; yield.

W09950302-A1

07 OCT-1999

31 MAR-1998;

98WO-CN00052 31-MAR-1998;

98WO-CN00052

(TONG:) TONGHUA GANTECH BIOTECHNOLOGY LID.

WPI: 1999-610839/52.

Gan 2;

New chimeric proteins containing human growth hormone fragment, used particularly for the production of human insulin ${}^{-}$

Claim 5; Page 28; 46pp; English.

sequence represents an N-terminal fragment of human growth hormone (hGH) which is a component of a chimeric protein (AAY42861) which also contains a human insulin precursor (AAY42859). The hGH portion of the chimeric protein acts as an intramolecular chaperone (IMC) for the

insulin precursor, enabling it to fold correctly. A cleavable peptide linker with a C-terminal Arg residue (AAY2887) enables the hdf portion of the chimeric protein to be removed after folding has taken place. Production of recombinant human insulin via an hdH-proinsulin chimeric protein can provide human insulin with correctly linked cysteine bridges with fewer necessary procedural steps, and hence resulting in a higher yield of human insulin. The IMC sequences not only protect insulin also promote the folding of the fused insulin precursor, facilitate the solubility of the fusion protein and decrease the intermigenlar. interactions among the fusion proteins, thus allowing folding of the fused insulin precursor at commercially useful high concentrations. The procedural steps of cyanogen bromide cleavage, oxidative sulphitolysis and related purification steps can thus be aliminated, along with the use of high concentrations of mercaptan or the use of hydrophobic absorbent resins

92 AA; Sequence

Gaps . O ; DB 20; Length 92; 4.6e-25; Indels 5 C: Mismatches 160.0%; Spore 260; 160.0%; Pred. No. 4 Pred. No. Best Local Similarity 100. Matches 49; Conservative Query Match

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1 MEPTIPLSRIFT-NAMERAHREHQLAFT-TYQEFEFAY LPKEQKYSFLONP 49

ŝ qq RESULT 3 AAY42860

AAY42860 standard; protein; 107 AA

AAY42860;

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(tirst entry) 19-JAN-2000

hGH mini-proinsulin chimeric protein.

insulin; precursor; growth hormone; chaperone; intramolecular; folding; conformation; chimeric protein; cleavable; recombinant; production; yield

Synthet ic.

Homo sapiens

WO9950302-A1

07-0CT-1999

98WO-CN00052 31-MAR-1998;

31-MAR-1998;

(TONG-) TONGHUA GANTECH BIOTECHNOLOGY LID

Gan 2;

WPI; 1999-610839/52.

New chimeric proteins containing human growth hormone fragment, used particularly for the production of human insulin

Claim 13; Page 30; 46pp; English.

This sequence represents a chimeric protein, high-mini-proinsulin.
This chimeric protein contains an N-terminal fragment of human growth hormone (htdl) of the sequence given in AAV42855, a cleavable peptide linker (AAV42857), and a human insulin precursor comprising insulin A and B chains (AAV42859). The hGH portion of the chimeric protein acts as an intramolecular chaperone (JMC) for the insulin precursor, enabling it to fold correctly. The cleavable peptide linker has a C-terminal Arg residue which enables the hGH portion of the chimeric protein to be removed after folding has taken place. Production

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of recombinant human insulin via an hGH-proinsulin chimeric protein can provide human insulin with correctly linked cysteine bridges with fewer necessary procedural steps, and hence resulting in a higher yield of human insulin. The IMC sequences not only protect insulin sequences from intracellular degradation by a microorganism host, but also promote the folding of the fused insulin precursor, facilitate the solubility of the fusion proteins and decrease the intermolecular interactions among the fusion proteins, thus allowing folding of the fused insulin precursor at commercially useful high concentrations. The procedural steps of cyanogen bromide cleavage, oxidative sulphitolysis and related purification steps can thus be eliminated, along with the use of high concentrations of mercaptan or the use of hydrophobic absorbent resins.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Human; anti anglogenic; prolactin; placentul lactogen; http: anglogenesis; quarath hormane; hGH; hGH-V. capullary endotherlal cen; proliferation; placentar vascularisation; pregnancy; treatment; anglosenic disease; tumbur; inhibitor; malignant; anglofibroma; arteriovenous malformation; would healing; proliferative retinopathy; nacusar degeneration; trachoma; granulation; glaucoma; coular, uvetis; 'cture; Osler Weber syndrome; psoriasis; fibroplasia; scleroderma; Rapus's sarcoma; vascular adhesion; quent therapy; pre-eclampsia; intrauterine growth retardation; placential dysfunction.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   This invention describes novel human anti-ar openic peptides derived from 10 to 150 consecutive amino acids selected from the N-terminal end of human placental lactogen (hPL), human growth hormone (hGH), growth hormone variant (hGH-V), or human projectin. Such peptides (i) Inhibit
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              New anti-andiogenic peptides · comprise N-terminal fragments of
human placental lactogen, human growth hormone, growth hormone
variant or human prolactin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          100.0%; Score 260; DB 20; Length 107; 100.0%; Pred. No. 5.4e-25; ive 0; Mismatches 0; Indels 6;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 MET TPLSRLEDNAMLRABRIHOLAFDTYQEFERAYTPKFÖKYSFLUNP 49
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                H. J. FELSTEIN MANDER HELD THE HELD THE PERSON PROPERTY FOR SYLVENIA SYLVEN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Human anti andiogenic peptide 16K hGH Met-1Prol33.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Claim 4: Page 49-50; 87pp; English,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Struman I, Taylor K,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAW92265 standard; Protein; 134 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           58WO - US09691
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   49; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (RESS ) UNIV CALIFORNIA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Ouery Match
Best Local Similarity
Matches 49; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    107 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            N-PSDB; AAX01707
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Martial JA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 19 NOV 1998.
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                                                                                                                                                                                                                                                                                                                                           Kaposi's sarcoma, trachoma, vascular adhesions, chronic varicose uloces, leukaemia, and reproductive disorders such as folicelar and luteal cysts and charicoarchoma. They can also be used as contraceptive agents. DNA encoding the peptides can be used in gene therapy. The measurement of abnorma, levels of Nierminal fragents of help with the help of the cast in assays for impairment of vascular development associated.
                                                                             diagnosing a probable abnormality of placental vascularisation during pregnancy. The peptides can be used for treating an angiogenic disease in a subject, for inhibiting tumour formation or growth in a patient or for modulating vascularisation of a patient's placenta. In particular, the peptides can be used for preventing or treating e.g. malignant tumours, angiofibroma, arteriovenous malformation, arthritic such as rheumatoid
                                                                                                                                                                                                 arthrilis, atherosclerotic plaques, corneal graft neovascularisation, delayed wound healing, proliferative retinopathy such as diabetic retinopathy, macular degeneration, granulations such as those occurring in Lacmophilic joints, inappropriate vascularisation in wound healing such as hypertrophic scars or keloid scars, neovascular glaucoma, ocular tumour, uveitis, non-union fractures, usler whober syndrome, psoriasis, pyogenic glaucoma, retrolental fibroplasia, scleroderma, solid tumours.
capillary endothelial cell proliteration and organisation (ii) inhibit angiogenesis in chick chorioallantoic membrane and (iii) binds to at least one specific receptor which does not bind an intact full length hGH, hPL, prolactin or hGH-V. The invention also describes a method for
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- having cleavage site for thrombin, useful for treating geriatric
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  with pre eclampsia, intrautering growth retardation, and placental dysfunction.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     100.0%; Srcie 260; DB 20; Length 134; 100.0%; Pred; No. 7e-25; ive 0; Mismatches 0; indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 MEPTIPLSKLEDNAMERABRUHOLAFOTYGEFSEAYIPKEOKYSFUJNP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Human growth hormone; fusion proteis; thrombin;
geriatric dementia; gervous disorders; human nerve factor.
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Best Local Similarity 100.0
Matches 49, Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                134 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        dementia, etc.
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Human growth hormone segment, used at the N terminal of a fusion

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of the chimeric protein acts as an intrandlecular chaperone (IMC) for the chimeric protein acts as an intrandlecular chaperone (IMC) for the insulin precursor, enabling it to told correctly. The cleavable period liner has a C-terminal Arg residue which enables the hGH portion of the chimeric protein to be removed retailed which enables the hGH portion of the chimeric protein to be removed received the hGH portion of the chimeric protein the man insulin with correctly linked cysteine bridges protein can provide human insulin with correctly linked cysteine bridges with fewer necessary procedural steps, and core resulting in a higher sequences from intracellular degradation by a microorganism host, but also promote the folding of the fuscon insulin precursor, facilitate the solubility of the fusion proteins, thus allowing folding of the interactions among the fusion proteins, thus allowing folding of the fusion proteins, thus allowing folding of the fusion proteins, thus allowing folding of the fusion protein and decrease the intermolecular increations among the fusion bromate cleavage, oxidative sulphitolysis and related purification steps can thus be eliminated, along with the use of high concentrations of mercaptan or the use of hydrophobic absorbent
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protein, which contains a thrombin recognition site, and human beta nerve growth factor (beta NGF) at the C-terminal. Beta-NF can be used to control geriatric dementia and other nervous disorders, and can be refeased from the fusion protein by incubation with thrombin (see AAN90577-8, AAP91034, AAP91299).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    This sequence represents a chimeric protein, which contains an N-terminal fragment of human growth hormone (hGH) of the sequence given in AAY42856, a cleavable peptide linker (AAY42857), and a human insulin precursor comprising insulin A and B chains (AAY42859). The hGH portion
                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    New chimeric proteins containing human grow:), hormone fragment, used particularly for the production of human insulin \cdot
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              avable; recombinant;
                                                                                                                                                                                                         ;
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                                                                                                                                                                                                                                                 5.
                                                                                                                                                                                                                                                                  e: intramolecular;
                                                                                                                                                                100.0%; Score 260; DB 10; Length 140; 100.0%; Pred. No. 7.3e-25;
                                                                                                                                                                                                                                           1 MEPTIPLSRLFDNAMLRAHRLHQLAFDTYQEFEEAYIPKEQKYSFUQNP
                                                                                                                                                                                                         Indels
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                                                                                                                                                                                                         Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Insulin; precursor; growth hormone; chap. folding; conformation; chimeric protein;
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                                                                                                                                                                                                                                                                                                                                                                                        AAY42861 Standard: protein:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Chimeric protein, SEQ ID 7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       19 JAN-2000 (lirst entry)
                                                                                                                                                                                                         49; Conservative
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                                                                                                                                                                                 Local Similarity
                                                                                                                       140 AA
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                                                                                                                       Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                 AAY42861;
                                                                                                                                                                Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Recombinant vector contg. fusion protein · consisting of human growth hormone or deriv. Ligated to foreign protein, for stability
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                                                                                                                                                                                                                                                          1 MEPTIPLSRIFONAMIRAHRIHQLAFOTYQEFEEAYIPKEQKYSFLONP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Human growth hormone; tusion protein; recombinant
                                                                                                                 Score 260; DB 20;
Pred. No. 7.9e-25;
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                                                                                                                                                                          Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A
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                                                                                                        100.0%;
ilarity 100.0%;
Conservative 0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (revised)
(first estry)
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N-PSDB: AAN90269.
                                                                                                                                         l Similarity
49; Conserv
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                                                     150 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          25 MAR-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        06-FEH-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                01 - N: v : 1985
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             07-JUN 1989
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAP90129;
                                                           Sedicence
                                                                                                              Query Match
Best Local S
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAW92264
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  vector
                                                                                                                                                                       Matches
                                                                                                                                                                                                                                                                                                                                                                      RESULT 7
                                                                                                                                                                                                                                                                                                                                                                                           AAP90129
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RESULT 8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAW92264
SXS
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Weiner RI;
       Human anti-angiogenic peptide hGH Met-1Phe191.
                                                                                                        Taylor R,
                                                                                                                                         Example 3: Page 49; 87pp; English.
                                                                                 15950SD + M86
                                                                                         97US-0046394
                                                                                                                                  variant or human prolactin
(first entry)
                                                                                                        Struman I,
                                                                                                 (REGC ) UNIV CALIFORNIA.
                                                                                                               WPI: 1999-045192/04
                                                                                                                                                                                                                                                                 192 AA:
                                                                                                                   N-PSDB: AAX01706
                                                           Homo sapiens
                                                                  W09851323-A1
                                                                                         13 MAY 1997;
                                                                                                        Martial JA,
                                                                                 12-MAY - 1998;
                                                                          6551 - AON 61
                                                                                                                                                                                                                                                                 Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          from 10 to 150 consecutive amino acids scretcul from the N-terminal end
of from 10 to 150 consecutive amino acids scretcul from the N-terminal end
of human placental lactogen (hPL), human rowth hormone (hGH), growth
bormone variant (hGH-V), or human prolac n Such peptides (1) inhibit
capillary endothelial cell proliferation uni organisation (11) inhibit
capillary endothelial cell proliferation uni organisation (12)
capillary endothelial cell proliferation or hid and intact tuil length
capillary probable abnormality of place (tal vascularisation disease in
a subject, for inhibiting tumour formatic or growth in a patient or for
modulating vascularisation of a patient's placenta. In particular, the
capillary accularisation or reventing or treating e.g. malignant tumours,
anticities a their selectic plaques, corneal graft necessorlarisation,
anticities a their selection pages. Corneal graft necessorlarisation,
anticities a their selection pages.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            delayed wound healing proliferative retinopathy such as diabetic retinopathy, macular degeneration, granulations such as those occurring in the momphilic joints, imappropriate vascularisation in wound healing such as hypertrophic scars or keloid scars, necovasion in wound healing such as hypertrophic scars or keloid scars, necovasion in wound healing such as hypertrophic scars or keloid scars, necovasional glancoma, occular pywenic glaucoma, retrolental fibroplasia, scheroderma, solid tumous. Kaposi's sarcoma, trachoma, vascular adhe ions, chronic varicose ulcers, lowacemia, and reproductive disorders such as follicular and luteal cysts and chorinoma. They can also be user as contraceptive agents, DNA encoding the peptides can be used in gene 'herapy, The measurement of abutormal levels of N-terminal fragments of how, prolactin or her
                                         Human: anti-angiogenic; prolactin; placental lactogen; hPL; angiogenesis; growth hormone; hGH; hGH-V; capillary endothelial cell proliferation; placental vascularisation; pregnancy; treatment; angiogenic disease; tumour; inhibitor; malignant; angiofibroma; arteriovenous malformation; arthritis; atherosclerotic plaques; corneal graft neovascularisation; wo.nd healing; proliferative retinopathy; macular degeneration; tractione; granulation; qlaucoma; ocular; uveilis; fracture; Osler Weber syndrome; psoriasis; fibroplasia; scleroderma; Kaposi's sarcoma; vascular adhesion; quene therapy; pre-eclampsia; intrauterine growth retardation;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     can be used in assays for impairment of vascular development associated with pre-eclampsia, intrauterine growth retardation, and placental
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            New anti-anglogenic peptides · comprise N-terminal fragments of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               human placental lactogen, human growth hor sone, growth hormone
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Score 260; DB 20; Length 192; Pred. No. 1e-24;

100.0%;

Best Local Similarity

Query Match

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Fusion protein consisting of human growth hormone at the N-terminal end (1st region), a 3 amino acid sequence representing thrombin recognition site, and human beta nerve growth factor (beta-NGF) at the C-terminal. Beta-NGF can be used to control geriatric dementia and other nervous disorders, and can be released from the tusion protein by incubation with thrombin (see AAN%0577-8, AAP91034,
Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    New human nerve growth factor gene encoding lusion protein having cleavage site for thrombin, useful for treating gerlatric
                                                                                                                                                                                                                                                                                                                  Human nerve growth factor and human growth hormone fusion protein
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O
                                       1 MEPTIPLSRLFDNAMLRAHRLHQLAFDTYQEFEEAYIPKEQKYSFLUNP 49
                                                              9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                100.0%; Score 260; DB 10; Length 261; 100.0%; Pred. No. 1.5e-24; ive 0; Mismatches 0; Indels 0
                                                                                                                                                                                                                                                                                                                                                          Human nerve growth Factor, tusion protein; thrombin, geriatric dementia, nervous disorders; human growth hormone.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 MEPTIPLSRLFDNAMLRAHRLHQLAFDTYOFFEEAY IPKEQKYSFLONP
  Indels
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0
  Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Claim 36; page 31-32; 38pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Local Fon/Jual Hers
                                                                                                                                                                                          AA
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                                                                                                                                                                                        AAP91299 standard; protein; 261
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                                                                                                                                                                                                                                                                            (first entry)
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Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Best Local Similarity
Matches 49; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (TOYJ ) TOSOH CORP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    261 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                dementia, etc.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          17-FEB-1989;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  19-FEB-1988;
                                                                                                                                                                                                                                                                          14 - DEC - 1989
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              23-AUG-1989.
49:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EP329175-A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Ohtsuka E;
                                                                                                                                                                                                                                    AAP91299;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Region
Region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Region
  Matches
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Location/Qualifiers 145..262

Bet.a-NGF; E.coli; ds

Homo sapiens

85.JP - 0045773 85JP-0045773

09-MAR-1985; 09-MAR-1985;

11 SEP-1986

JP61205485

Protein

Sapadese

Claim 32: Page 482; 71pp;

See also AAN60816-7

262 AA;

Sequence

WPI: 1986-281696/43

(CTSUZ) OTSUKA

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Purificn, of human neuron growth factor beta-subunit-contg. protein
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WPF: 1991-128768/18 N-PSDB: AAQ11578. (THYLL) TOSOH CORP

89JP-0202835 89JP-0202835

07-AUG 1989; 07 AUG-1989;

JP0+067598 A.

22 MAR-1991

Home sapiens

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The protein is produced by fusing DNA encoding BDF (11-) with DNA encoding BSF-2 (11.-5) and ligating the product into an expression vector See also AAR05311 and AAR05313.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Caps
                                                                                                                                                      A recombinant human nerve growth factor beta subunit-conig, protein can be produced as this fusion protein. It is purified by contacting a gel having a cation exchange gp. with the fusion protein, in the presence of urea. The purified protein is useful in a medicament for treating disorders of the nervous system, eg dementia.

(Updated on 25-MAR-2003 to correct PF field.)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           B-cell stirulatory factoriz: interlenkin 6; B cell differentiation:
interleukin-5; tusio: protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Preph. of human B-reil differentiation factor - from specified DNA sequence sequent, by recombinant DNA technique, gives protein of
by contacting with gel having cation exchange gp. in presence of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ·:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           100.0%; Score 260; DB 11; Length 310; ilarity 100.0%; Pred. No. 1.8e-24; Conservative 0; Mismatches 0; Indels 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Fusion protein of Breell stimulatory factor 2 and Breeil
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                    Ouery Match 100.0%; Score 260; DB 12; Best Local Similarity 100.0%; Pred. No. 1.5e-24; Matches 49; Conservative 9; Mismatches 9;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAR03255 standard; protein; 310 AA
                                                                                               Disclosure; fig 1; 7pp; Japanese
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Claim 31; Page 9: 17pp: Japanese
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  specified amino acid sequence.
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Best Local Similarity
Thes 49; Conserva
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WPI: 1990-062207/09
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                                                                                                                                                                                                                                                                                                                                                                                          262 AA;
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   # # X X X O O O O O C X & O
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   The protein is a direct translation of the upstream tryptophan promoter operator lacking its attenuation requence and human beta NGF sequence. The product may be efficiently expressed from a transformed E.coli expression system.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Human growth hormone/human nerve growth factor beta fusion protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ä
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Ouery Match
Best Local Similarity 100.0%; Pred, No. 1.5e-24,
Matches 49; Conservative U: Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 MEPTIPLSRIPDNAMLRAHREHULAFDTYGEFEBAYIPKEGKYSFLUNP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                used in produ.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NGF producting recombinant Excherichia strain
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             Human beta-nerve growth factor gene product
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ΑÀ

AAsli740 standard; Protein; 262

RESULT 11 AAR1174:

ò q AAR11740;

25 MAR-2003 (updated) 25 EUN-1993 (first entry)

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Song YH;
                                                                                                                                                                                                                                                       Synthetic.
                                                                                     Sequence
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                                                                                                                                                                                         AAP81226;
   YOO JG,
                                                                                                                                                               RESULT 15
                                                                                                                                                                     AAP81226
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O
                                                                                                                                                                                                                              The sequence encoding this protein can be fused with DNA encoding B-cell differentiation factor (1L-6) and liquted into an expression vector for prodn. of a fusion protein.
                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                     Prepa. of Euman B-cell differentiation factor - from specified DNA sequence segment, by recombinant DNA ter angue, gives protein of
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                                                                                                                                                                                                                                                                                                          Score 257; DB 11; Length 144;
Pred. No. i.8e-24;
1; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                              0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                    Human growth hormone with collagenase recognition site.
                                                                                                                                                                                                                                                                                                                                                                                                                  Human; growth hormone; collagenase; recognition site
                                                     Segment of B-cell stimulatory factor-2 (IL-5).
                                                                   B-cell stimulatory factor-2; interleukin-5.
             AAR05313 standard; protein; 144 AA
                                                                                                                                                                                                                  Disclosure: Page 9; 17pp; Japanese.
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                                                                                                                                                                                                                                                                                                                                                          ABB77327 standard; Protein; 204
                                                                                                                                                                                                    specified amino acid sequence.
                                                                                                                                                                                                                                                                                98.88;
                                                                                                                          88.19-0162555
                                                                                                                                       86.18-016.25%
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                                         (first entry)
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Best Local Similarity 98.09
                                                                                                                                                                                                                                                                                                                                                                                      (first entry)
                                                                                                                                                                  WP:: 1990-062207/09.
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                                                                                                                                                    (BOYJ ) TOSOB CORP.
                                                                                                                                                                                                                                                                   144 AA:
                                                                                                                                                                                                                                                    See also AAR05311.
                                                                                                                                                                         N PSDB; AAG02028
                                                                                                                                       C. JUL 1988;
                                                                                               JP62013375-A
                                                                                                                         01-JUL 1988;
                                                                                  Home sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         28 DEC-1993;
                                        19 . JUL- 1990
                                                                                                                                                                                                                                                                                                                                                                                                                                Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       28-DEC-1993;
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                                                                                                                                                                                                                                                                                                                                                                                                                                             KR289691-B
                          AAR05313;
                                                                                                                                                                                                                                                                   Sequence
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RESULT 13
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0
                                                                                                                                                            Recombinant human growth hormone having collagenase recognition region
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
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                                                                                                                                                                                                                                                                                                                                                               The invention relates to recombinant human growth hormone having collagenase recognition region.
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by culturing bacterium transformed by plasmid coutg. gene
segment with specified DNA sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence of protein with somatomedin-like activity
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Pred. No. 3.5e-24;
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                                                                                                                                                                                                                                                        Disclosure: Fig 3: 8pp; Korean.
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98.08;
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Best Local Similarity 100.
Matches 48: Conservative
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N-PSDB; AAN81605.
WPI; 2002-185396/24
N-PSDB; AHL55999.
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Search completed: September 15, 2003, 12:00:56 Job time: 15,4229 secs

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Sequence 1, Appli
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GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.
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US-08-1469-465-51
US-08-111-657-4
US-08-111-657-4
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Sequence 8, Appli Sequence 1, Appli Sequence 2, Appli Sequence 2, Appli Sequence 2, Appli Sequence 2, Appli Sequence 2, Appli Sequence 1, Appli Sequence 1, Appli Sequence 1, Appli Sequence 2, Appli Sequence 2, Appli Sequence 3, Appli Sequence 2, Appli Sequence 3, Appli Sequence 2, Appli Sequence 2, Appli Sequence 2, Appli Sequence 6, Appli Sequence 6, Appli Sequence 6, Appli	e Growth Hormone
191 1 US-08-468 924-8 176 3 US-08-791-728-1 176 4 US-08-990-774-1 190 1 US-08-388-267C-2 190 4 US-09-277-720-2 191 6 5210180-1 193 1 US-07-621-197C-2 193 2 US-08-383-982-2 193 2 US-08-165-651-1 193 2 US-08-165-651-1 194 2 US-09-165-651-3 176 4 US-08-791-728-2 177 1 US-08-191-728-2 177 1 US-08-191-756C-6 177 2 US-08-191-728-2 176 4 US-08-191-756C-6	ALICOMPINIS 08-093-383-1 08-093-383-1 08-093-383-1 Sequence 1. Application US/0809383 Setura 1. NFORMATION: APPLICANT: BENDERS: APPLICANT: BENDERS: APPLICANT: Sechura, Peter H. TITLE OF INVENTION: DNA for Expression of Bovine NUMBER OF SEQUENCE: 30 CORRESPONDER: ADDRESS: ADDRESSEE: Genentech, Inc. STREET: 460 Point San Brano H:vd CITY: South San Francisco STREET: 461 Point San Brano H:vd CITY: South San Francisco STREET: 461 Point San Brano H:vd CITY: South San Francisco STREET: 460 Point San Brano H:vd CITY: South San Francisco STREET: 460 Point San Brano H:vd COMPUTER: BN PC Compatible COMPUTER: BN PC Compatible COMPUTER: IBM PC Compatible COMPUTER: IBM PC Compatible COMPUTER: Satistonia SOFTHAND TYPE: 5.25 inch, 360 Kb iloppy disk COMPUTER: IBM PC Compatible APPLICATION NUMBER: 05/619827 FILING DATE: 28-KOV-1980 APPLICATION NUMBER: 06/63281 FILING DATE: 19-31-1984 PRIOR APPLICATION NUMBER: 06/63281 FILING DATE: 19-31-1984 PRIOR APPLICATION NUMBER: 06/63281 FILING DATE: 18-SEP-1981 ATTOCHENEY/AGENT INFORMATION: NAME: JOHNSTON SATOR 18-25-3562 TELEPHONE: 415/525-362 TELEPHONE CHARACTERISTICS: LEMENTION POS SPO ID NO: 1: SEQUENCE CHARACTERISTICS: LEMENTION AND ACID
28 164.5 63.3 30 164.5 63.1 33 159.5 61.3 34 159.5 61.3 34 159.5 61.3 34 159.5 61.3 34 159.5 61.3 36	RESULT 1 US-08-093-383-1 Sequence 1, Application US/0809383 Sequence 1, Application US/0809383 GEMERAL INFORMATION: APPLICANT: DeBoer, Herman A. APPLICANT: Secburg, Petch H. TITLE OF INVENTION: DNA for Express NUMBER OF SEQUENCES: 30 CORRESPONDENCE ADDRESS: 30 CORRESPONDENCE ADDRESS: 30 CONFESSE: Genentech, Inc. STREET: 460 Point San Brino Hivd SITRET: California COUNTHY: South San Francisco STATE: California COUNTHY: USA. ZIP: 94080 COMPUTER READABLE FURM: MEDIUM TYPE: California COUNTHY: USA. ZIP: 94080 COMPUTER READABLE FURM: MCONFORTION: WEBDIUM TYPE: Datin (Genentech) COMPUTER: Datin (Genentech) COMPUTER: Datin (Genentech) COMPUTER: 14 JUL-1993 CLASSIFICATION UNBER: US/08/093,38 FILING DATE: 28-NOV-1990 PRIOR APPLICATION NUMBER: US/08/3361 FILING DATE: 10-331-1984 PRIOR APPLICATION NUMBER: 05/632361 FILING DATE: 10-331-1984 PRIOR APPLICATION NUMBER: WS,910 REFERENCEOCKER INVERMATION: NAME: JOHNSTON SCAN A RECISTRATION NUMBER: PS,910 RECESTERATION NUMBER: PS,910 REFERENCEOCKER INVERMATION: TELEPONE: 415/225-3861 TELEX: 910/31-7168 INFORMATION FOR SED IN NO: 1: SEQUENCE CHARACTERISTICS: LENGTH: 1992 amino acids TYPE: amino acids

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) TOPOLOGY: linear
) MOLECULE TYPE: protein
US-08-459-906-4
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APPLICANT: Saidana, Hugo Farrera
APPLICANT: Saidana, Guese Maria Viader
TITLE DE INVENTION: Production and Secreti of the Busas drowth Rosmose
FILE REFERENCE: 1829, 60100-06
CURRENT FALING DATE: 1899 07-21
PRIOR FILING DATE: 1997-10-24
NUMBRE: OF SEQ ID NOS: 9
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                                                                                                                                                                  | FPTIPLSKLEDNAMLRAHKLHQUAFOTYQEFEEAY!PKEQKYSFLQNP 48
                                                                Length 192;
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                                                                                                                                            1 MFPTIPLSRLFDNAMLRAHRLHQLAFDTYQEFEEAYIPKEOKYSFLONP
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CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/383,621
FILLING DATE: 06-FEB-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         98.1%; Score 255; DB 4; 1
100.0%; Pred, No. 2.46-29;
                                                        Query Match 100.0%; Score 260; JR 1; Best Local Similarity 100.0%; Pred. No. 4.6r-30; Matches 49; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         i: Dr. Estelle J. Tsevdos
1937 West Main Street, P.O. Box 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       IBM PC compatible
SYSTEM: PC-DOS/MS-DOS
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APPLICANT: Buckwalter, Brian L.
APPLICANT: Cady, Susan M.
APPLICANT: Shieh, Hong-Minq
APPLICANT: Bohlen, Peter
APPLICANT: Seddon, Andrew P.
                                                                                                                                                                                                                                                                                      Sequence 5, Application US/09284878 Patent No. 6342375
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; Sequence 4, Application US/08383623
; Patent No. 5951972
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NUMBER OF SEQUENCES: 1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TYPE: PRT
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PERATING SYSTEM:
TOPOLOGY: linear
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Best Loval Similarity
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                                                                                                                                                                                                                                                                     US-09-284 878-5
                 US-08-093-383-1
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SEQ ID NO 5
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Gaps
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106.0%: Pred. No 2.5e 29;
ive 6; Mismatches 0; Indels
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OPERATING SYSTEM: PC-DOS/MS-NUS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
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One Cyanamid Plaza
                                                                                              NAME: TSEVdos, Estelle J.
REGISTRATION NUMBER: 31,145
REFERENCE/DOCKET NUMBER: 31,278.01
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/766.142
FILING DATE: 25.5EP-1991
ATTORNEY/AGENT INFORMATION:
NAME: Tsevdos, Estelle J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICATION NUMBER: US/08/459,906
FILING DATE: 02-JGN-1995
CLASSIFICATION: 5:4
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Patent No. 6010999
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APPLICANT: Daley, Michael J.
APPLICANT: Bickwalter, Brian ...
APPLICANT: Cady, Sissn M.
APPLICANT: Shieh, Hong-Ming
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NAME: Webster, Darry; L. REGISTRATION NUMBER: 34,276 REFERENCE/DOCKET NUMBER: 31, TELECOMMUNICATION: 101-831-3247
                                                                                                                                                                  TELECOMMUNICATION INFORMATION:
TELEPHONE: 203-321-2756
TELEFAX: 203-321-2971
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: Bohlen, Peter APPLICANT: Seddon, Andrew P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       INFORMATION FOR SEQ ID NO: 4:
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MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                            TELEFAX: 203-321-2971
TELEX: 203-310-474-4059
INFORMATION FOR SEQ ID NO: 8
SEQUENCE CHRARCTERISTICS:
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Bost Local Similarity 180 09
Matches 489 Conservative
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LENGTH: 194 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                                                                                             LENGIH: 194 amino acids
TYPE: amino acid
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MOLECHIE TYPE: protein
US-08-183-621-4
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CITY: Wayne
STATE: New Jersey
COUNIEY: U.S.A.
ZIP: 07470-8426
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CITY: Houston
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                                                APPLICANT:
APPLICANT:
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                                                                                                      4 FPTIPLSRLFDNAMLRAHRLHQLAFDTYQEFEEAYIPKEQKYSFLQNP 51
                                                                                                                                                                                                                                                                                                                                                                                                                         TITLE OF INVENTION: Accomptoner Expression of Proteins From
ITHE OF INVENTION; Secretary Oct., ands
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        Length 194;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        98.1%; Score 255; DB 3; Length 217; 100.0%; Pred. No. 2.9e-29;
                                             0; Indels
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SOFTWAME: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
Ouery Match 98.1%; Score 255; DB 3; I
Best Local Similarity 100.0%; Pred. No. 2.5e-29;
Matches 48; Conservative 0; Mismatches 0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ATTORNEY/AGENT INFORMATION:
NAME: H.shlander, Steven L.
KEGISTRATION NUMBER: 47,642
REFERENCE/INCKET NUMBER: UTSD:426\HYL.
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                               APPLICANT: Newgard, Christopher B. APPLICANT: Halban, Philippe APPLICANT: No. 6087129mington, Karl D. APPLICANT: Clark, Samuel A. APPLICANT: Thigpen, Anire E.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Halban, Philippe A.
No. 6110707mington, Karl D.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                NUMBER OF SEUBENCES: 50
CORRESPONDENCE ADDRESS:
ANDRESSEE: Arnold, White & Durkee
STREET: P. O. BOX 4433
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: Newgard, Christopher B. APPLICANT: Halban, Philippe A. APPLICANT: No. 6110707mington, Kar
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 10, Application US/08784582 Patent No. 6110707 GENERAL INFORMATION:
                                                                                                                                                                                                                         Sequence 10, Application US/08589028 Patent No. 6087129
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER: 18M PC COMPATIBLE UPERATING SYSTEM: PC-DOS/MS
                                                                                                                                                                                                                                                                                                                                                                                 Oldade, Christian
Kruse, Fred
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TELEPHONE: (512) 418-3000 (512) 474-757 INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
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MEDIUM TYPE: Floppy disk
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Matches 48; Conserva
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APPLICANT:
APPLICANT:
APPLICANT:
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                                                                                     APPLICANT: McGarry, Dennis
TITLE OF INVENTION: RECOMBINANT EXPRESSION OF PROTEINS FROM
TITLE OF INVENTION: SECRETORY CELL LINES
NUMBER OF SEQUENCES: 79
CORRESPONDINCE ADDRESS:
ADDRESSEE: Arnold, White & Durkee
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TITLE OF INVENTION: RECOMBINANT EXPRESSION OF PROTEINS FROM TITLE OF INVENTION: SECRETORY CELL LINES NUMBER OF SEQUENCES: 56
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 217;
                                                                                                                                                                                                                                                                                                                                                                                                                            SOFTWARE: Patenin Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/64/784,582
Fit.NS.IATE: Concerteniny Herewith
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match 98.1%; Score 25%; DB 3; L. Best Local Similarity 100.0%; Pred. No. 2.9e-29; Matches 48; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: Newgard, Christopher B. APPLICANT: Halban, Philippe A. APPLICANT: No. 6194176mington, Karl D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      REGISTRATION NUMBER 37,642
REFERENCE/DOCKET NUMBER: UTSD:514
TELECOMMUNICATION INFORMATION:
TELEPERSE: 512/418-3000
TELEFAX: 512/414-7577
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICATION NUMBER: US 08 :89,028 FILING DATE: 19-JAN-1996 ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICATION NUMBER: US 60/028,427 FILING DATE: 15-0CT-1996 PRIOR APPLICATION DATA:
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ADDRESSEE: Arnold, White & Durkee
STREET: P.O. Box 4433
                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     US-08-785-271-10
Sequence 10. Application US/08785271
Patent No. 6194176
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NAME: Highlander, Steven L.
Clark, Samuel A.
Thigpen, Anice E.
Ouaade, Christian
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TELEFAX: 512/474-7577 INFORMATION FOR SEQ ID NO: 10:
                                                                                                                                                                                                                                                                                                                                      COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               217 amino acids
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                                                                                                                                                                                                                           P.O. Box 4433
                                                                  Kruse, Fred
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CLASSIFICATION: 435
PRIOR APPLICATION DATA:
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STREET: P.C.
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TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-852-9196
TELEFAX: 415-496-1200
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LOCATION:
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LOGAT FON:
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                                                                                                                                                                                                                                                         LOCATION:
                                                                                                                                                                                                                                                                                                                                                                              LOCAL POR
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APPLICANT: Rock, Fernando L.
APPLICANT: Razal J. Fernando
APPLICANT: Kastelin. Robert A.
TITLE OP INVENTION: MUTATIONA, VARIANTS OF MAMMIJAN PROTEINS
NUMBER OF SEQUENCES: 11
CORRESPONDENCE ADDRESS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        98.1%; Score 255; OH 3; Length 217; 106.0%; Pred, No. 7 96.29; Live 0; Mismatch, s 0; Indels
                                                                               MEDIUM TYPE: Floppy disk
COMPUTER: 1BM PC compatible
COMPUTER: 1BM PC compatible
COMPUTER: 1RM PC compatible
COMPUTER: 1 PATEN: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
AFFL.CATION NUMBER: US/08/785,271
FILING DATE: CONCULTENTLY HEFEWITH
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APPLICATION NUMBER: US/08/759,628 FILING DATE: 05-DEC-1996
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                           NAME: Highlander, Steven L.
REGISTRATION NUMBER: 37,642
REFERENCE/COCKET NUMBER: 1550:53 (
TELEPHONE: 512/419-3000
TELEPHONE: 512/419-3000
TELEPHONE: 512/419-3000
TELEPHONE: 512/419-3000
SEQUENCE CHARACTERISTICS:
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                                                                                                                                                                                                                         CLASSIFICATION - 435
PRIOR APPLICATION DATA:
AFFLICATION NUMBER: US 08/589,028
FILING DATE: 19-JAN-1996
ATTORNEY/AGENT INFORMATION:
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APPLICATION NUMBER: US 60/008,574
FILING DATE: 06-DEC-1995
ATTORNEY/AGENT INFORMATION:
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CAMPUTER: 18M PC compatible
CPERATING SYSTEM: PC-DOS/MS-DOS
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STREET: 901 Cabifornia Avenue
CITY: Palo Alto
STATE: California
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TYPE: amino acid
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Best Local Similarity 100.0
Fost 48, conservative
                                                                     COMPUTER READABLE FORM:
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STATE: 1cm.
COUNTRY: USA
77210
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                  Texas
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APPLICANT: Olazaran, Mattha Guerrero
APPLICANT: Saldana, Hugo Barrera
TITLE OF INVENTION: Gree maria viader
TITLE OF INVENTION: Production and Secretion of the Human Growth Hormone
FILE KEPEBENCE: 1899-00-21
CURRENT APPLICATION NUMBER: US/U9/284,87#
CURRENT APPLICATION NUMBER: POT/MX97/Oc033
PRIOR FILING DATE: 1999-10-24
NUMBER OF SEQ ID NOS: 9
SOFTWARE: Patentin Ver: 2.1
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Pred. No. 2.9e-29;
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OTHER INFORMATION: Znote "The peptides above are
OTHER INFORMATION: depicted in Figure 1"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               98.1%; Sco., No. 2., 100.0%; Pred. No. 2., ..., 0; Mismatches
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Best Local Similarity 100.6%; Pred. No. 2.9
Matches 48; Conservative 0; Mismatches
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Patent No. 6391585
GENERAL INFORMATION:
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TELEFAX: 415-496-1200
INFORMATION FOR SEQ ID NO: 11:
SEQUENCE CHARACTERISTICS:
LENGTH: 217 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Best Local Similarity 100.
Matches 48: Conservative
                                                                                           TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                TOPOLOGY: linear
MOLECULE TYPE: protein
                                                                                                                                                                                                       Peptide
32..53
                                                                                                                                                                                                                                                                        Peptide
94..115
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                                                                                                                                                                                                                                                                                                                                            Peptide
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Gaps
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                         MCGarry, Dennis
ZENTION: RECOMBINANT EXPRESSION OF PROTEINS FROM
VENTION: SECRETORY CELL, LINES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     2 FPTIPLSRLFUNAMLRAHRUHQLAFDTYQEFEEAYIPKEQKYSFLONP 49
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       27 EPTIPISRLE NAMLRAHRLHOLAFDTYQEFEEAYIPKEGKYSFLQNP 74
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MEDIUM TYPE: Floppy disk
COMPUTER: Huppy disk
COMPUTER: Huppy disk
COMPUTER: Hup WC compatible
OPERATION SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTION DATA:
APPLICATION NUMBER: US/08/784,582
FILING DATE: CONCURRENTLY HERWITH
APPLICATION NUMBER: US/08/784,582
FILING DATE: CONCURRENTLY HERWITH
APPLICATION NUMBER: US 60/028,427
FILING DATE: 15-0CT-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/028,427
FILING DATE: 15-0CT-1996
PRIOR APPLICATION NUMBER: US 08/589,028
FILING DATE: 19-JAN-1996
ATTOMNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                              Halban, Philippe A.
No. 6110707minqton, Karl D.
Clark, Samuel A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    E: Arnold, White & Durkee
P.O. Box 4433
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                                                                                                                                                                               Sequence 71, Application US/08784582
Patent No. 6110707
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    US-08-784-582-73
; Sequence 73, Application US/08784582
; Patent No. 6110707
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NAME: Highlander, Steven L. REGISTRATION NUMBER: 37,642
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TELECOMMUNICATION INFORMATION:
TELEPHONE: 512/418-3000
                                                                                                                                                                                                                                                                                                                                   Thigpen, Anice E. Ocaade, Christian
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TELEFAX: 512/474-7577
INFORMATION FOR SEQ LUND: 71:
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Best Local Similarity 100.0
Matches 48; Conservative
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                                                                                                                                                                                                                                                                                                                                                                           Kruse, Fred
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CORRESPONDENCE ADDRESS
                                                                                                                                                                                                                                                                                                                                                                                                                  TITLE OF INVENTION:
TITLE OF INVENTION:
NUMBER OF SEQUENCES:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Texas
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APPLICANT:
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STATE:
                                                                                                                                                                                                                                                                   APPLICANT
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                                                                                                                             INVENTION: Process for pre-aring recombinant proteins using highly efficient expression vector from Sacharomyces cerevisiae
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ..
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: Sato, Seiji
APPLICANT: Kiqashikuni, Naohiko
APPLICANT: Kudo, Toshiyuki
APPLICANT: Kondo, Masaaki
TITLE OF INVENTION: DAMS ENCODING NEW FUSION PROTEINS AND IMCCESSES FOR
TITLE OF INVENTION: PREPARING USEFUL PALTYPEPTIDES THROUGH EXPRESSION OF THE
TITLE OF INVENTION: DNAS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  OTHER INFORMATION: Description of Artificial Sequence: Designated is OTHER INFORMATION: an amino acid Sequence of MMPSp-MWPmp20-TEV-G-GH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 0:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 241;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    98.1%; Score 255; DB 4; Length 245; 100.0%; Pred. No. 3.38-29; Live 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                          STATE: Connecticut.
COUNTRY: U.S.A.
ZIP: 06510-2802
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.5 inch, 1.44 ML storage
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Ouery Match
Best Local Similarity 100.0%; Pred. No. 3.3e-29;
Matches 48; Conservative 6; Mismatches 0;
                                                                                                                                                                                        CORRESPONDENCE ADDRESS:
AJDRESSEE: BACHMAN & LAPOINTE, P.C.
STREET: Suite 1201, 900 Chapel Street.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FILE REFERENCE: 382.1026
CURRENT APPLICATION NUMBER: US/09/280,030A
CURRENT PILLING DATE: 1999-03-26
EARLIER APPLICATION NUMBER: JP10-87339/1938
EARLIER FILLING DATE: 1998-03-31
NUMBER OF SEQ 1D NOS: 66
SOFTWARE: Patentin Ver. 2.0
SEQ 10 NO 66
LENGTH: 245
                                                                                                                                                                                                                                                                                                                                                                                                                                SOFTWARE: MS WORD
CURRENT APPLICATION CATA:
APPLICATION NORBER: US/25/424.1.00H
FILING DATE: 24-00. 6391585 1999
INFORMATION FOR SEQ ID NO: 25:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                         CHARUTER: IBM
OPERATING SYSTEM: WINDOWS 95/48
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TOPOLOGY: linear

MOLECULE TYPE: PROTEIN

SEQUENCE DESCRIPTION: SEQ ID NO: 25:
US-09-424-620R-25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 66, Application US/09280030A Patent No. 6505595
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LENGTH: 241 amino acids
                                                                                                        SEONG, Baik-Lin
JANG. Ki-Ryong
MOON, Jae-Woong
                                        BAE, Cheon-Soon
                                                           YANG, Doo-Suk
LEE, Jee-Won
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ORGANISM: Artificial Sequence
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Best Local Similarity 100.0
Matches 48; Conservative
                                                                                                                                                                                                                                                            CITY: New Haven
                                                                                                                                                                   NUMBER OF SEQUENCES:
                                                                                                                               TITLE OF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           08-08-580-030-66
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Length 191:

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2 FPTIPLSKLFUNAMLRAHRLHQLAFDTYGEFERAYIPKEGKYSFLONP 49
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97.9%; Pred. No. 2.1e-28;
tive 0; Mismatches 1;
                                                                                                      Score 249; DB 4;
Pred, No. 1.8e-28;
0; Mismatches 1.
                                                                                                                                                                                                                                                                                                                                                                                                           FITTE OF INVENTION: GOMEST GROWTH RETHOLD NUMBER OF SECTEMBES: 7 CORRESPONDENCE ANDRESS. 7 ANDRESSEE: CARELLA, BYRNE, BAIN, GILFILLAN, ADDRESSEE: CECCHI, STEWART & OLSTEIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Search completed: September 15, 2003, 12:05:30 Job time : 12.2401 secs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             OPERATING SYSTEM: MS-DOS
SOFTWARE: WAND PERFECT 5.1
CURRENT APPLICATION JAIA:
APPLICATION NUMBER: US/08/187,756C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      36,134
FR: 325800-55
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER READABLE FORM: MEDIUM TYPE: 3.5 INCH DISKETTE
                                                                                                                                                                                                                                                                                                                               Sequence 4. Application US/UB1877560 Patent No. 5597709 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                January 27, 1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NAME: FERRARO, GREGORY D. REGISTRATION NUMBER: 36,134 PEFERENCE/DOCKET NUMBER: 32 TELECOMMUNICATION INFORMATION: 201-994-1700
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STREET: 6 BECKER FARM RUAD CITY: ROSELAND
                                                                                                    95.8%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TELEFAX: 201-994-1744
INFORMATION FOR SEQ ID NO: 4:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               : 217 AMINO ACIDS
AMINO ACID
                                                                                             95.00
Best Local Similarity 97.99
Watches 47; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Best Local Similarity 97,99
Matches 47; Conservative
                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: ROSEN, EL AL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE CHARACTERISTICS:
LENGTH: 217 AMINO ACID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FILING DATE: January
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TOPOLOGY: LINEAR MOLECULE TYPE: PROTEIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER: IBM PS/2
OPERATING SYSTEM: M
                       TYPE: PRT
ORGANISM: homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CITY: ROSELAND
STATE: NEW JERSEY
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STRANDEDNESS
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                                                                                                                                                                                                                                                                                                              US-08-187-756C-4
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      LENGTH: 191
                                                                 US-09-465-461-1
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TITLE OF INVENTION: Human Growth Hormone to stimulate hematopoiesis and immune recons
TITLE OF INVENTION: after hematopoietic stem cell transplantation in humans
FILE OF FIREFERICE: CHAPPEL-6.
CURENT APPLICATION NUMBER: US/09/465,461
CURRENT FILING DATE: 1999-12-17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Caps
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                                                                                                                                                           TITLE OF INVENTION: RECOMBINANT EXPRESSION OF PROTEINS FROM TITLE OF INVENTION: SECRETORY CELL LINES NUMBER OF SEQUENCES: 79
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   27 FPTTPLSRLFDNAMLRAHRLHQLAFDTYGEFE! PREGKYSFLONP 74
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               98.1%; Score 255; DB 3; Length 360; 100.0%; Pred, No. 5.4e.29; tive 0; Mismarches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             2 FPTIPLSRLFDNAMLRAHRLHQLAFDTYGEFEEAYIPKEQKYSFLONP
                                                                                                                                                                                                                                                                                                                                                                                                                             SOFTWARE: Patentin Release #1.0, Version #1.35
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/784.562
FILING DATE: Concurrently Herewith
                   Halban, Philippe A.
No. 6110707mington, Karl D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/028,427
FILING DATE: 15-00T-1996
PHICK APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICATION NUMBER: US 08/589,028 FILING DATE: 19-JAN-1996 ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                          E: Arnold, White & Durkee P.O. Box 4433
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         UTSD:514
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRICH APPLICATION NUMBER: 60/112,668
PRICH FILING DATE: 1998-12-17
NUMBER OF SEQ ID NOS: 1
SOFTWARE: PatentIn version 3.1
SEQ ID NO ID NO ID
Newgard, Christopher B.
                                                                                                                                                                                                                                                                                                                                                                                      MEDIUM TYPE: Floppy disk
COMPUIEK: JHM PC compatille
OPERATING SYSTEM: PC DOS/MS:10:S
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ; Sequence 1, Application US/09465461; Patent No. 6348444; GENEMAL, INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 37,642
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NAME: Highlander, Steven L. REGISTRATION NUMBER: 37,642
                                                                              Thigpen, Anice E.
Quaade, Christian
Kruse, Fred
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  REFERENCE/DOCKET NUMBER: UT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   INFORMATION FOR SEQ TO NO. 73: SECUENCE CHARACTERISTICS:
                                                             Clark, Samuel A.
                                                                                                                                          McGarry, Dennis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               512/418-3000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Local Similarity
es 48; Conserv
                                                                                                                                                                                                                                                                                      Houston
                                                                                                                                                                                                                                                                                                              Texas
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                                                                                                                                                                                                                                                                                                                                                77210
                                                                                                                                                                                                                                              ADDRESSEE:
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US-08-784-582-73
                                                                            APPLICANT:
APPLICANT:
APPLICANT:
  APPLICANT:
                                        APPLICANT:
                                                                                                                                                                                                                                                                                                                           COUNTRY:
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                                                           APPLICANT:
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Sequence 23, Appli
Sequence 1, Appli
Sequence 1, Appli
Sequence 1, Appli
Sequence 6, Appli
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Sequence 4, Appli
Sequence 16, Appl
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                                                                                                     September 15, 2003, 12:03:35; Search time 20.5484 Seconds (without alignments) 347.945 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Pred. No. is the number of results projected by chance to have a score greater than or equal to the second the result being printed, and is derived by analysis of the total score distribution.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 9, #
Sequence 66,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 6, Sequence 7,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Descript ton
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1: Cgn2_6/ptodata/I/pubpaa/US07_PIBCOMB.pcp.*

2: /cgn2_6/ptodata/I/pubpaa/US07_PIBCOMB.pcp.*

3: /cgn2_6/ptodata/I/pubpaa/US06_BuB.pcp.*

3: /cgn2_6/ptodata/I/pubpaa/US06_BuBcOMB.pcp.*

3: /cgn2_6/ptodata/I/pubpaa/US06_BuBcOMB.pcp.*

4: /cgn2_6/ptodata/I/pubpaa/US08_BuBcOMB.pcp.*

5: /cgn2_6/ptodata/I/pubpaa/US08_BuBcOMB.pcp.*

6: /cgn2_6/ptodata/I/pubpaa/US08_BuBcOMB.pcp.*

7: /cgn2_6/ptodata/I/pubpaa/US08_BuBcOMB.pcp.*

9: /cgn2_6/ptodata/I/pubpaa/US08_PUBCOMB.pcp.*

10: /cgn2_6/ptodata/I/pubpaa/US08_PUBCOMB.pcp.*

12: /cgn2_6/ptodata/I/pubpaa/US09_BuBCOMB.pcp.*

13: /cgn2_6/ptodata/I/pubpaa/US09_BuBCOMB.pcp.*

14: /cgn2_6/ptodata/I/pubpaa/US09_BuBCOMB.pcp.*

15: /cgn2_6/ptodata/I/pubpaa/US09_RUB_COMB.pcp.*

16: /cgn2_6/ptodata/I/pubpaa/US10_RUB_COMB.pcp.*

16: /cgn2_6/ptodata/I/pubpaa/US10_RUB_COMB.pcp.*

16: /cgn2_6/ptodata/I/pubpaa/US10_RUB_PUBCOMB.pcp.*

16: /cgn2_6/ptodata/I/pubpaa/US10_RUB_PUBCOMB.pcp.*

17: /cgn2_6/ptodata/I/pubpaa/US10_RUB_PUBCOMB.pcp.*

18: /cgn2_6/ptodata/I/pubpaa/US10_RUB_PUBCOMB.pcp.*

18: /cgn2_6/ptodata/I/pubpaa/US10_RUB_PUBCOMB.pcp.*

18: /cgn2_6/ptodata/I/pubpaa/US10_RUB_PUBCOMB.pcp.*

18: /cgn2_6/ptodata/I/pubpaa/US10_RUB_PUBCOMB.pcp.*
                                                                                                                                                                                                             1 MF TIPLSRLFDNAMLRAHR.....OEFERAYIPKEOKYSFLONP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /cgn2_6/ptodata/1/pubpaa/3860_PUBCOMB.pep:*
                  ompagen Ltd
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US-10-654-873-7

US-10-984-010-23

US-10-153-237-1

US-10-400-7-1

US-10-153-237-1

US-10-400-7-1

US-10-153-7-6

US-10-153-7-6
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US-09-804-409A-16
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US-10-054-873-2
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US-09-853-648-2
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                                                                                                                                                                                                                                                                                                  541936 seqs, 145912426 residues
GenCore version
Copyright (c) 1993 - 2003
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                                                                        OM protein - protein search, using sw model
                                                                                                                                                                                                                                                                                                                                                                                                                                                             Listing first 45 summaries
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Gapop 10.0 , Gapext 0.5
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Sequence 12, Appl Sequence 3, Appli Sequence 350, App Sequence 2, Appli Sequence 411, App	Sequence 18, Appl Sequence 14, Appl Sequence 14, Appl Sequence 2, Appli	Sequence 4, Appli Sequence 7, Appli Sequence 6, Appli Sequence 6, Appli Sequence 22, Appl	Sequence 19, Appl Sequence 10, Appl Sequence 2, Appli Sequence 4, Appli		Sequence 63, Appl Sequence 25, Appl Sequence 13, Appl Sequence 22, Appl Sequence 23, Appl Sequence 23, Appl
12 US-09-824-200-12 9 US-09-850-887-3 15 US-10-043-487-350 12 US-10-153-207-2 15 US-10-103-313-411			15 US-10-191-879-19 15 US-10-191-879-10 10 US-09-887-569A-2 12 US-10-322-746-4	9 08-09-876-478-15 15 08-10 147-293-32 15 08-10 140-293-44 15 08-10-100-679-62 15 08-10 100-679-62	15 US-10-100-679-63 14 US-10-036-869-25 14 US-110-036-869-25 15 US-10-140-293-23 15 US-10-140-293-23 15 US-10-140-293-25
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ALIGNMENTS

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TITLE OF INVENTION: Chimeric Protein Containing an Intramolecular Chaperone-Like Sequence
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                                                                                                                                                                                                           CORRESPONDENCE ALDRESS:
ADDRESSEE: Townsend and Townsend and Grew LLP
STREET: Two Embarcadero Center, Eighth Floor
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FILINS DATE: 31.4MR-11998
APPLICATION NUMBER: US 09/423,100
FILING DATE: 11-DEG-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/054.873
FILING DATE: 22-Jan-2002
CLASSIFICATION: «Unknown»
                                                                                                                                                                                                                                                                                                                                                             COMPUTER READARLY FORM:
MEDIUM TYPE: FLOPBY JISK
COMPUTER: HAW PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NAME: Mycroit, Frank J
REGISTRATION NUMBER: 46,946
                             Sequence 1, Application US/16054673 Publication No. US20020164712A1
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LENGTH: 49 amino acids
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                                                                           GENERAL INFORMATION:
APPLICANT: Gan, Zhong Ru
                                                                                                                                                                                                                                                                                         CITY: San Francisco
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                    California
                                                                                                                                                                                        NUMBER OF SEQUENCES: 7
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                                                                                                                                                                                                                                                                                                                                             COUNTRY: USA
                                                                                                                                                                                                                                                                                                                       STATE:
US-10-054-873-1
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TYPE: amino acid

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APPLICATION NUMBER: US/10/054,873
FILING DATE: 22-Jan-2002
CLASSIFICATION: <UNKNOWN>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NAME: Mycroft, Frank J
REGISTRATION NUMBER: 46,946
                                                                                                                                                                                                                                                              COMPUTER: IBM PC compatible
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MEDIUM TYPE: Floppy disk
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Publication No. US20020:64712A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LENGTH: 107 amino acids
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                                                                                                                                              CITY: San Francisco
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COUNTRY: USA
21P: 94111-3834
COMPUTER READABLE FORM:
                                                                                                                                                             STATE: California
COUNTRY: USA
ZIP: 94111-3834
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FOPOLOGY: linear
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Best Local Similarity 100.
Matches 49; Conservative
                                                                NUMBER OF SEQUENCES:
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US:10:054 873-7
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TITLE DE INVENTION: Chimeric Protein Containing an
Intramolecular Chaperone-Like Sequence
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CORRESPONDENCE ADDRESS:
CORRESPONDENCE TOWNS and TOWNS and Grew LLP
STREET: Two Embarcadero Center, Eighth Floor
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100.0%; Pred. No. 1 26-27;
tive 0; Mismatche, 0;
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APPLICATION NUMBER: US 09/423,160
FILING DATE: 11-DEC-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-(x)S
: TOPOLOGY: linear
: MOLEGULE TYPE: protein
: SEQUENCE DESCRIPTION: SEQ ID NO: 1: US-10-054-873-1
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REGISTRATION NUMBER: 46,946
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                                                                                                   Query Match
Best Local Similarity 100.0.
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Matches 4% Conservative
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APPLICANT: Gam.
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US-10-054-873-6
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APPLICANT: Gan, Zhong Ru
TITLE OF INVENTION: Chimeric Protein Containing an
Intramolecular Chaperone-Like Sequence
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SOFTWARE: Patentin Release #1.0, Version #1.30
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SOFTWARE: Patentin Release #1.0, Version #1.30
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ADDRESSEE: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, Eighth Floor
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ADDRESSEE: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, Eigeth Floor
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FILLING DATE: 11-AMK-1998
APPLICATION NUMBER: US 09/423,100
FILLING DATE: 11-DEC-2000
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FILLING DATE: 22 Jan. 2602
CLASSIFICATION: CDRNOWN:
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SEQUENCE DESCRIPTION: SEQ ID NO: 6:
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2 FPTIPLSRLFDNAMLRAHRLHQLAFDTYQEFEEAYIPKEQKYSFLONP 49
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SOFTWARE: Patentin Ver. 3
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US-10-400-377-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ; ORGANISM: Home Sapiens
US-10-153-207:1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             191
                                                                                                                                                                                                     RESULT 6
US-10-153-207-1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEC ID NO 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TYPE: PRT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CORRESPONDENCE ADDRESS:
ADORESSEE: FINNEGAN, HENDERSON, FARABOW, GARRETT & DUNNER, LLP
STREET: 1300 I Street, NW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: BALIANCE, DAVID JAMES
TITLE OF INVENTION: RECOMBINANT FUSION PROTEINS TO GROWIH HORMONE
AND SERUM ALBUMIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sidne
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     166.0%; Shore 260; DR 14; Inhath 150; 100.0%; Pred, No. 2.1e 27; 100.0%; No. 2.1e 27; 100.0%; No. 2.1e 27; 100.0%; No. 2.1e 20; No. 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER READABLE FORM:
MEDIUM TYPE: FLORM:
MEDIUM TYPE: FLORPY disk
COMPUTER: IBM PC COMPATIBLE
OPFRATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN Release #1.0, Version #1.30 (EPO)
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 MEPTIPLSRLFDNAMLRAHRLHOLAFDTYCEFBEAYIPKEOKYSELUNP 49
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                                                                                                                                                                                                                    NAMÉ: Mycroft, Frank J
REGISTRATION NUMBER: 46,946
REFERENCE/DOCKET NUMBER: 020167-000130US
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 0
                               APPLICATION NUMBER: WO PCT/CN98/00052 FILING DATE: 31-MAR-1998
APPLICATION NUMBER: US 09/423,100 FILING DATE: 11-DEC-2000 ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICATION NUMBER: US 09/091.873
FILING DATE: 25-JUN-1958
APPLICATION NUMBER: PCT/GB96/33164
FILING DATE: 19-DEC-1996
INFORMATION FOR SEQ ID NO: 23:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICATION NUMBER: US/09/984.010 FILING DATE: 21-May-2002 PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE DESCRIPTION: SEQ ID NO: 23: US-09-984.010-23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TOPOLCOY: linear

MOLECULE TYPE: protein

SEQUENCE DESCRIPTION: SEQ ID NO: 7:
US-10-054-873-7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 23, Application US/09984010 Publication No. US20030104578A1
                                                                                                                                                                                                                                                                                                                                                                                                                  LENGTH: 150 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                     TYPE: amino acid
STRANDEDNESS: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LENGTH: 191 amino acids
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STRANDEDNESS: <Unknown>
                                                                                                                                                                                                                                                                                                                                       INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Ouery Match 166.0%;
Best Local Similarity 100.0%;
Matches 49; Conservative 0
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NUMBER OF SEQUENCES: 26
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MOLECULE TYPE: protein
HYPOTHETICAL: NO
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21P: 20005-3315
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Best Local Similarity
Matches 48; Conserva
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APPLICANT: Cox III. George N
APPLICANT: Bolder Biotechnology, Inc.
TITLE OF INVENTION: Derivative 3 of Growth Hormone and Related Proteins
FILE REPERENCE: 4152-1-PUS
CORRENT APPLICATION NUMBER: US/09/462,941
PRIOR APPLICATION NUMBER: US/09/462,941
PRIOR APPLICATION NUMBER: US/09/462,941
PRIOR APPLICATION NUMBER: US/09/462,516
PRIOR FILING DATE: 1997-07-14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
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                                1 FPTIPLSRLFDNAMLRAHRLHQLAFDTYQEFEEAYIPKEQKYSFLQNP 48
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 FPT:PLSRLFDNAMLRAHRLHQLAFDTYGEFEEAYIPKEGKYSFLONP 48
2 FPTIPLSRLFDNAMLRAHRLHQLAFDTYQEFEEAYIPKEQKYSFLQNP 49
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                                                                                                                                                                                                                                                                                              APPLICANT: James A. Wells
APPLICANT: James A. Wells
APPLICANT: Brian C. Cunningham
IITLE OF INVENTION: GROWTH HORMONE VARIANTS
FILE REFERENCE: 669.12-US-C7
CURRENT APPLICATION NUMBER: US/10/153,207
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SOFTWARE: FastSEQ for Windows Version 4.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                 CURRENT FILING DATE: 2002-05-22
PRIOR APPLICATION NUMBER: 08/479, 884
PRIOR FILING DATE: 1995-05-07
PRIOR FILING DATE: 1995-05-07
PRIOR PELLING DATE: 1995-05-07
PRIOR PELLING DATE: 1994-02-02
PRIOR APPLICATION NUMBER: 07/950,227
PRIOR PELLING DATE: 1992-10-13
PRIOR PELLING DATE: 1992-04-27
PRIOR FILING DATE: 1992-04-27
PRIOR FILING DATE: 1985-10-26
PRIOR PLING DATE: 1989-10-26
PRIOR PELLING DATE: 1988-10-26
                                                                                                                                                                                                          Sequence 1, Application US/10153207 Publication No. US/20030153003A1 GENERAL INFORMATION:
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Best Local Similarity 100.0
Matches 48; Conservative
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24 FPIIPLSRLFUNAMLRAHRLHQLAFDTYQEFEEAYIPKEQKYSFLQNP 71
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                                                                                                         US-09-929-918-9
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APPLICANT: COX III,
APPLICANT: Bolder Biotechnology, inc.
TITLE OF INVENTION: Derivatives of Growth Hormone and Related Proteins
FILE REFERENCE: 4152-1-PUS
CURRENT APPLICATION NUMBER: US/10/400,708
CURRENT FILING DATE: 2003-03-26
PRIOR FILING DATE: 2000-01-14
PRIOR FILING DATE: 2000-01-14
PRIOR FILING INTE: 1997-971-14
NUMBER OF SEU ID NOS: 4:
SOFTWARE: PATENTIN VET. 2.8
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APPLICANT: Brian C. Cunningham
TITLE SE INVENTION: GROWTH HORMONE VARIANT:
FILE REFERENCE: 669.12 US.C7
CURRENT APPLICATION NUMBER: US/10/153,267
CURRENT FILLNG DATE: 1995-06-07
PRIOR APPLICATION NUMBER: 08/190,723
PRIOR APPLICATION NUMBER: 07/960,227
PRIOR APPLICATION NUMBER: 07/960,277
PRIOR FILING DATE: 1992-10-13
PRIOR FILING DATE: 1992-10-13
PRIOR FILING DATE: 1999-10-26
PRIOR FILING DATE: 1999-10-26
PRIOR FILING DATE: 1999-10-26
PRIOR FILING DATE: 1999-10-26
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       : Sequence 6, Application US/10153207
; Publication No. US20030153003A1
; GENERAL INFORMATION:
                                                                                                                                              ; Sequence 1, Application US/10400708
; Publication No. US20030166865A1
; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NUMBER OF SEQ ID NOS: 20
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US-10-154-207-6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TYPE: PRT
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    161
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQ ID NO 1
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APPLICANT: Sato, Set);
APPLICANT: Higashikuni, Naohiko
APPLICANT: Higashikuni, Naohiko
APPLICANT: Higashikuni, Naohiko
APPLICANT: Kado, Toshiyuki
APPLICANT: Kado, Toshiyuki
APPLICANT: Kado, Masaaki
TITLE OF INVENTION: DRAS ENCODING NEW FUSION PHOTEINS AND PROCESSES FOR
TITLE OF INVENTION: DRAS PRING USEFUL, POLYPEPTINES THROUGH EXPRESSION OF TITLE OF INVENTION: UNMER: US/09/280.03vA
CURRENT APPLICATION NUMBER: US/09/280.03vA
CUBRENT FILING DATE: 1999-03-26
EARLIER APPLICATION NUMBER: JPI0-87x35/1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GENERAL INFORMATION:
APPLICANT: Kordyum, Vitaliy A.
APPLICANT: Chernykh, Svitlana 1.
APPLICANT: Slavchenko, Iryna Yu.
APPLICANT: Vozianov, Oleksandr
TITLE OF INVENTION: PHAGE-DEPENDENT SUPER PRODUCTION OF
TITLE OF INVENTION: BIOLOGICALLY ACTIVE PROTEIN AND PEFTIDES
FILE REFERENCE: PHAGE.006A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Ouery Match 98.1%: Score 255; DB 9; Length 245; Best Local Similarity 100.0%; Pred. No. 1.7e-26; Matches 48; Conservative 0; Mismatches 0; Indels
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Bost Local Similarity 100.0%; Pred. No. 1.5e-26;
Matches 48; Conservative ); Mismatches 0;
                                                                                                                                                                                                                                                                                       CURRENT APPLICATION NUMBER: US/09/929,918
CURRENT FILING DATE: 2001-08-15
PRIOR APPLICATION NUMBER: 09/314,288
PRIOR DATE: 1409-05-25
NUMBER: JE SEO IL NOS: 11
SOFTWARE: PASLSEQ IOF WILLOWS VERSIO: 4.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 66, Application US/0928303UA Patent No. US20010021515A1
; Sequence 9, Application US/09929918 ; Patent No. US20020090678A1
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SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 66
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APPLICANT: CCOPER, DAVID N.
APPLICANT: CCOPER, DAVID N.
APPLICANT: GREGORY, JOHN E.
APPLICANT: MILLAR, DAVID S.
TITLE OF INVENTION: METHOD FOR DETECTING GROWTH HORMONE VARIATIONS IN
TITLE OF INVENTION: HUMANS, THE VARIATIONS AND IHEIR USES
FILE REFERENCE: WCM78
                                                                                                                                                                                                                   TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR REGULATED PROTEIN TITLE OF INVENTION: EXPRESSION IN GUT FILE REFERENCE: 029996/027 8721
CURRENT APPLICATION NUMBER: US/05/804.405A
CURRENT FILING DATE: 2001-03-12
NUMBER OF SEQ 1D NOS: 18
SOFTWARE: PALENTIN VET. 2.1
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Live 0; Mismatches 2; Indels
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97.9%; Pred. No. 1.36-25;
UVC 0; Mismatches 1:
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Job time : 21.5484 secs
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CURRENT FILING DATE: 2001-05-14
NUMBER OF SEQ ID NOS: 66
SOFTWARE: Patentin Ver: 2.1
SEQ ID NO 4
         RESULT 14
US-09-3804-409A-16
Sequence 16, Application US/09804409A
Patent No. US20020155100A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      // Sequence 4, Application 05/09853688
// Patent No. US20020081605A1
                                                                                                                             GENERAL INFORMATION:
APPLICANT: KIEFFER, TIMOTHY J.
APPLICANT: CHEUNG, ANTHONY T.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               95.4%
Best Local Similarity 97.9%
Matches 47; Conservative
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Matches 46; Conservative
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US-09-853-688 4
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US-09-853-688-4
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APPLICANT: HOUSTON. LOU, L.
APPLICANT: HOUSTON. LOU, L.
APPLICANT: HOUSTON. LOU, L.
APPLICANT: HOUSTON. LOU, L.
APPLICANT: HAWLEY, Stephen
APPLICANT: GLYNN, Jacqueline, M.
APPLICANT: CHAPIN. Steven
APPLICANT: MARIERS
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE TRANSPORT OF BIOLOGICALLY ACTIVE
TITLE OF INVENTION: AGENTS ACKOSS CELOU."R HARRIERS
TITLE OF INVENTION: AGENTS ACKOSS CELOU."R HARRIERS
TILLE OF INVENTION: AGENTS ACKOSS CELOU."R HARRIERS
TILLE OF INVENTION: AGENTS ACKOSS CELOU."R HARRIERS
FILLE OF INVENTION NUMBER: US 60/267,60;
PRIOR APPLICATION NUMBER: US 60/248,819
PRIOR APPLICATION NUMBER: US 60/248,478
PRIOR APPLICATION NUMBER: US 60/248,478
PRIOR PILLING DATE: 2000-11-14
PRIOR APPLICATION NUMBER: US 60/248,478
PRIOR FILLING DATE: 2000-11-14
PRIOR FILLING DATE: 2000-11-14
PRIOR FILLING DATE: 2000-11-14
PRIOR FILLING DATE: 2000-11-14
PRIOR APPLICATION NUMBER: US 60/248,478
PRIOR APPLICATION NUMBER: US 60/248,478
PRIOR FILLING DATE: 2000-11-14
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PRIOR APPLICANTION NUMBER: US 60/248,478
PRIOR FILLING DATE: 2000-11-14
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                                                                                                                                             APPLICANT: COOPER, ANNIE M.
APPLICANT: COOPER, ANNIE M.
APPLICANT: PROCTER, ANNIE M.
APPLICANT: GREGORY, JOHN
APPLICANT: MILLAR, DAVID S.
TITLE OF INVENTION: HITHOD FOR DETECTING GROWTH HORMONE VARIATIONS IN TITLE OF INVENTION: HUMANS, THE VARIATIONS AND THEIR USES CURRENT APPLICATION NUMBER: US/09/853,688
CURRENT FILING DATE: 2001-05-14
NUMBER OF SEQ ID NOS: 66
SOFTWARE: PATENTIN VET. 2.1
SEQ ID NO 2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     95.8%; Score 24.; DB 12; Length 217; 97.9%; Pred. No. 9.8e-26; tive 0; Mismatches 1; Indels (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       95.8%; Score 249; #8-9; Length 217;
97.9%; Pred. No. 9.8e-26;
Live 0: Mismatches 1; Indols
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                                                           Sequence 2, Application US/09853688 Patent No. US20020081605Al GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Best Local Similarity 97.9
Matches 47; Conservative
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Best Local Similarity 97.9
Matches 47; Conservative
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RESULT 12
US-09-853-688-2
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GenCore version 5.1.6
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OM protein - protein search, using sw model

September 15, 2003, 11:56:45; Search time B.07885 Seconds (without alignments) 583.284 Million cell updates/sec Run on:

Title: Perfect score: Sequence:

US-09-423-100-1 260 1 MFPTIPLSRLFUNAMLRAHR.....QEFEEAYIPKEOKYSFLONP 49

Scoring table:

BLOSUM62 Gapop 10.0 , Gapext 0.5

283308 seqs, 96168682 resignes Searched:

878 H H Z Total number of hits satistying chosen parameters:

length: 0 length: 200000000 Minimum DB seq Maximum DB seq Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

1: pirl:* 2: pir2:* 3: pir3:* 4: pir4:* PIR_76:* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

	Description	sometofrom 1 ore		~	^	na t			chorionic somatoma	choriomammotropin	choriomammotropin	choriomammotropin	scmatotropin precu		somatotropin - hor	•		pr		somatotropin precu	somatotropin precu	somatotropin - gol	somatotropin precu	somatotropin precu	somatotropin - alp	Id		•	,	pr
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æ	Ouery Match	98.1	58.1		87.7	H1.9	81.9	78.8	17 4	75.8		75.8		61.7	61.3	61.3	61.3	61.3	61.3	61.3	61.3	61.3	61.3	60.2	59.8	57.7	56.9	56.2	55.4	55.4
	Score	255	255	22H	228	713	213	202	20;	197	197	o-			159.5	159.5	159.5	159.5	159.5	159.5		159.5	159.5	156.5	S	150	148	146	144	144
	Result No.		7	~	4	5	9	7	œ	5	10	11	12	13	14	1.5	16	17	18	19	50	21	22	23	24	25	56	27	28	59

somatotropin precu	somatotropin precu	somatotropin precu	somatotropin - dom	somatotropin precu	somatotropin - bul	somatotropin - bul	somatotropin - bow	somatotropin precu	choriomammotropin-	somatotropin - blu	EST/beta-Gal mutan	growth hormone - g	growth hormone II	growth hormone I p	somatotropin precu
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217	217	217	217	216	190	215	195	215	199	183	87	200	210	210	210
54.8	54.8	54.8	54.8	53.8	50.8	50.8	49.2	49.2	46.9	44.6	37.9	37.3	33.5	33.5	33.5
142.5	142.5	142.5	142.5	140	132	132	128	128	122	116	98.5	65	87	87	87
30	31	32	33	34	32	36	37	38	39	4 0	4.	4.2	43	44	4 5

AL LGNMENTS

RESULT 1

STHU	
Sometotropin precursor (validated) - human N:Alternate names growth hormone : http://www.simatotropin	testary semalolropin
N.Contains: growth hormone 5K peptide; somatotropin 1, long torm; somatotropin 1, sh	stropin 1, long torm; somatotropin 1, sh
C:Species: Homo sapions (man)	
C;Date: 24-Aptr-1984 Resquence_revision 10-Feb 1995 Retx. Change Us-DeC-2000 C:Accession Ag3731 A3245 Ag4844 Ag427 A90551 A933437 A93778 A91764 A90217) 1995 #text_change 08-Dec-2000 A90051: A93397: A93778: A91764: A90217:
R; DeNoto, F.M.; Moore, D.D.; Goodhan, H.M.	
Nucleic Acids Res. 9, 3719-3730, 981	
AJTitle: Human growth hormone DNA sequence and mRNA structure: possible alternative	id mKNA structure: possible alternative
A; Reference number: A93731; MUID:82014939; PMID:6269091	(ID:6269091
A; Accession: A93731	
A; Molecule type: DNA	
A; Residues: 1-217 <den></den>	
A;Cross-references: GB:V00520	
A; Note: the 20K short form somatotropin lacks residues 58.72 (32-46 in the active h	s residues 58.72 (32-46 in the active he
R;Chen, E.Y.: Liao, Y.C.: Smith, D.H.: Barrera-Saldana, H.A.: Gelinas, R.E.: Seebur-	a-Saldana, H.A.; Gelinas, R.E.; Seebur-
Genomics 4, 479-497, 1989	
A:Title: The human growth hormone locus: nucleotide segmence: biology, and evolution	entide sequence, biology, and evolution

A:ille: ine numan growin hormone locus: nucleotide sequence, A:Reference number: A32435; MUID:89307277; PM:D:2744760 A:Accession: A32435

A;Molecule type: DNA A;Residues: 1-217 cCHE> A;Cross.references: GB:J0:3071; NID:g183148; PIDN:AAA52549.1; PiD:g183149 B;Roskam, M.; Rougeon, E. Nucleic Acids Ros. 7, 305-320, 1979 A;Tille: Molecular cloning and nucleotide sequence of the human growth hormone struc A;Reference number: A93694; MUID:80034477; PMID:386281

A.Molecule type: mRNA
A.Residues: 1-217 <RGS>
A.Cross-references: 6B-V06519
A.Note: 35-Pro was also found
B.Martial, J.A.: Hallewell, R.A.; Baxter, J.D.; Guodman, H.M.
Science 205, 602-607, 1979
A.Inile: Human growth hormone: complementary DNA cloning and expression in bacteria.
A.Reference number: A94247; MUID:79203293; PMID:377496
A.Rocession: A94247
A.Molecule type: mRNA
A.Residues: 1-217 <AMA>
A.Residues: 1-217 <AMA>
A.Relerence number: A90048; MUID:69289202; PMID:5810834
A.Title: Human pituitary growth hormone. XIX. The primary structure of the hormone.
A.Reference number: A90048; MUID:69289202; PMID:5810834

A:Contents: annotation
R:Li, C.H.; Dixon, J.S.
Arch. Biochem. Biophys. 146, 233-236, 1971
A;Title: Human pituitary growth hormone. XXXII. The primary structure of the hormone A;Reference number: A90051; MUID:72143935; PMID:5:44027
A;Accession: A90051
A;Molecule type: protein

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Alternate names: growth hormone
Coperation and an analyse maraque
Nighternate names: growth hormone
Coperation and alta freesus maraque
Redolos, 16. burning, wh. Fisher, J.M.; Fowler, P.D.
Redolos, 16. during of four growth hormone/choriconic somatomammos ropin-related complement
Accession: 167410
A
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N.Alternate names: growth hormone 2; growth hormone variant; hGH-V; placental somator
N.Contains: somatotropin 2, long splice form: somatotropin 2, short splice form
C:Species: Homo sapiens (man)
C:Date: 17-bec-1982 *sequence_revision 10-Feb-1995 *text_change 21-Jul-2000
C:Accession: D32435; #28072; A01511; 152104; A6071;
R:Chen, E.Y: Liao, Y.C.; Smith, D.H.; Barrera-Saldana, H.A.; Gelinas, R.E.; Seeburg
             C:Comment: The gene for this hormone is transcribed only in somatotrophic cells of C:Comment: About 90% of somatotropin is the 22K long form. C:Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Ö,
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0
                                                                                                                                 A.Gene: GDB:GHJ
A.Cross-references: GDB:119982; GMIM:139250
A.Map position: 17q23.1-17q23.3
A.Map position: 17q23.1-17q23.3
A.Introns: 4/1: 57/3; 9/2; 152/3
G.Superfamily: prolactin
C.Keywords: alternative splicing; hormone; pituitary
C.Keywords: alternative splicing; hormone; pituitary
F.1-26/70omain: signal sequence #status predicted <SIG>F.27-217/Product: somatotropin 1, long form *status experimental <SG;>F:27-69/Product: gromatotropin 1, short form *status experimental <SG>F:27-55/733-217/Product: somatotropin 1, short form *status experimental <SG>F:79-191,208-215/Disulfide honds: *status experimental
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 98.1%; Score 255; DB 1; Length 217;
100.0%; Pred. No. 2e-24;
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C.Superfamily: revision:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        :
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Affitle: Preparation of gro
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Matches 48; Conserv
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Matches 48; Conserv
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A; Reference number: A94427

A; Contents: annotation: Somatotropin revision

R; Bewley, T.A.; (pixun, J.S.; il) 2.8.

Int. J. Pept. Protein Res. 4, 281-281

A; Title: Sequence comparison of bursa; prinitary growth crimone, human cherronic somatomal A; Reference number: A97744; MUD0:73042428; PR:15-467454
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A.Residues: 46-57:73-80 cLEW>
R.Chapman, G.E.; Rogers, K.M.; Brittain, T.; Bradshaw, R.A.; Bates, G.I.; Turner, C.; Ca
J. Biol. Chem. 256, 2395-2401, 1981
A.Title: The 20.000 molecular weight variant of human growth hormone. Preparation and so
A.Reference number: A92311; MUID:81117361; PMID:7462247
A.Contents: somatotropin, 20K short variant
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A;Accession: 184549
                                                                                                                                                                                                                                                                                                                                             Riviall, H.D.; Hogan, M.L.; Sauer, R.; Rosenblum, L.Y.; Greenwood, F.C.
Proc. Nat. Acad. Sci. U.S.A. 68, 866-869, 1971
A.Title: Sequences of pitultary and placental lactogenic and growth hormones: evolution A;Reference number: A93778; MUID:71153968; PMID:5279528
A;Accession: A94778
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A.Residues: 27-217 cBEN>
A.Residues: 27-217 cBEN>
B.S.Lewis, U.G.; Bootewald, L.F.; Lewis, L.J.
Blochem. Riophys. Res. Commun. 92, 511-516, 1980
A.Title: The 20,000-dalton variant of human growth hormone: location of the amino acid. A.Reference numbor: A90217; MUID:80130196; PMID:7356479
A.Contents: somatotropin, 20K short variant
A.Accession: A90217
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Affiller: Identification of the aspartimide structure in a previously-reported peptide.
A; Reference number: 809688; MUID:90334745; PMID:2378679
A; Accession: $09688
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            in Prolactin and Carcinogenesis, Proc. Fourth Tenovus Workshop Prolactin, Griffiths,
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A:Note: the structure of the complex with growth hormone receptor is described
R:Gray, G.L.; Baldridge, J.S.; McKeown, K.S.; Hoyneker, H.L.; Chang, C.N.
Gene 19, 247-254, 1985
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A.Molecuia type: protein
A.Molecuia type: 27-37.73-79 CCHA>
R.Singh, R.N.P.: Saavey, B.K.: Lewis, L.J.: [ewis, U.J.
A. Protein Chem. 2, 425-436, 1983
A.Tille: Human growth hormone peptide 1 43: isolation from pituitary gladds.
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                                R;Niall, H.D.
Nature New Biol. 230, 90-91, 1971
A;Title: Revised primary structure for human growth hormone. A;Reference number: A93397; MUID:71139765; PMID:5279046
A;Accession: A93397
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A;Molecule type: mkNA
A;Residues: 1-26 <RES>
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R;de Vos. A.M.; Uitsch, M.; Kossiakott, A.A.
Science 255, 306-312, 1992
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A)Molecule type: protein
A;Residues: 119-120;157-159 <NI2>
R;Niall, H.D.
27-94;96-217 <LIC>
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A; Residues: 27-69 <SIN>
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C,Accession: 167408
R;Golos, T.G.; Durning, M.; Fisher, J.M.; Fowler, P.D.
Endocrinology 133, 1744-7752, 1993
A;Title: Cloning of four growth hormone/chorionic somatomammotropin-related compleme A;Reference number: 153267; MJID: 94008724; PMID: 8404617
A;Recession: 167408
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C:Species: Macaca mulatia (rhesus macaque)
C:Date: 31-May-1956 Wsequence_revision 31-May-1956 #text_chande 16-Jul-1999
C:Accession: 153267
R:Golos, T. O.: Durning, M.; Fisher, J.M.; Fowler, P.D.
Brocorinology 133, 1744-1752, 1993
A;Title: Cloning of four growth hormone/chorionic somatomnmotropin-related compleme
A;Reference number: 153267; MUID:94008724; PMID:8404617
A;Rccession: 153267
A;Status: preliminary: translated from GB/EMBL/DDBJ
A;Rcsidues: 1-217 <RES.
A;Residues: 1-217 <RES.
A;Cross-references: GB:116552; NID:9293108; PIDN:AAA18839.1; PID:9293109
C:Superfamily: prolactin
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C:Species: Macaca mulat: (rhesus maraque)
C:Date: 11-May-1996 #sequence_revision 31-May-1996 #text_change 16-Jul-1999
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A;Residues: 1-212 <RES>
A;Cross-references: GB:L16553; NID:q293110; FIDN:AAA18840.1; FID:g293111
C;Superfamily: prolactin
                                                                                                                                                                                                                                                                                                                                                      C;Superfamily: prolactin
C;Keywords: alternative splicing; hormone; placenta
F:1-26/Domain: signal sequence #status predicted <SIG>
F:27-256/Product: somatotropin 2 splice form 2 *status predicted <MAI>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      81.9%; Score 213; DB 2; Length 217; 78.7%; Pred. No. 3.5e-19; Live 9; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                3 PTIPLSRLFDNAMLRAHRLHQLAFDTYQFFEEAYIPKEQKYSFLQNP 49
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                                                                                                                                 A:Note: an alternative splice junction for intron 4 is used Cygenetics: COB:GH2 A:Gene: COB:GH2 A:Cross-references: GDB:119983; OMIM:139240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A:Status: preliminary: translated from GB/EMBL/DDBJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 2: Mismatches
                                                                                                                                                                                                                                                                               A:Map position: 17q22-17q24
A:Introns: 4/1; 57/3; 97/3; 152/3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               87.78;
91.78;
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Matches 44; Conservative
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Best Local Similarity 78.71
Matches 37, Conservative
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Matches 37; Conservative
                                                          A; Molecule type: mRNA
A; Residues: 1-256 <COO>
                           A; Accession: A28072
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                                                                                                                         C.Accession: A28072
R.COOKE, N.E.; Ray, J.; Emery, J.G.; Liebhabor, S.A.
J. Biol. Chem. 263, 9001-9006, 1988
A.Title: Two distinct species of human growth hormone-variant mRNA in the human placental A:Reference number: A92725; MUID:88243769; PMID:3379057
Genomics 4, 479-497, 1989
A.Title: The human growth hormone locus: nucleotide sequence, biology, and evolution.
A.Reference number: A32435; MUID:89307277; PMID:2744760
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  F:27-217/Product: somatotropin 2, long splice form *status predicted <sol>
F:27-57,73-217/Product: somatotropin 2, short splice form *status predicted <sos>
F:79-191,208-215/Disultide bonds: *status predicted
F:166/Binding site: carbohydrate (Asn) (covalent) *status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ..
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N:Alternate names: growth hormone variant-2; placental somatotropin form 2
C:Species: Homo sapiens (man)
C:Date: 10.Sep:1989 #sequence_revision 10.Fet:-1995 #text_change 02-Sep-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Saps
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A:Introns: 4/1: 57/3: 97/3: 152/3
C:Superfamily: prolactin
C:Keywords: alternative splicing; qlycoprotain; hormone; placenta
F:1-25/Domain: signal sequence Estatus predicted <81G>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                2 FPTIPLSRLFDNAMLRAHRLHQLAFDTYQEFEEAYIPKEQKYSFLQNP 49
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tive 2; Mismatches 2; Indels
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A:Cross references: GDB:L19983: OMIM:139240
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Best Local Similarity
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Matches

RESULT 4

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R:Tanaka, M.; Masuda, N.; Watahiki, M.; Yamukawa, M.; Slimiku, K.; Naqai, J.; Nakash)
Biochem. Int. 16, 287-292, 1988
A:Title: cDNA cloning of human chorionic socatomanmotropin-l DRNA whose transcription
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A:Molecule type: protein
A:Residues: 1,3-26 (SHE)
A:Experimental source: placenta
R:Shine, J.; Seeburg, P.H.; Martial, J.A.; Baxter, J.D.; Goodman, H.M.
Nature 270, 494 499, 1977
Nature: 270, 494 499, 1977
A:Tille: Construction and analysis of recombinant DNA for human chorionic somatomammer A:Reference number: A93192; MUID:78671761; PMIL:593368
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A;Residues: 27-217 <NIA>
A;Experimental source: placenta
A;Experimental source: placenta
Biochem. Soc. Trans. 19, 208, 1991
A;Title: Catechol-O-methyltransferase from human placenta: purification and some prol
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               R:Goodman, H.M.; DeNoto, F.: Fiddes, J.C.; Hallewell, R.A.; Paqo, G.S.; Smith, S.; Ti
in Mobilization and Reassembly of Genetic Information, Scott, M.A., Werner, R., Josep
A:Reference number: A94422
                                                                                                                                                                                                                                                                                                                                                                                                                                            C:Date: 23-Oct. 1981 #sequence_revision 23-Oct. 1981 #text_change 08-Dac-2000
C:Accession: C:22435, A94422; I52342; A93833; A93192; A90054; A94427; A61283; I55229;
R:Chen, E.Y.: Liao, Y.C.: Smith, D.H.; Barrera-Saldana, H.A.; Gelinas, R.E.; Seeburg,
Genomics 4, 479-497, 1989
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A:Title: The human drowf: hormone locus: naciestide sequence, biology, and evolution.
A:Reference number: A*24*5; MGHD:R9*07277; PRED:2744765
A:Accession: c*24*5
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A;Reference number: A944.7
A;Reference number: A944.7
                                           ö
                                       Gaps
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N;Alternate names: chorionic somatomanmotropin 1; piacental lactogen
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A:Residues: 50-217 <SB1>
A:Experimental source: placenta
B:Li, C:H.: Dixon, J:S.: Chung, D.
R:Li, C:H.: Dixon, J:S.: Chung, D.
R:Li, C:H.: Acchem: Riophys: J:S.; 95-710, 1973
A:Title: Amino acid acquence of human chorionic somatomammotropin.
A:Reference number: A90054: MUID:73201971; PMID:47:2456
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A; Molecule type: mRNA
A; Residues: 1-3 <TAN>
A; Cross-references: GB:M:5419; NID:9506822
A; Cross-references: GB:M:5419; NID:9506822
R:Sherwood, L.M.; Burstein, Y.; Schechter, I.
Proc. Natl. Acad. Sci. U.S.A. 76, 3819-3823, 1979
A; Tible: Primary structure of the NH-2-termina: extra piece of
A:Reference number: A93833; MUID:80034970; PMID:291043
A:Accession: A93833
                                                                                                        4 TIPLSRLFDNAMLRAHRLHQLAFDTYQEFEEAYIPKEQKYSFLON 48
                                                                                                                                            1:1111.11:11:11:11 1:11 1:11 1111111 1111:11111 : 29 TVPLSRLFDHAMLQAHRAHQLAIDTYQEFEETYIPKIXQKYSFLHD 73
                                           Indels
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          Pred. No. 3.4e-17;
                                       5; Mismatches
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80.08;
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A;Residues: 27-217 <LIC>
A;Experimental source: placenta
   Best Local Similarity 80.0
Matches 36; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                   C:Species: Homo sapiens (man)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A;Molecule type: DNA
A;Residues: 1-217 cCHE>
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A:Residues: 1-217 <000>
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Ridolos, T.G.: Durning, M.: Fisher, J.M.: Fowler, P.D.
Endocrinology 133, 1744-1752, 1993
A;Title: Cloning of four growth hormone/chorionic somatomamnotropin-related complementar
A;Reference number: 153267; MUID:94008724; PMID:8404617
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DNA 6, 59-70, 1987
ArTitle: The human growth hormone gene locus: structure, evolution, and allelic variation
A.Reference number: A26449; MUID:87161235; PMID:8030680
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Ridolos, T.3.: Durning, M.: Fisher, J.M.: Fowler, P.D.
Andocrinology 13, 7744-1752, 1993
A.TILle: Cloning of four growth hormone/chorionic sonatomammotropin-related complementar
A:Reference number: 153267; MUID:94008724; PMID:8404617
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C.Accession: A26449
R.Hirt, H.: Kimelman, J.: Birnbaum, M.J.: Chen, E.Y.: Seeburg, P.H.: Eherhardt, N.L.: Ba
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                                                                                                                                                                     N:Allernate names: growth hormone
C:Species: Macaca mulatta (rhesus macaque)
C:Date: 31 May:1996 #sequence_revision 31:Ma; 1996 #text_change 16-Jul-1999
C;Accession: 167411
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     C;Species: Macaca mulatta (rhesus macaque)
C;Date: 31 May-1996 #sequence_revision 31 May-1996 #text_change 16-Jal 1999
C;Accession: 167409
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C; Superlamniy: prolactin
F;1.26/komain: Signal sequence #status predicted <SIG>
F;27-215/kroduct: choriomammotropin, hCS-3 allele #status predicted <MAT>
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A:Residues: 1-217 <RES>
A:Cross:references: GB:L16554: NID:q293112: PIDN:AAA18841.1: PID:g293113
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A;Molecule Type: mRNA
A;Residues: 1-27 - KESS
A;Cross:references: 1-27 - KESS
C;Superfamily: prolactio
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79.2%: Fred. No. 4 Serial
79.2%: Mismatology 55
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Best Loval Similarity 74.59
Matches 35; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Best Local Similarity 79.2
Matches 38: Conservative
                                                                                                                                     somatotropin - rhesus macaque
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       C;Supertamily: prolactin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A;Molecule type: DNA
A;Residues: 1-215 <HIR>
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C:Species: Mus muscuius (house mouse)
C:Species: Mus muscuius (house mouse)
C:Accession: B2311
R:Linzer, D.1.H.: Taiamantes, F.
J. Balol. Chem. 260, 9574-9579, 1985
A:Title: Nucleotide sequence of mouse prolactin and growth hormone mKNAs and expres A:Reference number: A92548; MulD:85261358; PMID:2991252
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A.Molecule type: mRNA
A.Residues: 1-216 <LIN>
A.Cross references: GB:X02891; GB:K03232; N:D:95i067; PIDN:CAA26650.1; PID:951068
A.Cross references: GB:X02891; GB:K03232; N:D:95i067; PIDN:CAA26650.1; PID:951068
C.Supertamily: prolacting
C.Supertamily: prolacting
C.Keywords: anterior pitultary; growth factor; hormone
F:1-26/Domain: signal sequence #status predicted <SIG>
F:27-216/Product: somatotropin #status predicted
F:78-189,206-214/Disulfide bonds: #status predicted
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C:Species: Balaenoptera borealis (sei whale)
C:Date: 07-May-1993 #sequence_revision 07-May-1999 #text_change 07-May-1999
C:Accession: PN0140
R:Yudaev, N.A.; Pankov, Y.A.; Bulatov, A.A.; Osipova, T.A.
                                                            A;Cross-references: (GB:J03071; NID:g183148; PIDN:AAA52553.1; PID:g183153
C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          27 FPAMPLSSLFSNAVLRAQHLHQLAADTYKEFERAY:PEGGRYS-1QN 72
                                                                                                                                                                                                                                                                                                                                                                                      Score 197; DB 2; Length 217;
Pred. No. 3.5e-17;
5; Mismatches 4; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 29 TVPLSKLEDHAMIQAHRANGLAIDTYQEFEETYIPKDQKYSFLHD 73
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      4 TIPLSELFDNAMLRAHREHULHULAFDTYOEFEEAYIPKEOKYSFLON 48
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A;Title: Amino acid sequence of seiwhale somatotropin.
A;Reference number: PN0140; MUID:83000569; PMID:7115813
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             62.1%; Score 161.5; DB 1; 68.1%; Pred. No. 9.40-13; Mismatches 8;
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68.1%; Pred. No. 1.1e-12;
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C:Superfamily: prolactin
C:Keywords: growth factor: hormone
F:52-163,180-188/Disulfide bonds: *status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              6; Mismatches
                                                                                                                                                                                A;Gene: GDB:CSH2
A;Cross-references: GDB:119813; OMIM:118820
                                                                                                                                                                                                                                                                                                                                                                                           75.8%;
80.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                N/Alternate names: growth Lormone
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Rest Local Similarity 80.0%
These 36; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          somatotropin precursor - mouse
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Tes 32: Conservative
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                                                                                                                                                                                                                                                              A:Map position: 17q22-17q24
C;Superfamily: prolactin
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Best Local Similarity
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A;Residues: 1-190 <YUD>
            A; Molecule type: DNA
A; Residues: 1-217 <CHE>
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                                                                                                                                                      ANote: choriomammotropin apparently copurified with placental catechol-O-methyltransfer Rysherwood, L.M.; Handwerger, S.; McLaurin, W.D.; Lanner, M. Mature New Hol. 233, 59-61, 1971.
Affile: New Hol. 233, 59-61, 1971.
Affile: Amino-acid sequence of human placental lactogen.
A.Reference number: A93401; MUID:72016313; PMID:5286363
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Rischneider, A.B.: Kowalski, K.; Russell, J.; Sherwood, L.M.
J. Biol. Chem. 254, 3782-3787, 1979
A.Tille: Identification of the interchain disulfide bonds of dimeric human placental laq
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A; Contents: attactation; dimeric disultide base
R; Selby, M.J., brita, A., Baster, E., Ferl, D.L., Fberhard, N.E.,
J. Biol. Chem. 259, 1831-18354; 1944
A; Title: Analysis of a major human choicents sematemanentropin gene. Evidence for two A; Reference number: 155229; MUID:85030426; PMID:6208192
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N;Alternate names: chorionic somatomammotropin 2
Species: Brown Sapiens (man)
C;Date: 24:Dec-1989 scaquence_revision 29:Dec-1989 stext_change 16-Jul-1999
C;Date: 24:Dec-1989 scaquence_revision 29:Dec-1989 stext_change 16-Jul-1999
C;Accession: E:34.35
R;Chen E: Y: Liao, Y.C.; Smith, D.H.; Barrera-Saldana, H.A.; Gelinas, R.E.; Seeburg, Genomics 4, 479-497, 1989
A;Title: The human growth hormone locus: nucleotide sequence, biology, and evolution.
A;Reference number: A12435; MUID:89307277; PMID:2744760
A;Status: preliminary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         F:208-215/Disulfide bonds: (in monomeric form) *status experimental
F:208/bisuifide bonds: interchain (to 215 in dimeric form) *status experimental
F:215/bisulfide bonds: interchain (to 208 in dimeric form) *status experimental
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A:Molecule type: mRNA
A:Residues: 160-217 <RE2>
A:Cross-references: GB:M25118; NID:9181124; PIDN:AAA35721.1; PID:9181125
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A:Introns: 4/1: 57/3; 97/3; 152/3
C.Superfamily: prolactin
C:Keywords: hormone: placenta
F:1-26/10mmain: signal sequence *status experimental <SIG>
F:27-217/Product: chorlomammotropin A *status experimental <MAT>
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Areference number: A93405
A;Contents: annotation
R;Schneider, A.B.; Kowalski, K.; Russell, J.; Sherwood, L.
A;Reference number: A61283; MUID:91244006; PMID:2037148
A;Accession: A61283
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Pred. No. 3.5e-17;
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R:Secburg, P.H.; Shine, J.; Martial, J.A.;
Trans. Assoc. Am. Physicians 90, 109-116,
A.Fille: Nucleotide sequence of a human ger
A.Reference number: 159658: MUID:78160787;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Cross-references: GDB:119084; OMIM:150200
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A:Status: translated from GB/EMBL/DDBJ
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80.0%;
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Best Local Similarity 80.00
Best Local Similarity 80.00
Social Similarity 80.00
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                                                                                 A; Molecule type: protein
A; Residues: 27-46 <NIC>
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A; Residues: 1-217 <RES>
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2 FPTIPLSRIFDNAMLRAHRLHQLAFDTYQEFEEAYIPKEQKYSFLQN 48
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Chacession: Agi372; Agi385; Agi381; Ag0240; A01514
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A.Residues: 1-190 <2AKs
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FEBS Lett. 44, 453-756, 1974
A.Fille: The among and Sequence of equine as with hormore,
A.Reference number: A91395, Mille:7402(462): 10.4747849
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68.1%: Pred. No. 1.4e-12;
live 6; Mismatches 8; Indels 1
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A:Residues: 1-190 <HUL>
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F:1-190/Froduct: somatotropin #status exper. *ntal <MAT>
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6; Mismatches
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C:Species: Equus caballus (domestic horse)
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OM protein - protein search, using sw model

September 15, 2003, 11:54:00; Search time 4,56631 Seconds (without alignments) 504.633 Million cell updates/sec Run on:

US-09-423-100-1 260 | MFPTIPLSRLEDNAMLRAHR.....QEFEEAYIPKEOKYSFLONP 49 Title: Perfect score:

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Scoring table:

127861 seqs, 47026705 residues BLCSUM62 Gapop 10.0 , Gapext 0.5 Searched:

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution. SwissProt_41:* Database :

SUMMARIES

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ع	98.7		217	_	SOM2_PANTR	P58757	pan trodlod
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У	197	75.8	217	-	PLIHUMAN	P01243	homo sapien
10		62.1	216	-	SOMA_MOUSE	P06880	mus musculu
=			190	-	SOMA_BALHO	P33092	balaenopter
12	159.5		190	-	SOMA_LOXAF	P20392	loxodonta a
13		61.3	190	-	SOMA_VUI.VU	P10766	vulpes vulp
14	٠. ص		216	~	SOMA_CANFA	P33711	canis famil
15		61.3	216	-	SOMA_FELCA	P46404	felis silve
16	159.5		216	-	SOMA_HORSE	P01245	equus cabal
17		61.3	216	_	SOMA_MESAU	P37886	mesocriceta
æ :	159.5		216	-	SOMA_PIG	P01248	sus scrofa
9	159.5	61.3	216	-	SOMA_RABIT	P46407	oryctolagus
50	159.5	61.3	216	-	SOMA_RAT	P01244	rattus norv
7		61.3	217	_	SCMA_GALSE	09gkal	qalaqo sene
22	159.5	63.3	217	-	SOMA_NYCPY	09qmb2	nycticebus
£	156.5	60.2	216	-	SOMA_MUSVI	P19795	mustela vis
7	155.5	59.8	150	-	SOMA_LAMPA	P37885	lama guanic
52	150	\sim		-	SOMA_MELGA	P22077	meleagris q
56	148	Ø		-	SOMA_CHEMY	P34005	chelonia my
27	145	ഹ		-	SOMA_MONDO	09160	monodelphis
28	145	55.8	215	-	SOMA_TRIVU	062754	trichosurus
58		u٠	190	_	SOM1_ACIGU	P26773	acipenser g
30	144	L'I	190	_	SOM2_ACIGU	P26774	acipenser g
31	144	Š	216	~	SOMA_CHICK	P08998	gallus gall
35	142.5	₹.	217	-	SOMA_BOVIN	P01246	bos taurus
33	142.5	54.8	217	-	SOMA_CEREL	P56437	cervus elap

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MEDLINE-80130196; Pubmed-7356479;
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MEDLINE-71139765; PubMed+5279046;
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          SECUENCE FROM N.A. (ISOFORM 4).
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SEQUENCE OF 1-26 FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sundstroem M., Lundgvist I., Roedin J., Giebel L.B., Millian D.
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Pohen F.E., Kuntz 1.10-3
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Lander E.S.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Nat. Genet.
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differentiation and proliferation of myoblasts. It also stimulates

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SIGNAL
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                                                                                            SOMA_PANTR
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                                                                                                               This SWISS-PROT entry is copyright, it is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation of the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license?isb-sib.ch).
                                 ö
                                                                                                                                                                                                                                                                                                                                             Somatotrep is precursor (drewth terrore) (dB) (SB N) (Pituriar) growth
                                 Gaps
                                                                                                                                                                                                                                                                                    complementary deoxyribonucleic acids diff. entially expressed during pregnancy in the rhesus monkey placenta."; entially expressed during Endocrinclosy 133:1744-1752(1993).
                                                                                                                                                                                                Macara mulatta (Brosas macaque).
Enkaryota: Mehazoa: Chordata: Graniata: Vertebrata: Esteleostuma:
Mammalia; Entheria: Primates: Catarrión: Perropithecidae;
                                0
                                                          SIMILARITY: BELONGS TO THE SOMATOTROPIN/PROLACTIN FAMILY.
                                                 2 FPTIPLSRLFDNAMLRAHRLHQLAFDTYC :FEEAYIPKEQKYSFLQNP 49
            Length 217;
                                Indels
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E -> 0 (IN REF. 2).

N -> D (IN REF. 2).

W; 2C5180341EEC46D0 CRC64;
Score 255; DB 1; Len.
b; Pred. No. 6.6e-25;
                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
MEDLINE:94008724: PubMed:8464617;
Golos T.G., Durning M., Fisher J.M., Fox r P.D.;
"Cloning of four growth hormone/chorinon amatom."
                                                                                                                                                 01-00T 1594 (Rel. 30, Last segmence update)
28 FER-2014 (Rel. 41, Tast annotation update)
                                                                                                                    217 AA
                100.0%; Pred. ....
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SOMATOTROPIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PROSITE: PSUU338: SOMATOTKOPIN_1: 1. PROSITE: PSUU338: SOMATOTKOPIN_2: 1.
                                                                                                                    PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                               SUBCELLULAR LOCATION: Secreted.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     InterPro: IPR001400: Somatotropin.
                                                                                                                                       01-OCT 1993 (Rel. 27, Created)
01-OCT 1994 (Rel. 30, Last Seq
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 24913 MW;
                                                                                                                                                                              horson) (drawth horsone 1)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Pituitary; Signal.
1 26
     Query Match
Best Local Similarity 100.0
                                                                                                                     STANDARD:
                                                                                                                                                                                                                              Cercopithecinae; Macada
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   215
100
179
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HSSP: P01241; 1AXI.
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100
179
217 AA;
                                                                                                                                                                                                                                                                                                                                      SEQUENCE OF 27-217
                                                                                                                                                                                                                                       NCB1_TaxID~9544;
                                                                                                                    SOMA_MACMU
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CONFLICT
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                                                                                                                               P33093;
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Length 217;

DB 1;

Score 255;

98.18;

Query Match

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    -i- FUNCIION: Plays an important role in growth control. Its major role in stimulating body growth is to stimulate the liver and other tissues to secrete 1GF-1. It stimulates both the differentiation and proliferation of myoblasts. It also stimulates amino acid uptake and protein synthesis in muscle and other
                                                                                                                                                                                                                                                                                                     28-FEB-2003 (Rel. 41, Created)
28-FEB-2003 (Rel. 41, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Somatofropin precursor (Growth hormone) (GH-N) (Piluitary growth
                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
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Mammalla; Butheria; Primates; Catarthin; Botinidae; Pan.
                          Ö
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                                                                             49
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Revol A., Esquivei D., Santiago D., Barrera-Saldana H.;
*Independent diplication of the growt; hormone gene is three
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 tissues (By Similarity).
-!- SUBCELLULAR LOCATION: Secreted.
-!- SIMILARITY: BELONSS TO THE SOMATOTROPIN/PROLACTIN FAMILY.
                                                                                                                          74
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                                                                          2 FPTIPLSKLFINAMLKAHRLHÖLAFDTYQEFEBAYIPKEGKYSFLONP
                             Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Anthropoidean lineages.":
Submitted (APR-2001) to the EMBL/GenBank/DOBJ databases.
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  100.0%; Pred. No. 6.6e-25;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                98.1%; Score 255; DB 1; 1
100.0%; Pred, No. 6.6e-25;
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28-FEB-2003 (Rel. 41, Last sequence update)
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Conservative 0; Mismatches
                          Mismatches
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BY SIMILARITY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SOMATOTROPIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PROSITE: PS00266; SOMATOTROPIN_1; 1.
PROSITE: PS00338; SOMATOTROPIN_2; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRT;
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InterPro; 1PR001406; Somatotropin.
                        0;
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                                                                                                                                                                                                                                                                                                                                                                                                                   hormone) (Growth hormone 1).
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                          Conservative
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Best Local Similarity
Matches 48; Conserv
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Matches 48: Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NCBI_TaxID-9598;
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Q9GMB3;
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DISULFID
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                                                                                                                                                                                                                                                                                                      SIGNAL
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                                                                                                                                                                                                                                                                                This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the Buropean Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (see http://www.isb-sib.ch/announce/or send an email to licenselisb-sib.ch).
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O
                                                                                                                                                                    -i- FUNCTION: Plays an important role in growth control. Its major role in stimulating body growth is to stimulate the liver and other tissues to secrete IGF-1. It stimulates both the differentiation and proliferation of myoblasts. It also stimulates
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDLINE-21265430: PubMed-11371582;
Liu J.C., Makova K.D., Adkins R.M., Gibsol. S., Li W.H.;
"Episodic evolution of growth hormone in primates and emergence of the
species specificity of human growth hormone receptor.";
MOI. Biol. Evol. 18:945-953(2001).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GHI.
Saimiri boliviensis boliviensis (Bolivian squirrel monkey).
Eukaryota, Metazoa; Chordata; Craniata; Verlebrata; Euteleostom;
Mammalia: Eutheria; Primates; Platyrrhin;; Cebidae; Cebinae; Saimiri.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Caps
                                                                                                                       Wallis O.C., Wallis M., "Cloning and characterisation of a putative growth hormone encoding gene from the marmoset (Callithrix jacchus)."; Submitted (AUG-2000) to the EMBL/GenBank/DDBJ databases.
                                                 Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Eutheria; Primates; Platyrrhini; Callitrichidae;
                                                                                                                                                                                                                        amino acid uptake and protein synthesis in muscle and other
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         <u>ن</u>
                                                                                                                                                                                                                                                          SIMILARITY: BELONGS TO THE SOMALOTPOPIN/PROLACTIN FAMILY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                2 FPTIPLSRLFDNAMLRAHRLHQLAFDTYQEFEEAYIPKFOKYSFLQNP 49
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DB 1: Length 217;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     i.7e-24;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         E102151A12CE6192 CRC64;
28-FEB-2003 (Rel. 41, Last annotation update) Somatotrupin precursor (Growth hormone).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         28-FEB-2003 (Rel. 41, Created)
28 FEB-2003 (Rel. 41, Last sequence update)
28 FEB-2004 (Rel. 41, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     217 AM.
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0; Mismat .em
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BY SIMILARITY
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                         BY SIMILA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SOMATOTRO
                                    Callithrix jacchus (Common marmoset).
                                                                                                                                                                                                                                                                                                                                                                                                                    PFOSITE: PSO0266, SOMATOTROPIN 1: PROSITE: PSO0388: SOMATOTROPIN 2: 1.
                                                                                                                                                                                                                                    tissues (8y simitarity).
-1- SUBCELLULAR LOCATION: Secreted.
                                                                                                                                                                                                                                                                                                                                                                                                         InterPro: IPR001400; Somatotropin.
                                                                                                                                                                                                                                                                                                                                                                                 EMBL: AJ297563; CAC03481.1; ..
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          208 215 B<sup>3</sup>
217 AA; 24959 MW;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                              Hormone; Pituitary; Signal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Best Local Similarity 97.99
Matches 47, Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STANDARD;
                                                Eukaryota; Metazoa;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
                                                                                                           SEQUENCE FROM N.A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NCBI_TaxID=39432;
                                                                                   NCBI_TaxID=9483;
                                                                                                                                                                                                                                                                                                                                                                                                P51241;
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P58343;
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between the Swiss Institute of Rioinformatics and the EMBL outstation-
the European Bioinformatics Institute. There are no restrictions on its
use by non-profit institutions as long as its content is in no way
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O
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                                                                                                                                                                                                                                                                                                    This SWISS-PROT entry is copyright. It is produced through a collaboration
                                  role in stimulating body growth is to stimulate the liver and other tissues to secrete 10F-1. It stimulates both the differentiation and proliferation of myoblasts. It also stimulates amino acid uptake and protein synthesis in muscle and other
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        differentiation and proliferation of myoblasts. It also stimulates amino acid uptake and protein synthesis in muscle and other
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
-!- FUNCTION: Plays an important role in growth control. Its major
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28-FEB-2003 (Rel. 41, fast sequence update)
28-FEB-2003 (Rel. 41, fast annotation update)
Growth hormone variant precursor (GH-V) (Placenta-specific growth
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-!- FUNCTION: Plays an important role in growth control. Its major role in stimulating body growth is to stimulate the liver and other issues to secrete [GF-1]. It stimulates both the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Pan.
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O
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-:- TISSUE SPECIFICITY: Expressed in the placenta.
-:- SIMILARITY: BELONGS TO THE SOMATOTROPIN/PROLACTIN FAMILY.
                                                                                                                                                                   Lissues (By similarity).
SUBCELLULAR LOCATION: Secreted.
SIMILARITY: BELONGS TO THE SOMATOTROPIN/PROLACTIN FAMILY.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 217;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   2 FPT:PLSKLFDNAMLRAHKLHQLAFDTYQEFEEAY:PKEQKYSFLQNP
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SCHATOTROPIN.
BY SIMILAKITY.
BY SIMILAKITY.
W. 9515289992C529F7 CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      95.8%: Score 249;
97.9%; Pred. No. 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRINTS: FROUBBE, SOMALTROPIN.
PROSITE: PS00266; SOMATOTROFIN_1; PROSITE: PS00338; SOMATOTROPIN_2; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EMBG, AF339060; AAK62287.1;
InterPro; PR601400; Somatofropin,
Pfam: PF60104; Bormone; 1,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Conservative
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217 AA:
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nes 47; Conserv
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P01242 P005587:
21-JUL-1986 (Rel. 01, Created)
28-FEB 2003 (Rel. 41, Last sequence update)
15-SEP-2003 (Rel. 42, Last annotation update)
Growth hormone variant precursor (GH-V) (Placenta-specific growth
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                rmone variant mRNA in the novel growth hormone
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sceburg P.H.; *The human growth hormone gene family: nuclectide sequences show recent divergence and predict a new polypeptide hormone.*;

    60.8%; Score 2.65; DR 1; Length 217;
    93.6%; Prod No. 1.66; 22;
    (IVC Z. Misharonos 1; Edels

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Chen E.Y., Liao Y.C., Smith D.H., Barryra-Saldana H.A.,
Gelinas R.E., Seeburg P.H.;
                  Usage by
                                                                                                                                                                                                                                                                                                                         GROWTH HERMONE VARIANT.
BY SIMILARITY.
BY SIMILARITY.
1592A429075677DE CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Cooke N.E., Ray J., Emery J.G., Liebh or S.A.; "Two distinct species of human growth ormone va
modified and this statement is not rem rel. entities requires a license agreement ree hor send an email to license@isb-sib.ch.,
                                                                                                                                                                                                                                                                Hormone; Placenta; Signal; Glycoprotein.
SIGNAL 1 26 BY SIMILARITY
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MEDLINE-88243769: PubMed-3379057;
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                                                                                                                                                                        Pfam; PF00103; hormone; 1.
PMOSITE: PS00266; SOMATOTROPIN_1; 1.
PROSITE: PS00338; SOMATOTROPIN_2: 1.
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                                                                                                                                                   InterPro; IPR001400; Somatotropin.
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MEDLINE-83182010; PubMed-7169009;
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GH2.
                                                                                                                  EMBL; AF374233; AAL72285.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               L Somitarity 93.8
45. Conservative
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191
215
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SEQUENCE
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between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/
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Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D., Alschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Hhat N.K., A Hopkins R.E., Jordan H., Moore T., Max S.I., Mang J., Hsieh F., Diatchenko L., Marusiana K., Farmer A.A., Rubin G.M., Hong L., A Stapleton M., Soares M.B., Ronaldo M.F., Casavant T.L., Scheetz T.E., Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C., A Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J., AR Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaraine P.H., Richards S., Worley K.C., Hule S., Garcia A.M., Gay L.J., Hulyk S.W., Willalon D.K., Mazny D.M., Sodergren E.J., Lu X., Gibbs R.A., Willalon D.K., Wazny D.M., Sodergren E.J., Lu X., Gibbs R.A., Mhiting M., Madan A., Wodrigues S., Sanchez A., Mhiting M., Madan A., Green E.D., Dickson M.C., Grimwood J., Schmutz J., Myers R.M.,
                                                                                                                                                                                                                                                                                                                                                                                                                      -: SUBBUNT: Monomer, dimer, trimer, tetramer and pontamer, disulfide-
linked or non-covalently associated in homopolymeric and
heteropolymeric combin lions. Can also form a complex either with
GHBP or with the alphax-macroglobulin complex.
                                                                                                                                                                                                                                                         Butterfield Y.S.N., Krzywinski M.T., Skalska U., Smailus D.E., Schnerch A., Schein J.E., Jones S.J.M., Marra M.A., Generation and intial analysis of m.go than 15,000 full-length brand and mouse cDNA sequences."
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            isold-P01242-2: Sequence-VSP_006203;
Note-wo experimental confirmation available:
-!- TISSUE SPECIFICITY: Expressed in the placenta.
-!- SIMILARITY: BELONGS TO THE SOMATOTROPIN/PROLACTIN FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Event=Alternative splicing: Named isoforms=2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                           MEDLINE 99321812; PubMed-10393484;
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EMBL: J03756; AAB59547.1; -.
EMBL: J03756; AAB59548.1; -.
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MIM; 139240; -.
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PIR: D32435; STHUV.
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SIGNAL
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                                                                                                            KDMDKVETFLRIVQCRSVEGSCGF -> VRVAPGIPNPGAP
LASRDWGEKHCCPLFSSQALIQFNSPYSSFPLVNPPGI.SLQ
PGGEGGKWMNERGREQCPSAWPI.LELHFAEAGRWQPPDWA
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MEDLINE-94008724: PubMed-8404617;
Golos T.G., Durning M., Fisher J.M., Fox er P.D.;
Golos T.G., Durning M., Fisher J.M., Fox er P.D.;
Coloning of growth hormone-chorionic somatomamotropin-related complementary droxyribonucleic acids differentially expressed during pregnancy in the rhesus monkey placenta.";
Endocrinology 33:1744-1752(1993).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SOM2_MACMU STANDARD: PRI: 217 AA.
007376: Q28494:
01 NOV-1997 (Rel. 35, Created)
01 -NOV-1997 (Rel. 35, Last sequence update)
28-FER-2003 (Rel. 41, Last annotation update)
Growth hormone variant precursor (GH-V) (Placenta-specific growth
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Macaca mulatra (Rhesus macaque).
Eukaryota: Metazoa; Chordata; Cramiata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhin; Cercopithecidae;
                                                                       ( POTENTIAL)
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TISSUE SPECIFICITY: Expressed in th. placenta.
SIMILARITY: BELONGS TO THE SOMAIOTM (IN/PROLACTIN FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                       Z. 1911 PERSKLEDNAMERAHREHUL APPERORY PREGRYSSELUNE 33
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                                                                                                                                                                                                                                                                                                                                  Score 228: DB 1; Length 217;
Pred. No 1.6e-21;
                                                                                                                                                                          DLQSVLOOV (in isoform 2).
/FTId+VSP_006203.
R -> W (IN dDSNP:5389).
/FTId-VAR_014591.
I -> T (IN REF. 2).
W; 789324698E822F96 CRC64;
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    HORMONE VARIANT
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                                                                  N-LINKED (GLCNAC.
                                                                                                                                                                                                                                                                                                                                                                              Mismatches
                       BY SIMILARITY
BY SIMILARITY
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217 AA; 24999 MW;
                                                                                                                                                                                                                                                                                                                                87.7%;
Harity 91.7%;
Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              hormone) (Growth hormone 2)
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  217
191
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166
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es 44; Conserv
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SEQUENCE FROM N.A
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27
79
208
166
153
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SEQUENCE
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  CHAIN
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EMBL: U02293; AAA03391.1; -. EMBL: L16555; AAA20180.1; -.

PIR; 167411; 167411.

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Selby M.J., Barta A., Baxter J.D., Bell G.J., Eberhardt N.L.,
"Analysis of a major human chortonic somatomamotropin gene. Evidence
for two functional promoter elements.",
D. Biol. Chem. 259:1417-1318(1984).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    21-Jub-1986 (Rel. 01, Created)
01-APR-1988 (Rel. 07, Last equence update)
15-SFP-2003 (Rel. 42, Last equence update)
Lactogen precursor (Chorlomanmotropin) (Chorlonic somatomanmotropin).
CSH1 AND CSH2.
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MEDLINE: 89307227; Pubmed-2744760;
Chen E.Y., Liao Y.C., Smith D.H., Barrera-Saldana H.A., Gelinas R.E.,
Seeburg P.H.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Homo sapiens (Human).
Eukaryota: Metazoa; chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Eberhardt N.L., Harta A.;
"The human growth hormone gene locus: structure, evolution, and
allelic variations.";
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7e-18;
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BY SIMILARITY.
L -> F (IN REF. 2).
E -> 6 (IN REF. 2).
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SIGNAL 1 26 BY SIMILARITY.
CHAIN 27 217 GROWTH HORMONE VARIANT.
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Pred. No. 7
                                                                                                                                                                                                  PROSITE; PS00266; SOMATOTROPIN_1; 1.
PROSITE; PS00338; SCMATOTROPIN_2; 1.
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HSSP; P01241; 1HGU,
InterPro; 1PR001400; Somatotropin.
Pfam: PF00103; hormone; 1.
PRINTS; PR00836; SOMATOTROPIN.
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J. Biol. Chem. 258:3787-3793(1983)
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MEDLINE-85030426; Pubmed=6208192;
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MEDLINE*87161235; PubMed-3036680;
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79 191 BY
208 215 BY
57 57 L
152 152 E
217 AA; 25221 MW;
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                                                                       TISSUE-Placenta, and Oterus;

MEDINE-2288257; PubMed-12477932;

MEDINE-2288257; PubMed-12477932;

MEDINE-2288257; PubMed-12477932;

MISTAL REPUBDICE EA., GCOUSE L.B., Derge J.G.,

MISTAL REPUBDICE E.S., Wadner C.E., Bhat N.K.,

A Hopkins R.E., Jordan H., Moore T., Max S.I., Wang J., Hsich, F.,

MISTAL REPUBDICE E.S., Madner C.E., Bhat N.K.,

MISTAL REPUBDICE E.S., Madner C.E., May J., Waich, F.,

MISTAL REPUBDICE E.S., Madner C.E., Mark S.I., Wang J., Hsich, F.,

MISTAL REPUBDICE E.S., Moore T., Max S.I., Wang J., Hsich, F.,

MISTAL REPUBDICE E.S., Moore T., Max S.I., Wang J., Hsich, F.,

MISTAL REPUBDICE E.S., Moore T., Mark S.I., Wallank, S.J.,

MISTAL REPUBDICE E.S., Moore T., Male R.J., Male R.J.,

MISTAL REPUBDICE E.S., Moore T., Male R.J., Male R.J.,

MISTAL REPUBDICE E.S., Worley R.C., Shervishek, V. M., Mallank, S. Mancher, R. M.,

Mistal R.M., Madan A., Wong A.C., Shervishek, V. M., Mallank, S. M.,

Maltinis M., Madan A., Wong A.C., Shervishek, V. M., Malting M., Madner, M. M.,

Maltinis M., Madan A., Wong, M., Maltin, M., Madner, M.,

Maltinish M., Madan A., Schein, J. J., Mysts R.M.,

Matterfield V.S.N., Krzywinski M. L., Skaiska U., Small is D.E.,

Manna and mouse CDA, Sequences. T., Manna M.A.,

"Generation and initial analysis of more than 15,000 fall-length human and mouse CDA."
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Schneider A.B., Kowalski K., Russell J., Sherwood L.K.;
"Ideutification of the interchain disulfide bonds of dimerse human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Shine J., Seeburg P.H., Martial J.A., Gaster J.D., Goodman H.H., "Construction and analysis of recombinant DNA for human chorionic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Li C.H., Dixon J.S., Chung D.; "Amino deid sequence of human chorienic sematemammetropin.";
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sherwood L.M., Handwerger S., McLaurin W.D., Lanner M.;
Nature New Hiol. 235:64-64(1972).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE OF 27-117.
MEDLINE-22016313: Pubmed 5286363;
Sherwood L.M., Handwerger S., McLaurin W.D., Lanner M. Amnino-scala sequence of human placental lactogen.";
Nature New Biol. 233:59-61(1971).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Natl. Acad. Sci. U.S.A. 99:16849 16903(2002).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   somatomammotropin.";
Nature 270:494-499(1977).
DNA 1:239-249(1982)
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J00289; AAA98747.1; -. K02401; AAA52115.1; -. M15894; AAA52116.1; -. J03071; AAA52551.1; -.

EMBL;

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Gene 169:209-213(1996).
-!- FUNCTION: Plays an important role in growth control. Its major role in stimulating body growth is to stimulate the liver and other tissues to secrete IGF-1. It stimulates both the differentiation and proliferation of myoblasts. It also stimulates
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Caps
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Das P., Meyer L., Seytert L.-M., Brockmann G., Schwerin M.:
"Structure of the growth Limone encoding gene and its promoter in
                                                                                                                                                                                                                                                                                                   INTERCHAIN (WITH C-215 IN A DIMER).
INTERCHAIN (WITH C-206 IN A DIMER).
P -> A (IN CSH2).
/FIId **VAR_007166.
IS -> L (IN CSH2).
/FIId **VAR_007167.
I -> T (IN REF. 9).
MISSING (IN REF. 9).
MISSING (IN REF. 9).
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Mammalia; Eutheria; Rodent a; Sciurognathi; Muridae; Murinae; Mus.
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23580D07A713F431 CRC64;
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80.0%; Pred. No. 1.3e-17;
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01-JAN-1988 (Rel. 06, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
GABATOLFOPIN Precursor (Growth hormone).
                                                                                                                                 MIM: 150200;

GO: GO:0007565; P:pregnancy; TAS.
InterPro; IPRE01400; Somatotropin.
Prim: PF00103; .cormone: 1.
PROSITE; PS00260; SOMATOTROPIN.1: 1.
PROSITE; PS00388; SOMATOTROPIN.2: 1.
FORMOME: Placepita: Multique: family; Signal.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Mismatches
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JOULTB: AAA98621.1; -- BC002717; AAH02717.1; -- BC005921; AAH05921.1; -- BC020756; AAH20756.1; --
                                                                                                                                                                                                                                                                                                                                                                                                                                                       25020 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STRAIN-F2TDU; TISSUE Liver:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STANDARD;
                                                                                                      Genew: HGNC:2440; CSH1.
Genew: HGNC:2441; CSH2.
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                                                            PIR: A26449: A26449.
PIR: C32435: LCHUC.
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95
116
134
217 AA:
                                                                                         HSSP; P01241: 1A22.
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                                                                                                                                                                                                                                                                                                                                                                  104
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ID SOMA_MOUSE
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D1831,F11)
D1831,F11)
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                                                                                                                                                                                                                                             SIGNAL
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                              EMBL;
                                                                                                                                                                                                                                                           CHAIN
                                              EMB.:
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bloinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as its eventent is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             role in stimulating body growth is to stimulate the liver and other tissues to secrete IGF1. It stimulates both the differentiation and proliferation of mybblasts. It also stimulates amino acid uptake and protein synthesis in muscle and other
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Caps
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OSIDOVA I.A., Bulatov A.A., Pankov Y.A.;
Structural studies of trypic peptides from large cyanogen bromide fragments of sei whale (Balalnoptera borealis) somatotropin.";
History, Khim, 4:1884-1899(1978).

PROCTION: Plays an important role in growth control. Its major
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Eukaryota: Metazoa; Chordata; Craciatu: Vertebrata; Eufeleostomi:
Mammalia; Eutheria; Cetartiodactyla; Cetacea; Mysticeti;
Baluenopteridae; Balaenoptora
amino acid uptake and protein synthesis in muscle and other
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-:- SIMILARITY: BELONGS TO THE SOMATOTROPIN/PROLACTIN FAMILY.
                             SUBCELLULAR LOCATION: Secreted. SIMILARITY: BELONGS TO THE SOMATOTROPIN/PROLACTIN FAMILY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      62.1%; Score 161.5; DH 1; Length 21 illarity 68.1%; Pred, No. 3.6e-13; Conservative 6; Mismatches 8; Indels
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01 odr-1993 (Rel. 22, Last Septence up.1 to)
01 FEB-2004 (Rel. 41, Last annotation u.date)
Somatotropis (Growth hormone).
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BY SIMILAR: TV.
BY SIMILAR IV.
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                                                                                                                                                                                                                         EMBL: X02891; CAA26650.1; -. EMBL: 246663; CAA86658.1; -.
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MGD; M31:95207; Ch.
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es 42; Conserv
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78
206
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P34692;
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Matches
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"Primary structure of elephant growth hormone.";
"Thindry structure of elephant growth hormone.";
"Int. J. Pept. Protein Res. 31:368-372(1984)
"!- FUNCTION: Plays an important role in growth control. Its major role in strainglating body growth is to stimulate the liver and other tissues to secrete igF-1 I: stimulates both the differentiation and proliferation of myoblasts. It also stimulates
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Saps
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Eukaryotu, Metazoa, Chordata, Craniuta, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Proboscidea, Elephantidae, Loxodonta.
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                                                                                                                                                                                                                                                                                                                                                                                           61.7%; Score 160.5; DB 1; Length 190; 68.1%; Fred. No. 4.1e-13;
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    -1- SUBSELLUIAR DOCATION, Secreted.
    -1- SUBSELLUIAR DOCATION, Secreted.
    -1- SUMLARITY, BELONGS TO THE SOMATOTRUPIN/PROLACTIN FAMILY.
    -1- SUBSELLANDIA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                         8; Indels
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BY SIMILARITY.

05H8608130B741F2 (1RC64).
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68.1%; Pred. No. 5.5e-13;
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01-JUL-1989 (Rel. 11, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Somatotropin (Growth hormone).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          01-FEB-1991 (Ref. ?, Last sequence uplate)
28-FEB-2003 (Ref. Last annotation opdate)
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BY SIMILARITY.
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HSSP; P01241: 1AX1.
InterPro: JPR001400: SomatoLropin
Pfam: PF00103: hormone: 1.
PROSITE: PS00266: SOMATOTROPIN_1: 1.
PROSITE: PS00338: SOMATOTROPIN_2: 1.
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                                                                                                                                                                                                                                                                                                                     190 AA: 21835 MW;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                     32: Conservative
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Matches 32; Conservative
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188
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180
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P10766;
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                                                                                                                                                TISSUE*Pituitary;

#BEDL(RF 99524575; PubMed*2722401;

Li C. H., Ladebski J., Chung D.;

Int. G. H., Protein Res. 33:70*72(1989).

1nt. J. Pept. Protein Res. 33:70*72(1989).

-1. FUNCTION: Plays an important role in growth control. Its major role in stimulating body growth is to stimulate the liver and other tissues to secrete LGP-1. It stimulates both the differentiation and proliferation of myobiasts. It also stimulates amino wrid uptake and protein synthesis in massiv and short
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       van Leeuwen I.S., Teske E., van Garderen E., Rutteman G.R., Moi J.A.; "Extrapituitary growth hormone expression in the dog is initiated at the normal pituitary transcription start site in the mammary gland and at multiple upstream sites in lymphoid cells."; Submitted (MAR-1997) to the EMBL/GenBank/DDBJ databases.
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MEDLINE-99337113; PubMed-10411306;
Lantingar-van Leeuwen I.S., Oudshoorn M., Mol J.A.;
"Cantine mammary growth hormone gene transcription initiates at the pituitary-specific start site in the absence of pit-1.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDIJNE-94266166; Pubmed-8206387;
Ascacio-Martinez J.A., Barrera-Saldana H.A.;
"A dow growth hormone cDNA codes for a mature protein identical to
                Vulpes vulpes (Red fox).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Vulpes.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Carnivora, Fissipedia, Canidae, Canis,
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                                                                                                                                                                                                                                                                                                                                                                                                                  SIMILANITY: BELCINIS TO THE SOMAL OF PLINZEPOLACTIN PARTLY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       2 FPTIPLSRLFDNAMLRAHRLHQLAFDTYOEFERAYIPKEOKYSFLON
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         51.3%; Score 159.5; DH 1
68.1%; Pred. No. 5.5e-13;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         6: Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PROSITE: PS00266; SOMATOTROPIN_; 1. PROSITE: PS00386; SOMATOTROPIN_; 1. PROSITE; PS00338; SOMATOTROPIN_2; 1
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InterPro: IPR001400; Somatotropin.
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Matches 42: Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Hormone; Pituitary.
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                                                                                    NCBI_TaxID-9627;
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                                                                                                                                SEQUENCE
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                                                       role in stimulating body growth is to stimulate the liver and other tissues to secrete 1GF-1. It stimulates both the differentiation and proliferation of myoblasts. It also stimulates amino acid uptake and protein synthesis in muscle and other
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TISSUE-Pituitary:
PEDLINE-S7359713; pubMed-7642118;
Castro-Peralta F., Barrera-Saldana H.A.;
Castro-Peralta G., Barrera-Saldana H.A.;
Cloning and Sequencing of cDNA encoding the cat growth hormone.";
Gene 160:311-312(1995).
Mol. Cell. Endocrinol. 150:121-128(1999).
-!- FUNCTION: Plays an important role in growth control. Its major
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Mammalia, Eutheria, Carnivora, Fissipedia, Felidae, Felis.
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                                                                                                                                                                                                                                               -!- SIMILARITY: BELONGS TO THE SOMATOTROPIN/PROLACTIN FAMILY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Indels
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BY SIMILARITY.
S YS G (IN REF. 1).
N -> T (IN REF. 1).
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01-NOV-1995 (Rei. 32, Last sequence update)
28-FEB-2003 (Rei. 41, Last annotation update)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PROSITE: PS00266; SOMATOTROPIN_1: 1. PROSITE: PS00338; SOMATOTROPIN_2: 1.
                                                                                                                                                                                                                     SUBCELLULAR LOCATION: Secreted.
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HSSP; P01246, 16ST,
InterPro: IPR001400, Somatotropia.
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MEDLINE-96194906; PubMed~8654953;
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PRINTS; PR00836; SOMATOTROPIN.
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FUNCTION: Plays an important role in growth control. Its major role in stimulating body growth is to stimulate the liver and other tissues to secrete 16F1. It stimulates both the differentiation and proliferation of i, blasts. It also stimulates amino acid uptake and protein synthesis in muscle and other tissues. SUBCENTICLER LOCATION: Secreted.
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Live 6; Mismatches 8; Indels 1
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SOMATOTR 1.
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N -> T (1 REF. 2).
T -> A (1. REF. 2).
T -> A (1. REF. 2).
L -> P (1. REF. 2).
L -> P (1. REF. 2).
M. 05820239A7D292C6 CRC64:
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SIGNAL 1 26
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EMBL: 013393; AAA56142.1;
PTR: 304632; J04632;
HSSP: F01246; TBS1.
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216 AA:
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Search completed: September 15, 2003, 12:01:29 Job time : 5.56631 secs

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GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.
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OM protein - protein search, using sw model

September 15, 2003, 11:54:30; Search time 19.1434 Seconds (without alignments) 660.520 Million cell updates/sec Run on:

US-09-423-100-1 260 1 MFPTIPLSRLFDNAMLRAHR......QEFEEAYIPKEQKYSFLQNP 49 Title: Perfect score: Sequence:

Gapop 10.0 , Gapext 3.5 BLOSUM62 Scoring table:

830525 seqs, 258052634 residues Searched:

830525 Total number of Lits satisfying chosen paramayers:

Length: 0 length: 200000000 Minimum DB seq Maximum DB seq

Post processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

SPTREMBL_23: * Database :

sp_vertebrate:* sp_unclassified:* sp_invertebrate:* sp_bacteriap:*
sp_archeap:* sp_organelle:* sp_archea:* sp_bacteria.* sp_rvirus:* sp_rodent:* sp_virus:* sp_phage:* sp_plant:* sp_mammal:* sp_fungi:*

Pred, No. is the number of results predicted by charce to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

014644 home sapies, 007368 macaca mula 007467 macaca mula 007869 macaca mula 014407 home sapien 08wd9 ateles geor 07615 spalax leuc 09tv91 equus cabal 08m173 delphinus d O9r2c3 mus musculu O9jkm4 cavia porce 095mj5 tarsius ban 095205 ovis aries OBwne0 ateles geof O8hye5 ailuropoda Description 070615 09TV91 09R2C3 09JKM4 007367 014407 08WND9 007458 **Q8MI74** 08M173 QUAYES 4 6 6 6 7 6 Ouery Match Length DB Secre 159.5 159.5 159.5 159.5 155.5 154 228 213 213 201 197 195 170 Result

014643 homo sapien 095mj6 tarsius syr 091400 cavia porce 09tu21 capra hircu 0919w9 bos indicus	V8M1/5 CallIlfrix Q28957 sus scrofa Q9bec0 tragulus ja Q9beb9 tragulus ja	090472 cynops pyrr 091386 amia calva 095240 canis famil 014406 homo sapien	Usegas arises of 1904 orise arises of 46474 telis silve P78451 homo sapien Ofform Clarias bat Ufbort quiaqo cras	Udqqjl heteropneus Qdqfn2 clarias qar Q9prp5 clarias qar Q9pr82 silurus aso Q90283 carassius a	OBuvez cirrhinus m 090w26 carassius a 090w27 carassius a 098sr7 cyprinus ca
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17 18 19 20 20 21	22 23 24 25 26	27 28 29 30	- W W E E E - U J 4 E E E	3.7 3.8 3.9 4.0 4.1	4444 9447

ALIGNMENTS

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Platyrrnini; Cebidae; Atelinae; Ateles. NCBL_TaxID-9509; Gaps 0 Revoi A., Esquivel D., Santiago D., Barrera-Saldana H.,
Revoi A., Esquivel D., Santiago D., Barrera-Saldana H.,
Independent duplication of the growth hormone gene in three
Anthropoldean lineages.'
Submitted (APR-2001) to the EMBL/GenHank/DDHJ databases.
EMBL. AR7A234, AAL72286.1:
InterPro I PR001400: Somatotropin.
Pram: PF00103: hormone: 1. Pram: PF00103: hormone: 1. PR051EP.
PROSITE: PS00266: SOMATOTROPIN_2: 1.
SEQUENCE 217 AA: 24894 MM: 425829FF41EEAAE6 CRC64: 2 FPTIPLSRLFDNAMLRAHRUHQLAFDTYGEFEEAYIPKFOKYSFLONP 49 27 FPTIPLSRLLDNAMLRA KLHQLAFDTYĞEFERAYIPKEGKYSFLÖNP 74 Query Match 95.8%, Score 249; UH 6; Length 217; Best Local Similarity 97.9%; Pred. No. 1.2e-25; Matches 47; Conservative 0; Mismatches 1; Indels 01-MAR-2002 (TrEMBLrel. 20, Created) 01-MAR-2002 (TrEMBLrel. 20, Last sequence update) 01-MAR-2003 (TrEMBLrel. 23, Last annotation update) Ateles geoffroyi (Black-handed spider monkey). 217 AA PRT: PRELIMINARY; Growth hormone, 08WNE0; 08WNE0 RESULT 2 014644 ID 01464 AC 01464 RESULT 1 OBWNEO Š

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007 369 ;
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"Cloning of four growth hormone/chorisonic somatomagnotropin-related complementary decxyribonucleic acids differentially expressed during pregnancy in the rhesus mockey placental.";
Endocrinology 13:1744-1752(1993).
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                                                                                                                                                                                                                                 TISSUE Term placenta:
MEDLINE:983737; PubMed-9709963;
MEDLINE:983737; PubMed-9709963;
MEDGUASEWSKI C.L., Svensson P.A., Jansson T., Clark R.,
Carisson L.M.S., Carisson B.;
"Cioning of two novel growth hormone transcripts expressed in human
                                                                                                         Homo sapiens (Human).
Eskaryota: Metazoa; Chordata; Craniata; Vertebrata; Esteleostomi;
Mammalia; Estheria; Primates; Catarrhini; Hominsidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Eukaryota: Metazoa: Chordată: Craniata: Vertebrata: Euroleostemi:
Mammalia: Eutheria: Primates: Catarrhiui: Cercopithecidae:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 2 PPTIPLSRIFDNAMI, RAHRI, HOLA PUTY OFFEE AY IPKEOKY SFI, UNP 49
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               87.7%; Score 22%; DB 4; Length 245; 91.7%; Pred, No. 9.5e-24;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    81.9%; Score 213; DB 6; Length 212; 78.7%; Pred. No. 8.7e-21;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FP71PLSRLFDNAMLARRELYQLAYDTYQEFEBAY11.KEQKYSF1ONP
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01.60V-1996 (TrEMBLrel, 01, Last sequence update)
01.60V-2003 (TrEMBLrel, 23, Last annotation update)
Somatotropin 2 precursor (Growth hormone 2) (Fraqment).
Maraca Autatta (Rhesus macaque).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    14CC7F8CD75D91C8 CRC64;
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0:-JAN-1998 (TrEMBLrel. 05, Created)
01-JAN-1998 (TrEMBLrel. 05, Last sequence update)
01-JEC-2001 (TrEMBLrel. 19, Last annotation update)
Placental growth hormone isoform hGH-V3 precursor.
                                                                                                                                                                                                                                                                                                                                        placenta.":
J. Clin. Endocrinol. Metab. 83:2878-2685(1998).
EMBL. Apricocl. A871829.1;
InterProc. Proc. 441: 1A.2.
InterProc. Proc. Proc. 1990[460]. Semotor opin
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PROSITE: PS00338; SOMATOTROPIN_2: 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PROSTIE: PS 6/266; SOMATGTEGGIN, 1; ..
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE 245 AA; 27101 MW;
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                                                                                                                                                                     NCHI_Tax (D-9606;
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Q67368;
Q1:NOV 1996 (
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Colos T.G., During M., Fisher J.M., Fowler P.D.,
"Cloning of tour growth hormone/chorionic somatomammotropin-related complementary deoxyribonucleic acids differentially expressed during pregnancy in the rhesus monkey placenta.";

Endocrinology 133.1744-1752(1993).

EMBL, Di6554: AAA18841.1;

HSSP: P01241: 1AXI.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 complementary devixitionarless acris differentially expressed during prequancy in the ricesus monkey placenta."; Endocrinclogy 14:1744-1752(1993).
EMBL: L16552; AAA18839.1; -...
HSSP; P01241; TAXI.
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                                                                                                                                                                                                   Eukaryota, Metazoa, Chordata, Cranjata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catairhidi, Gercopithecidae,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Cercopithecidae,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 217;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 217;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      24942 MW; FF5AA8915131F2BC CRC64;
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                                                                             01-NOV-1996 (TrEMBLrel. 01, last sequence update)
01-NAY-2003 (TrEMBLrel. 23, Last annotation update)
Chorronic somatomammotropin-1.
Macaca muiatta (Rhesus macaque).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         01-NOV-1996 (TrEMBLrel. 01, Last sequence update) 01-MAR-2003 (TrEMBLrel. 23, Last annotation update) Chorionic somatomammotropin-3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        81.9%; Score 21%; DB 6;
78.7%; Pred. No. 9e 21;
live 9; Mismatches 1.
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217 AA
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                                                 01-NOV-1996 (TrEMBLrel, 01, Created)
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PROSITE; PS00266: SOMATOTROPIN_1; 1.
PROSITE; PS00338: SOMATOTROPIN_2; 1.
PRT;
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Pfam; PF00103; hormone; 1.
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                                                                                                                                                                                                                                                                                                                                                                                 TISSUE-Midprequancy placenta;
MEDLINE-94008724; PubMed:8404617;
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MEDLINE-94008724; Pubmed-8464617;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Macaca mulatta (Rhesus macaque)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Best Local Similarity 78.7
Matches 37, Conservative
PRELIMINARY;
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                                                                                                                                                                                                                                                                  Cercopithecinae; Macara
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                                                                                                                                                                                                                                                                                              NCB:_TaxID-9544;
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Eukaryota: Metazoa; Chordata; Craniata; Vertebrata; Futeleostomi; Mammalia; Eutheria; Primates; Platyrrhini; Cebidae; Atelinae; Ateles. NCBI_TaxID=9509;
                                        Ateles geoffroyi (Black-handed spider monkey).
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Wallis O.C., Wallis M.;
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08M174
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                                                                                                                                                                                                                                                                                                                        01-NOV-1996 (TrEMBLrel. 01, Created)
01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
Chorionic somatomammotropin CS-2 (Chorionic somatomammotropin horsone
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDLINE-89307277, PubMed-2744760;
Chen E.Y., Liao Y.C., Smith D.H., Barrera-Saldana H.A., Gelinas R.E.,
Seeburg P.H.;
      Gaps
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Mammalia, Entherias Primates Primates Pranains necisidae, Hemo
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                                                        3 PTIPLSRLFDNAMLRAHRLHQLAFDTYQEFEEAYIPKEQKYSFLQNP 49
                                                                                             75.8%; Score 1-7; DB 4; Length 217;
80.0%; Pred. No. 1.30-18;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       4: Indels
      4; Indels
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Strausberg E.:
Schmitted (JUL-2002) to the EMBL/GenBank/EDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Submitted (JAN-2002) to the EMBL/GenBank/DDBJ databases
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Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                      217 AA
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8; Mismatches
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                                                                                                                                                                                                                                                                          PRT;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             outside of Alu repeats.";
Science 250:1745-1748(1990).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EMBL, JU3071; AAAS2553.;;
EMBL, H1022044; AAH22044.);
EMBL, H1035965; AAH35965.];
HSSP; P01241; 1A22.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   01-MAR-2002 (TrEMBLrel. 20, 01-MAR-2002 (TrEMBLrel. 20, 01-(XTY-2002 (TrEMBLrel. 22,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   46; Conservative
35; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Genomics 4:479-497(1989)
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                                                                                                                                                                                                                                                                          PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                      2).
Home sapiens (Buzan).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Growth hormone.
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Matches
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Mammalia; Eutheria; Primates; Platyrrhini; Callitrichidae; Callithrix.
                                                                                                                                                                                                                                                                                                                                                                  Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               "Characterisation of the GH gene cluster in a new-world monkey, the marmoset (Callithrix jacchus).":
J. Mol. Endocrinol. 0:0.0(2002).
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SEQUENCE FROM N.A.

Revol A., Esquivel D., Santiago D., Harrera-Saldana H.;

Independent duplication of the growth hormone gene in three
Anthropoldean lineages.";

Submitted (APR-2001) to the EMBL/GenBank/DDBJ databases.

EMBL, AFRASS; AAL72287.1;

FILITEPPO. IPROD1400; Somatotropin.

PFO0103; hormone: 1.
                                                                                                                                                                                                                                                                                                                                                                                                             49
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 217;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GROWTH HORMONE LIKE PROTEIN 6
                                                                                                                                                                                                                                                                                                                                                                                                                                        2 FPFIPISRI TUNAMIRAHRIHQLAFDTYQEFEEAYLPKEUKYSFLCNP
                                                                                                                                                                                            PRINTS; PRO0836; SOMATOTROFIN,
PROSTITE; PS00266; SIMATOTROFIN 1; i
PROSTITE; PS05388; SIMATOTROFIN 1; i
SECREXITE; TAX: JC233 MW; 741745A1875A188 IPRO643;
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Last sequence update)
Last annotation update)
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Last annotation update)
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9
                                                                                                                                                                                                                                                                                                                75,0%; Score 195; FB 6; 77,1%; Pred. No. 2.5e-18;
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68.1%; Pred, No. 5.1e 15;
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                                                                                                                                                                                                                                                                                                                                                               5; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Growth hormone-like protein 6 precursor.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Callithrix jacchus (Common marmoset).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRINTS; PROOB36; SOMATOTROPIN.
PROSITE: PSO0338; SOMATOTROPIN_2: i.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRT;
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InterPro; IPR061409; Somatotropin.
Pfam: PF00103; hormone: 1.
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SEQUENCE 217 AA: 25177 MW:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             01-OCT-2002 (TrEMBLrel. 22, 01-OCT-2002 (TrEMBLrel. 22, 01-MAR-2003 (TrEMBLrel. 23,
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                                                                                                                                                                                                                                                                                                        Obery Match
Bost Local Similarity 77.14
Matches 37: Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Best Local Similarity 68.1
Matches 32: Conservative
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SEQUENCE
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        ACCOCCOS OCC CONTRACT CONTRACT
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                                                                                                                                                           MEDLINE-99124645; PubMed-9924177; Libupis A., Nevo E., Mallis M.; Libupis A., Nevo E., Mallis M.; Cibning and characterisation of the gene encoding mole rat (Spalax ehrenberg) growth hormone."; J. Mol. Endocrinol. 22:29-36(1999). EBBLS. AndOSB19; CAA06716.1; C., HSSP; PG1241; JAX1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDITNE: 99160468; PubMed 10051324;
Pertaino A.E., Pomp D., Murray J.D., Howing A.T.;
"Comparative mapping of 18 equine type I genes assigned by somatic
cell hybrid analysis.";
               Spalax leucodon ehrenbergi (Ehrenberg's mole rat).
Eukaryota: Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Spalacinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Eukaryota, Metazoa, Chordata, Craniatu, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Perissodactyla, Equidae, Equus,
NCBL_Taxlb*9796;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match 61.7%; Score 160.5; DB :1: Length 216; Best Local Similarity 68.1%; Pred. No. 1.20-13; Matches 42; Conservative 6: Mismatcher 8; Indels 1;
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01 MAY 2000 (TrEMBLrel. 13, Last sequence update)
01 MAR 2003 (TrEMBLrel. 23, Last annotation update)
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                                                                                                                                                                                                                                                                                                                                             PRINTS, PROBACE SCHARLOTERS IN.
PROSTIE: (SOULEE) SOMALOTER FOR I.
PROSTIE: PSOUCCES, SCHARLOTER FOR I.
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Ptam; PF00103; hormone; 1.
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EMBL; AF097589; AAD25992.1;
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GH.
Equus caballus (Horse).
Growth hormone precursor
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SEUCENCE FROM N.A.
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os 32: Conserv
                                                                                                                                            SEQUENCE FROM N.A.
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                                                                                                   NCBI_TaxID=30637;
                                                                                 Nannospalax.
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                                                                                                                                                                                  Delphinus delphis (Saddleback dolphin) (Black sea dolphin).
Bukaryota: Metazoa: Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia: Euthoria: Cetarliodactyla; Cetacea: Odontoceti: Delphinidae;
                                                                                                                                                                                                                                                                                                                                                                                         Maniou 2., Wallis O.C., Wallis M.; "Clouing and characterisation of the off sere from the examon desphin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
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Skafyoha Metaxoa, Chordata, Craniata, Vertebratu, Euteleostomi,
Mammalia, Euthoria, Carnivora, Fissipedia, Ursidae, Alluropoda.
NCRI_TaxiD-9646.
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Liao M., Zhu M., Zhang A.;
Liao M., Zhu M., Zhang A.;
*Cloning and expression of cDNA encoding growth hormone from Alluropoda melanoleura.";
*Alluropoda melanoleura.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  27 FPAMPLSSLE-LNAVLRAQH:HQLAADTYKEFERAYIPEGGRYS-1QN 72
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       48
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                                                                                                                                                                                                                                                                                                                                                                                                                                          (Delptin is delphis).";
Submitted (JUN 2022) to the EMSL/Aberrank/Cabl Astabases
EMBL: A3492191; CAD37292.);
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Submitted (AUG-2002) to the EMBL/GenBank/DDBJ databases
EMBL; AF540936; AAN77228.1; -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  27 216 GROWTH HORMONS.
216 AA; 24509 MW, 1EC467A84CCFFH02 CR:64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 26 PSTENTIAL.
216 AA: 24.583 MW; 44E017E044B0B056 CR064.
OBMI73 PRELIMINARY; PRT; 216 AA. 08MI73: 010-OCT 2002 (TrEMELrel. 22, Created) 01-OCT-2002 (TrEMELrel. 22, Last sequence update) 01-ORT-2003 (TrEMELrel. 23, Last annotation update) 01-MAR-2003 (TrEMELrel. 23, Last annotation update) Growth hormone precursor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          01-MAR-2003 (TrEMBLrol, 23, Last sequence update)
01-MAR-2003 (TrEMBLrol, 23, Last annotation update)
Growth hormone precursor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1.6e 14;
thes 8;
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6; Mismatches
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68.3%; Pred. No. 1.6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               OBHYES;
01-MAR-2003 (TrEMBLrel. 23, Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PROSITE: PS00266; SOMATOTROPIN_1: 1. PROSITE: PS00338; SOMATOTROPIN_2: 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PKT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     InterFro: IPRUU1406; Somato'ropin.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Pfam; PF00103; Hormone; 1.
PRINTS; PR00836; SOMATOTROPIN.
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Matches 32, Conservative
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216
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                                                                                                                                                                                                                                                                                        NCBI_TaxID=5728;
                                                                                                                                                                                                                                                                                                                                                                    TISSUE LIVER;
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RESULT 11 Q8M173

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SEQUENCE
  RESULT 15
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01-00T-2000 (TFBMBLrel. 15, Created)

01-00T-2000 (TFBMBLrel. 15, Last. sequence update)

01 MAK-2004 (TFBMBLrel. 13, Last. annotation update)

Growth hormone precursor.

Gavia porcellus (Guinea piq).

Eukaryota Metazoa, Chordata: Craniata; Vertebrata; Euteleostomi;

Mammalia: Eutheria: Rodentia: Hystricoquushi: Caviidae: Cavia.

NGHI_TaxID:10141;
                                                                                                                                                                          Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Eutoleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
NCBI_Taxib*10090;
                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
Nauyen I.N.K., Liebhaber S.A.;
"Mouse Growth Hormone Locus: Nurieotide Sequence and Phylogenetic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     27 FPAMPLSSEFSNAVLRACHLHOLAADTYKIJJERAYIPEGGRYS-10N 72
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        6e-13;
es 9; Indels
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Submitted (AUG-1995) to the EMRE/Scorkbox/^{\prime} 4d databases
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27 216 GROWTH HORMONE.
216 AA; 24822 MW; 45996BEL19R08DD3 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       536B18 CRC64:
                                                                   01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update).
101-MAR-2003 (TrEMBLrel. 23, Last annotation update)
Growth hormome.
                           216 AA
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66.0%; Pred. No. 5e
live 6; Mismatches
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PROSITE: PS00246; SOMATOTROPIN.1: i.
PROSITE: PS00348; SOMATOTROPIN.2: 1.
SEQUENCE: 216 AA: 24682 MM: F.22A061
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PHINTS: PROUBTS: SOMATOTROPIN.
PROSITE: PS00266; SOMATOTROPIN_1: 1.
PROSITE: PS00388: SOMATOTROPIN_2: 1.
                        PRT;
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Pfam: PF00103: hormone: 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                       EMBL: U34362; AAC99988.1;
HSSP: P01241; 1AX1.
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Best Local Similarity 66.0
Matches 31; Conservative
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                        PRELIMINARY;
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Matches 29; Conserv
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                           09R2C3
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09JKM4
Q9R2C3
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                   Tarsius bancanus (Western tarsier) (Horsfield's tarsier).
Eukaryota, Motazoa, Chordata, Craniata, Vertobrata, Euteiecstomi,
Mammalia, Eutheria, Primates, Tarsii, Tarsiidae, Tarsius.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   .,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 178;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 58.5%; Score 152; DB 6; Length 17 65.1%; Pred. No. 1.3e 12; ative 8; Mismatches 7; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 20038 MW; F678087512F9H7F0 CRC64;
                                               01-DEC-2001 (TrEMBLrel. 19, Created)
01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-NAR-2003 (TrEMBLrel. 23, Last annotation update)
Growth hormone (Fragment).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Search completed: September 15, 2003, 12:03:27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRINTS: PRO0836: SOMATOTROPIN.
PROSITE: PSO0266: SOMATOTROPIN_1: 1.
PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRELLIMINARY;
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178 AA;
                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
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Human anti-angioge
Chimeric protein,
Human growth hormo
Human growth hormo
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Human nerve growth
Human growth hormo
Fusion protein of
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                                                                                                  September 15, 2003, 11:44:15; Search time 64.6308 Seconds (without alignments) 225.942 Million cell updates/sec
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Cupyright (c) 1993 - 2003 Compugen Ltd.
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    protein search, using sw model

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Listing first 45 summaries
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Match I
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Perfect score:
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Maximum DB seq
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		particularly for the production of human insulin	Nov	obinerio		or seign	. 6	ning human growth borms			_

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chimeric profein acts as an intramolecular chaparone (IMC) for the linsuin precursor, enabling it to fold correctly. A cleavable peptide linsuin precursor enabling it to fold correctly. A cleavable peptide of the chimeric protein to be removed after folding has taken place. Production of recombinant human insulin via an hGH-proinsulin chimeric protein can provide human insulin with correctly linked cystein cridges with fewer necessary procedural steps, and hence resulting in a higher sequences from intracellular degradation by a microorganism host, but also promote the folding of the fused issulin precursor, facilitate the colour, in the folding of the fused issuling precursor, facilitate the colour.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             interactions among the tuston proteins, thus a leaving fielding of the fused hash as processor a recentrally used that can entrations, the procedural steps of cyanamic behavior and related puritized in a respect to this telefinities and related puritized for steps can thus be obtained a grand with the use of high cyanecutations of mercaptan or the use of hydrophobic
                                                                                    sequence represents an N-terminal 1 agment of human growth hormone
                                                                                                            (ACH) which is a component of a chimeric protein (AAY42861) which also contains a human insulin precursor (AAY4289). The AGH portion of the
                        Claim 5; Page 28; 46pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 absorbent resins
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42 AA: Sequence

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1 MEPTIPLSRLFDNAMLRAHRLHQLAFDIYQLE BFAYIPKEQKYSFLQNPQTSLSFSTR 50
                                              0; Caps
               100.0%; Score 47.0; DB 20; Length 92; 100.0%; Pred, No. 5,884.40;
                                              Indels
                                               0:
                                            0; Mismatch s
Ouery Match
Bost Lucai Similarity 100.0
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61 TPSNREETQQKSNLELLRISLLLTQSWLEPVQ 92 င်

RESULT 2 AAW92265

AAW92265 Standard: Protein: 134 AA

08-JUN-1999 (first entry)

AAW92265:

Human acti angloqenic peptide 19K how Met-1Prol33.

Human: anti-angiogenic; prolactin; planeatai lactogen; EFE; angiogenesss; quowth hormone; hGE; hGE; vcapilary endothelial cell proliferation; placeatai vascularisation; pregnancy; treatment; angiogenic disease; tumcur; inhibitor; malignant; angiofibrom; atteriovecous malformation; arthritis; atherosclerotic plaques; corneal graft neovascularisation; wound healing; proliferative relingially in menular degeneration; trachomaternical and alarcoma; occilar, uvellis; fracture; OsleryGeber syndrome; pseriasis; tibroplasia; scleroderma, Raposi's sarcoma; vascular adiosion; quinter; indivadia; reproductive disorder, cantrareptive agent; quent library; pre-eclampsia; intradientic growth retardation;

Home sapiens

W09851323 A1

19-Nov-1998

58WO-US09691 12-MAY-1998; 97US - 0046394. 13-MAY 1997;

(REGC) UNIV CALIFORNIA.

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This invention describes nove; human auti-angiogenic peptides derived from 19 to 150 consecutive amino acids selected from the N-terminal end of from 19 to 150 consecutive amino acids selected from the N-terminal end of human placental hardogen (http://p. human growth hormone (http://p. growth formone variant (hdHvV), or human production, such peptides (i) inhibit capillary endothellal cell proliferation and organisation (ii) inhibit capillary endothellal cell proliferation and organisation (ii) inhibit conferences: in chick chokindal attoic merbrane and (iii) binds to attoin the base of the capillary endothellal cell proliferation and organisation of programmes and products and products and products of the capillary of placental vascularisation during programs are protected and production or growth in a patient or for a subject, for inhibiting tumour formation or growth in a patient or for codulating variant sation of a patient's placental in particulary the codulation variation variations and reprosorous malformation, arthritic such as rheumatoid arthritis, attended proliferative retinopathy such as those occurring or harmony manual proportiate vascular sation in wound healing on harmony proliferative retinopathy such as those occurring or harmony proliferative retinopathy such as diabetic continous, avoitis, and reproductive disorders such as follicalar and tumour. Socilasis, pyoyenic glaucoma, retrolental fibroplasia, schedering variation of conditional levels of N-terminal Iraques can be used as contraceptive agents. DNA conditional levels of N-terminal Iraques of both with pro-eciampsia, intraductine growth retardation, and placental
                                                                                                                       New asti-anglogenic peptides - comprise N-terminal fragments of
                                                                                                                                           human placental lactogen, human growth hormone, growth hormone
  Weiner Ri;
  raylor R,
                                                                                                                                                                                                                 Claim 4: Page 49-50: 87pp; English.
                                                                                                                                                                     variant or human prolactin
  Struman 1,
                                            WPI: 1999 045192/04.
                                                                     N-PSDB; AAX01707
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144 AA; Sedmonse

.. O DB 20; Length 134; Indeis 0 E.86-40; Mismatches 150.0%: Score 470; 100.0%; Pred. No. E .; Conservative Local Similarity 92; Ouery Match

3

61 TPSNREETQCKSNLELLR1 ILLIQSWLEPVQ 92

3

61 IPSNREETOGKSNLELLRISLLIGSWLEPVO 92

AAY42841 standard: proteis: 150 AA AAY42861 KES: H.T

AAY42F61;

19-JAN-2000 (first entry)

Chimeric protein, SEC ID 7.

Insulin: precursor; growth h rmone; chaperone; intramolecular; folding; conformation; chimeric protein; cleavable; recombinant; production; yield

Synthetic

Homo sapiens

Gan Z:

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Human growth hormonic sequent, used at the N-terminal of a fusion profess, which contains a thrombin recognition site, and himan beta nerve growth factor (beta-NGF) at the Citerminal. Heta-NGF can be used to control geriatric dementia and other nervous disorders, and can be released from the fusion protein by incubation with thrombin (see AAN90577-8, AAP91034, AAP91299).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 MEPTIPLSRLFUNAMLRAHRLHULAFDTYQEFEEAYIPKEQKYSFLUNPOTSLSFSESIP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           New human nerve growth factor gene encoding fusion profein
- having cleavage site for thrombin, useful for treating gerlatric
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Recombinant vector contg. fusion protein - consisting of human growth hormone or deriv. ligated to foreign protein, for stability and high yield.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DB 10; Length 140;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               98.9%; Score 465; DB 3 98.9%; Pred. No. 3e-39;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               61 IPSNREETQOKSNLELLRISLLLIQSWLEPVQ 92
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Disclosure; page 21: 38pp; English
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                                                                                                                                     88JP-0035042.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (first entry)
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Best Local Similarity 98.35
Fac 91: Conservative
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                                                                                                                                                                                                                                                                                                                       WPI; 1989-243092/34
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                                                                                                                                                                                               (TOYJ ) TOSOH CORP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 140 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     N-PSDB: AAN90269
                                                                       17.FEB-1989;
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                                                                                                                                     19-FEB-1988;
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                23-AUG-1989.
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01-NOV-1989
                                                                                                                                                                                                                                                             Ohtsuka E:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Niteriniai tradment of human grawt, harmone (http:) of the sequence given in AAY42856, a cleavable peptide linker (AAY42857), and a human masuin of the precursor comprising insulin A and B chains (AAY42859). The http portion of the chimeric protein acts as an intramolecular chaperone (LMC) for the insulin precursor, enabling it to foid correctly. The cleavable of the insulin precursor neabling it to foid correctly. The cleavable of the chimeric protein to be removed after folding has taken place. Production of recombinant human insulin as high profinsulin chimeric protein can provide human insulin with contributing in a higher yield of human insulin with contributing in a higher sequences from intracellular devradation by a microorganism host, but also product the folding of the fused insulin precursor, inclinate the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               interactions among the fusion proteins, thus allowing folding of the fused instill in precursor at commercially useful high concentrations. The procedural steps of cyanogen bromide cleavage, oxidative suphtholysis and related putitication steps can thus be eliminated, along with the use of high concentrations of mercaptan or the use of hydrophobic absorbent.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        solubility of the fusion protein and decrease the intermolecular
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    .;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                100.0%: Score 476; 18 20; Length 150; 100.0%; Pred. No. 1e-39;
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                                                                                                                                                                                                                                             (TONG - ) TONGHUA GANTECH BIOTECHNOLOGY LTD.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Claim 14g taxes to vis 46ppg Baglish
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                                                                                                                           98WO-CN00052
                                                                                                                                                                                     98WO-CN00052
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                                                                                                                                                                                                                                                                                                                                                                     WPI: 1999-610839/52.
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Best Local Similarity
Matches 92: Conserv
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W09950302-A1
                                                                                                                                                                                     31-MAR 1998;
                                                                                                                        31 MAR-1998;
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Sequences

AAP9:041;

RESULT 4 AAP91041

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Gaps

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us-09-423-100-2.rag

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Human: anti-angiogenic; prolactin; placental lactogen; hPL; angiogenesis; quewth hormone; hGH; hGH-V; capillary e dothelial cell proliferation; placental vascuiarisation; pregnancy; i tutment; angiogenic disease; tumout; inhibitor; malignant; angiodibi mu; arteriovenous malformation; arthritis; atherosclerotic plaques; cornwal graft neovascularisation; wound healing; proliferative retinopothy; macular degeneration; trachona; granulation; qlaucomo; ocular; uveitis; fracture; osiar-weber syndrome; psoriasis; tibroplasia; scleroderma; Karosi's sarcoma; vascular adhesion; glere therapy; pre-reclampsia; intraufer; ormitaceptive agent; placention; plucental dystunction.
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                                                                                The invention consists of a vector contq. a fusion protein which is formed by inquting, downstream of a promoter, hGH or a deriv. (pret. formed by subtstn. of Met.-14 with Leu) and a foreign protein. Stability of the vector in the host is greatly increased so the protein yield is higher. (Updated on 25-MAR-2003 to correct PA field.)
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                                                                                                                                                                                                                                                                                                                                                                                 DB 10; Length 192;
                                                                                                                                                                                                                                                                                                                                                                                                                                             1ndels
                                                                                                                                                                                                                                                                                                                                                                             Score 465; DB 10;
Pred. No. 4.2e·39;
0; Mismatches 1
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                       Disclosure: Fig 1: 19pp: Japanese.
                                                                                                                                                                                                                                                                                                                                                                             98.98;
98.98;
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                                                                                                                                                                                                                                                                                                                 192 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Homo Sapiens
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hormone variant (hGH-V), or human prolactin. Such peptides (i) inhibit capillary endothelial cell proliferation and organisation (ii) inhibit angiogenesis in chick chorioallantoic membrane and (iii) binds to at least one specific receptor which does not bind an intact full length hGH, hPL, prolactin or hGH-V. The invention also describes a method for diagnosing a probable abnormality of placental vascularisation during pregnaticy. The peptides can be used for treating an angiogenic disease in a subject, for inhibiting tumour formation or growth in a patient or for
                                                                                                                                                                                          peptidos can be used for proventing or treating e.g. malignant tumours, anglofibroma, arteriovenous mallormation, arthritic such as rheumatoid arthritis, atheroselerotic plaques, corneal graft neovascularisation, delayed wound healing, proliferative retinopathy such as diabetic retinopathy, macular dogeneration, granulations such as those occurring in haemophilic joints, inappropriate vascularisation in wound healing such as hypertrophic sears or begind a reevascular glaucoma, ocular tumour, uveltis, non-union tractures, usier wheer syndrome, psoriasis, pyoqenic alauroma, turnoma, vascularistandi throplasia, scleroderra, solid tumours, feukascia, and reproductive disorders such as foilieu ar and luteal cysts and choricoarcinoma, they can also te used as contraceptive agents. DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 MFPTIPLSRLFGNAMLRAHRLHQLAFDTYQEFEEAYIPKEQKYSFLONPQTSLSFSESIP 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         and choriocarcinemd, they can also be used as contraceptive agents. DNA encoding the peptides can be used in gone therapy. The measurement of abnormal levels of Noterinal fragments of high higher, projectin or hPL can be used in assays for impairment of vascalar development associated with pre-eclampsia, intranterine growth retardation, and placental dystunction.
                                                                                                                                                                           modulating vascularisation of a patient's placenta. In particular, the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Human nerve growth lactor and human growth hormone fision protein.
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geriatric dementia; nervous disorders; human growth hormone.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             98.98; Score 46%; DB 20; 98.98; Pred. No. 4.2e-3%;
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Matches 91, Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Homo sapiens (human).
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AAP91299
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Ohtsuka E;

This invention describes novel human anti-angiogenic peptides derived from 10 to 150 consecutive amino acids selected from the N-terminal end of human placental lactogen (hPL), human growth hormone (hGH), growth

New anti-anglogenic peptides - comprise N-terminal fragments of human placental lactogen, human growth hormone, growth hormone variant or human prolactin

Example 3; Page 49; 87pp; English.

us-09-423-100-2.rag

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262 AA;
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                                                                                                                                                                                             Fision protein consisting of human growth hormone at the Niterminal end (lst region), a 3 amino ucid sequence representing thrombin recoy ition site, and human beta nerve growth factor (beta-NGF) at the C-ferminal. Beta-NGF can be used to control geriatric dementia and other nervous disorders, and can be released from the fusion protein by incubation with thrombin (see AAN96577-8, AAP91634).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 MEPTIPLSRLFDNAMLRAHRLHQLAFDTYÇEFEFAYIPKEQKYSFLÜNPQTSLSFSESIP 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Purifien, of Buman neuron growth factor beta-subunit-contq, protein
by contacting with gel having cation exemange gp. in presence of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Ruman growth hormone/human nerve growth factor beta insion protein.
                                                               New human nerve growth factor gene encoding fusion protein - having cleavage site for thrombin, useful for treating geriatric
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                                                                                                                                                                                                                                                                                                                                                                                                                             Score 465.
Pred. No. :
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                                                                                                                                                     Claim 36; page 31-32; 38pp; English
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98,9%;
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(first entry)
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Matches 91; Conservative
                     WPI; 1989-243092/34
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                                                                                                                                                                                                                                                                                                                                                                                 ZFI AA.
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                                                                                                             dementia, etc.
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25-JUN-1991
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                                                                                                                                                                                                              1 MEPTIPLSRLFONAMLRAHRLHQLAFDTYQEFEEAYIPKEQKYSFLONPQTSLSFSESIP
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                                                                                                                      Gaps
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O
                    DB 12; Length 262;
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Pred. No. 7.3e-39;
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                                                                                                            1; Indels
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               Score 465; DB 12
Pred. No. 6e-39;
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               98.98;
98.98;
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Query Match
Best Local Similarity 98.99
Matches 91; Conservative
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ID AARC
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Gaps

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The polypeptide (AAPB1226) with somatomedin-like activity and the DNA (AANB1605) encoding it are claimed. A Met resicual gp. may be added to the Niterminal. The polypeptide acts on the bone structure of mammals, including humans, to promote bone growth. The polypeptide has high production rate and is easily extracted from bacterial culture medium and refined for use as a bone growth accelerator. (Updated on 25-MAR-2003 to correct PA field.)
                                                                                                                                                        The protein is a direct translation of the upstream tryptophan promoter operator lacking its attenuation sequence and human becances sequence. The product may be efficiently expressed from a transformed E.coli expression system.
                                                                                  Gene segment of human nerve growth factor - used in prodn. of
                                                                                                                                                                                                                                                                                Guery March.

Best Local Similarity 97.8%; Pred. No. 1.2e-59;
Matches 96; Conservative 1; Miscatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Polypeptide with sometomedin like activity by culturing bacterium transformed by plasmid conto, gene segment with specificd DNA sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence of protein with somatomedin-like activity.
                                                                                                 NGF-producing recombinant Escherichia strain.
                                                                                                                                                                                                                                                                                                                                                                                                       Claim 2(1): Page 509: 9pp: Japanese.
                                                                                                                            Claim 32; Page 482; 71pp; Japanese.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAP81226 standard; protein; 138 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (TOY) ) TOYO SODA MES CO LTD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                86JP-0410177
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (updated)
                                                   WPI; 1986-281696/43.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WPI: 1988-232632/33.
N-PSDB: AAN81605.
                                                                                                                                                                                                                                                      26.2 AA:
                     (OTSU/) OTSUKA E.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Growth hormone
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 JP63167798-A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               29-DEC-1986;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            29-DEC 1986;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               25-MAR-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            20-NOV-1990
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 11-300-1988
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Synthetic.
                                                                                                                                                                                                                                                      Sequences
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAP81226;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RESULT 12
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O
                                                                                                                                                                                                                                                                                                                                                                                                                                                 The sequence encoding this protein can be fused with DNA encoding B-cell differentiation factor (1L-6) and lighted into an expression vector for produ. of a fusion protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 MEPTIPLSRLFONAMLRAHRIHQLAFOTYCHER AKIPKEQKYSFLONPQTSLSFSESIP 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Saps
                                                                                                                                                                                                                                                                                                                                                       Preph. of human B-cell differentiation factor - from specified DNA sequence sequence, by recombinant DNA technique, gives protein of specified amino acid sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DB 11; Length 144;
16 39;
s 1; Indels
                                                          Segment of B-cell stimulatory factor-2 (IL-5)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 61 TPSNREETQQKSNLELLHISLLLIGSWLEPVL 92
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Human betainerve growth factor gene prodit
                                                                                          B-cell stimulatory factor-2: interleukin-5.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 462;
Pred. No. 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Mismate
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145..262
                                                                                                                                                                                                                                                                                                                                                                                                                     Disclosure; Page 9; 17pp; Japanese
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Α¥
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAP61633 standard; Protein: 262
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          98.38;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         85JP-0045773
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        85JP-0045773
                                                                                                                                                                                                                  88JP-0162556
                                                                                                                                                                                                                                                88.12-0162556
                             19-JUL-1990 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    25 OCT-1991 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       toral Similarity 97.8 es 90; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                BetainGF: E.coli; ds
                                                                                                                                                                                                                                                                                                          MPI: 1990-062207/09.
N-PSDB: AAQU2028.
                                                                                                                                                                                                                                                                             ARCH HOSCI ( FAOI)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           144 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                See also AAR05311
                                                                                                                                                      JP02013375-A
                                                                                                                                                                                                                                                01 -JUL-1983
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          JP51205485-A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         09-MAR-1985;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        09-MAR-1985;
                                                                                                                           Homo sapiens
                                                                                                                                                                                                                  01 JUL-1988;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Home sapiens
                                                                                                                                                                                     17-JAN-1990
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          11-SEP-1986
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence
AAR05313;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
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Matches

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RESULT :1

Protein

RESULT 13 AAO20110

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The specification describes a method of detecting an exogenously administered substance from a naturally occurring endogenous substance. The exogenous substance being tagged so that it fluoresces differently from the endogenous one at a surtable wavelength. The tagging may consist of one or more substitutions in tagged growth hormone selected from 640%, F52%, W86F, Y, L, I or V F63% or 113%. The method is used to distinguish between exogenously administered substances as compared to naturally occurring endogenous substances. Especially mentioned is the illegal misuse of growth substances by athletes or in domesticated farm animals e.g. cattle. The present sequence represents native finant growth hormone which may be used in the method of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Detection; fluoresce; illegal misuse; growth substance; athlete; domesticated farm animal; cattle; human growth hormone.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               22kDa growth hormone; hGH; mutant; thrombin; resistance,
                                                                      Primary amino acid sequence of native human growth hormone.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 460; DB 20;
Pred. No. 1.3e·38;
0; Mismatches 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               62 PSNREETOOKSNLELLRISHLIJOSWLEPVQ 92
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PSNREETOOKSALELLRISHLIJOSWLEPVO 91
                                                                                                                                                                                                                                                                                                                                                                                                                   Use of tagged exogenous polypeptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Š
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Natural human 22kDa growth Lormone.
                                                                                                                                                                                                                                                                                                                                                                                                                                                 Disclosure, Fig 1; 38pp; English.
                                                                                                                                                                                                                                                                                                                  (GENE-) GENERIC BIOLOGICALS LTD.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               97.98;
98.98;
                                                                                                                                                                                                                                                                                    97GB 0024955
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAY04396 standard; protein;
                                    28-JUL-1999 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Ouery Match
Best Local Similarity 98.95
- has 90; Conservative
                                                                                                                                                                                                                                                                                                                                                   Atkinson A. Marphy JP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  plasmin: decomposition
                                                                                                                                                                                                                                                                                                                                                                                    WPI; 1999-338072/28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 191 AA:
                                                                                                                                                                                                                                                   16-NOV-1998;
                                                                                                                                                                                                                                                                                  14-NW 1997;
                                                                                                                                                      Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             JP11092499-A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              29-JUN-1999
                                                                                                                                                                                                                    27-MAY-1999
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAY04396;
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                                                                  :
:
                                                                                            Z FPTIPLSKLFDNAMLKAHKLHQLAFDTYGEFEEAYIPKEQKYSFLÇNPQTSLSFSSSIPT 61
                                                                                                               2 FPTIPESRLFONAMLRAHKLHQLAFOTYQEFEEAYIPKEQKYSFJONPOISLSFSFSIPT 61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            The invention relates to a serum albumin-growth hormone fusion protein -
useful to treat growth hormone related diseases such as Down's syndrome.
This sequence represents a protein of the serum albumin-growth hormone
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               useful to treat growth
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        97.9%; Score 460; DB 18: Length 191; 98.9%; Pred. No. 1.3e-38;
Live O: Mismatches I: Indels (
                                                                                                                                                                                                                                                                                                                                                                                                            Serum albumin-growth hormone fusion profein; growth hormone;
                                  Length 138;
                                                                 1: Indels
                                DB 9;
3e-39;
                                                                                                                                                                                                                                                                                                                                                                           Protein sequence of the hGH growth hormone cDNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Serum albumin growth hormone fusion protein - i
hormone related diseases, e.g. Down's syndrome
                              Score 460; DB
Pred. No. 3e-
0; Mismatc: s
                                                                                                                                                             62 PSNREETOOKSNLELLRISLLLIQSWLEPVQ 92
                                                                                                                                                                              PSNREETOOKSNLELLRISLLLIOSWLEPVO 91
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PSNREETOOKSNLELLRISLLLIQSWLEPVQ 92
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PSNREETOOKSNLELLRISLLIIOSWLEPVO 91
                                                                                                                                                                                                                                                                                  ξ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Disclosure: Fig 1: 21pp: Korean.
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                              97.98;
98.98;
                                                                                                                                                                                                                                                                             AANZOllo stanfard: Froreign
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         95GB-0026733
96WO-GB03164
                                                                                                                                                                                                                                                                                                                                              (first entry)
                                                               Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        90; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CONA of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WP1: 1997 363680/55
                                              Best Local Similarity
Matches 90; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           141 AA;
138 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              N-PSDB; AAK99565
                                                                                                                                                                                                                                                                                                                                                                                                                               Down's syndrome
                                                                                                                                                                                                                                                                                                                                          06-AUG-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            KR99076789-A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           30 - DEC - 1995;
19 - DEC - 1996;
                                                                                                                                                                                                                                                                                                                                                                                                                                                             Unidentitied
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            25 JUN-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           15-OCT 1999
Seguence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence
                                                                                                                                                                                                                                                                                                            AAG231103
                             Query Match
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Indeis

Length 19 ;

9 61

Query Match

g ó RESULT 14 AAY15809 ID AAY1

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The prosect invention describes a human erach harmone and and the 18th The and the 18th The are replaced respectively by Aspland From the 18th The and sequence of statual type human az king growth harmone (half) and which has a resistance adalost decomposition by thrombin. The present sequence represents the natural half. Also and the 14th has a resistance adalost the 18th The and the 140 hubbs are placed respectively by Asp. Pro and Ala in the amino acid sequence of natural type holf and which has a resistance amino acid sequence of natural type holf and which has a resistance preparation containing the above holf mut at as the active component. The mutant holf shows a nactivity approximately equivalent to that of natural type holf and solve the active component.
                                                                                                                                                                                                              A human growth hormone mutant - with equivalent activity to natural human growth hormone
                                                                                                                                                                                                                                                                       Example 1: Page 5-6; 10pp; Japanese,
                                                       97JP-0275277.
                                                                                            97JP-0275277
                                                                                                                                   (SUMU ) SUMITOMO SEIYAKU KK
                                                                                                                                                                        WPI; 1999-283567/24
                                                       22 · SEP - 1997;
                                                                                            22-SEP-1997;
                  06-APR-1999
```

Sequence 191 AA;

Gaps Ouery Match 97.9%; Score 460; DB 20; Length 191; Best Local Similarity 98.9%; Pred. No. 1.3e-38; Matches 90; Conservative 0; Mismatches 1; Indels 0;

2 FPTIPLSRLFDNAMLRAHRLHQLAFDTYOEFEEAYIPKEOKYSFLONPQISLSFSFSIPT 61

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Search completed: September 15, 2003, 12:00:57 Job time : 65,6408 secs

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GenCore version 5.1.6
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OM protein . protein search, using sw model

September 15, 2003, 11:57:40; Search time 21.1039 Seconds (without alignments) 184.449 Million cell updates/sec Run on:

US-09-423-100-2 470 1 MFPTIPLSRLEDNAMLRAHR......NJELLRISIALIQSWLEPVO 92 Title: Perfect score:

Scoring table:

Sequence:

(28317 seqs, 42 (19458 residues BLOSUM62 Gapop 10:0 - Gapoxt 0.5 Searched:

Total number of hits satisfying chosen parameters:

length: 2000000000 length: 0 Minimum DB seq Maximum DB seq Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Issued_Patents_AA:* Database :

/cqn2_6/ptodata/1/jaa/6B_COMB.pep:*/cqn2_6/ptodata/1/jaa/PCTUS_COMB.pep:*/cqn2_6/ptodata/1/jaa/ba kfiles1.pep:* 1: /cgn2_6/ptodata/1/iaa/5A 'OMB. pep:* 2: /cgn2_6/ptodata/1/iaa/5B COMB. pep:* 3: /cgn2_6/ptodata/1/iaa/6A_COMB. pep:*

Pred. No. is the number of results producted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Posmili		ر اورون				
NO.	Score	Match	Length	DB	ſſ	Description
	465	6.85	192		US-08-093-383-1	Sequence 1, Appli
2	460	97.9	191	4	US-09-284 878-5	2
~	460	97.9	194	~	US-08-383-621-4	4
4	460	97.9	194		US-08-459-906-4	4
2	460	97.9	217	~	US-08-589-028-10	10,
ۍ	460	97.6	217	m.	US 08-784-582 0	10,
7	460	97.9	217	~	US-08-785-271	10,
ထ	460	97.9	217	~	US-08-759-628	-
ಶ	460	67.6	217	4	US-09-284-878-1	_`
10	460	67.6	241	4	US-09-424-620B-25	Sequence 25, Appl
11	460	97.9	245	ಶ	US-08-280-030-66	99
12	460	9.79	274	~	US-08-784 582-71	71,
13	460	97.9	360	٣.	US-08-784-582-73	73,
14	454	9.96	191	4	US-09-465-461 1	'n
7.5	454	9.96	217	-	US-08-187-756C-4	4
16	454	9.96	217	-	US-08-469-486.51	51
17	454	9.96	217	7	US-08-469-658-51	51
18	454	9.95	217	~	US-08-710-324A-4	4
19	454	9.96	217	4	US-09-411-657-4	Sequence 4. Appli
20	453	4.96	400	❖	US-09-420-819-17	Sequence 37, Appl
21	453	96.4	401	₹	US-09-420-819	36,
22	447	95.1	191	~	US-08-800-215t. 8	Sequence 18, Appl
23	445	94.7	191	~	US-08-800-215C-16	16,
24	4	94.7		m	-08	Sequence 20, Appl
25	364.5	•	176	٣	US-08-791-728-1	٦, ٩
56	364.5	77.6	176	❖	- 08 -	'n
27	358.5	76.3	176	m	US-08-791-728-2	Sequence 2, Appli

LENGTH: 192 amino acids TYPE: amino acid

sednence : Appli	1 878 776-79-86	 	6.4.7	2.887	î.
Sequence 3, Appli	05-07-963-3310-3	1.40	63.7	5.667	44
Sequence 3, Appli	US-09:105:651-3	216 2	64.1	401.5	43
Sequence 1, Appli	US-08-459-906-1	193 3	64.1	301.5	42
Sequence 1, Appli	US-08-383-621-:	193 2	64.1	301.5	41
7	US-08-363-582-2	193]	64.3	301.5	0 \$
2,	US-07-621-197C-2	193 1	64.1	301.5	39
Patent No. 521018	5210180-1	191 6	54.1	301.5	38
Sequence 2, Appl.	US-09-277-720-2	190 4	54.1	301.5	37
Sequence 2, Appl	US-08-388-267C-2	190 1	64.1	301.5	36
Sequence 1, Appl.	US-09-105-651-1	216 2	64.4	302.5	35
	US-07-963-331D-4	191 1	64.8	304.5	34
Sequence 8, Appli	US-08-468-824-8	191 1	65.2	306.5	33
Sequence 5, Appl	US-09-411 657.5	198 4	71.0	333.5	32
	US-08-710-324A-5	198 2	71.0	333.5	31
Sequence 5, Appl	US-08-187-756C-5	158 1	71.0	333.5	30
Patent No. 542419	5424199-3	168 6	72.3	340	58
Sequence 2, Appli	US-08-990-774-2	176 4	76.3	358.5	78

ALLIGNMENTS

```
APPLICANT: DeBoer, Herman A.
APPLICANT: Beyneker, Herman A.
APPLICANT: Beyneker, Herbert I.
APPLICANT: Seeburg, Peter H.
TITLE OF INVENTION: DNA for Expression of Bovine Growth Hormone CORRESPONDENCE ADDRESS:
ADDRESSEE: Geneblech, Inc.
STREET: 460 Point San Bruno Blvd
CITY: South San Francisco
STATE: California
                                                                                                                                                                                                                                                                                                                                                                                                      ZIP: 94080
COMPUTER READABLE FORM:
MEDIUM TYPE: 5.25 inch, 360 Kb floppy disk
COMPUTER: 1BM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SOFTWARE: pails (Generated)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/093,383
FILING DATE: 14-34L-1993
CLASSIFICATION NUMBER: US/08/093,383
FILING DATE: 28-NOV-1990
PRIOR APPLICATION NUMBER: 07/19824
FILING DATE: 28-NOV-1990
APPLICATION NUMBER: 07/19834
FILING DATE: 05-APK-1988
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 06/3361
FILING DATE: 19-3UL-1984
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 06/30367
FILING DATE: 18-SEP-1981
ATTORNEY AGENT: 18-SEP-1981
ATTORNEY AGENT: 18-SEP-1981
                                                Sequence 1, Application US/08093383
Patent No. 5489529
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NAME: Johnston, Sean A. RECISTRATION NUMBER: P35,910 REFERENCE/DOCKET NUMBER: 46c4 TELECOMMUNICATION INFORMATION: TELECOMMUNICATION 18F025-3562
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TELEX: 910/371-7168
INFORMATION FOR SEQ 1D NO: 1:
SEQUENCE CHARACTERISTICS:
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RESULT 1
US-08-093-383-1
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Webster, Darryl L
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Matches 90; Conservative
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COMPUTER READABLE FORM:
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FRY: U.S.A.
07470-8426
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                                                                                                                            FILING DATE:
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STREET: On
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                                                                                                                                         0: Caps
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                                                                                      0:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 460, DB 4; Length 191;
Pred. No. 60-51;
0; Mismatches i: Indels
                                                    Score 465; DB 1; Length 192;
Pred. No. 1.4e-51;
                                                                                      1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  E: Dr. Estelle J. Tsevdos
1937 West Main Street, P.O. Box 60
                                                                                                                                                                                        61 TPSNREETQQKSNLELLRISLLIJQSWLEPVQ 92
                                                                                                                                                                                                          6: TPSNREETOOKSNLELLRISLLLIGSWLEPVO 92
                                                                                                                                                                                                                                                                                                                                                        APPLICANT: Saldana, Martha Guerrero
APPLICANT: Saldana, Hugo Barrera
APPLICANT: Saldana, Hugo Barrera
APPLICANT: Salvado, Jose Maria Viader
TITLE OF INVENTION: Genetically Modified of
TITLE OF INVENTION: Production and Secretic Bride Represence: 1829-0010000
CORRENT APPLICATION NUMBER: US/09/284,87b
CORRENT FILLNG DATE: 1999-07-21
PRIOR FILING DATE: 1997-10-24
NUMBER OF SEQ ID NOS: 9
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                                                                                     0; Mismatches
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Patent No. 5951972
GENERAL INFORMATION:
APPLICANT: Daley, Michael 3.
APPLICANT: Buckwalter, Brian L.
APPLICANT: Cady, Susan M.
APPLICANT: Chay, Susan M.
                                                                                                                                                                                                                                                                                                          Sequence 5, Apr. Cation US/UC244878; Patent No. 6442375; GENERAL INFORMATION:
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                                                98.98;
98.98;
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                                       Ouery Match
Best Local Similarity 98.98
Watches 91; Conservative
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Best Local Similarity 98.9%
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ; ORGANISM: Homo sapiens
US-09-264-878-5
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TOPULOGY: linear
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US-09-284-878-5
     ) 10FCLVO1
US-08-093-383-1
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2 FPTIPLSRLFUNAMLKAHRLHQLAFUTYQEFEBAYIPKEQKYSFLQNPQTSLSFSESIPT 61
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APPLICANT: Buckwalter, Brian I.
APPLICANT: Buckwalter, Brian I.
APPLICANT: Carly, Susan M.
APPLICANT: Shieh, Hong-Ming
APPLICANT: Solich, Peter
APPLICANT: Soldon, Andrew P.
TITLE OF INVENTION: Stabilization of SomatoLropins and Other
TITLE OF INVENTION: Proteins by Modification of Cysteine Residues
CORRESPONDENCES: 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     97.9%; Score 460; DB 2; Length 194;
98.9%; Pred. No. 6.1e-51;
Live 0; Mismatches 1; Indels
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/183.621
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COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
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One Cyanamid Plaza
                                                                                                                                                                                                                                                                                                                           NAME: Tsevdos, Estelle J.
RECISTRATION NUMBER: 31,145
REFERENCE/DOCKET NOMBER: 31,278-01
TELECOMMUNICATION: INFORMATION:
                                                                                                                                                                                                 CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/766,142
FILING DATE: 25-5EP-1991
ATTORNEY/AGENT INFORMATION:
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FILING DATE: 02-JUN-1995
CLASSIFICATION: 514
                                                                                                                                            UMBER: US/08/383,621
06-FEB-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 4, Application US/08459906
Patent No. 6010999
                                                                                                                                                                                                                                                                                                                                                                                                                                                       TELLEFAX: 203-321-2971
TELLERX: 203-770-474-4059
INFORMATION FOR SEQ ID NO: 4.
SEQUENCE CHARACTERISTICS:
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amino acid
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38.9%;

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Best Local Similarity 98.9
Matches 90; Conservative
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                                                                                                                                                                                                                                                                                        C, Gaps
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Pred. No. 6.1e-51;
0; M.Smarches 1; indels
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SVETWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                 62 PSNREETQQKSNLELLRISLLLIQSWLEPVU 32
                                                                                                                                                                                                                                                                                                                                                                                                                   NAME: Highlander, Sloven I.
REGISTATION NUMBER: 47,642
REFERENE, DOCKET NUMBER: UISD: 426-HY
TELEY AMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: Newgard, Christopher B. APPLICANT: Halban, Philippe APPLICANT: Ho. 6087129mington, Karl D. APPLICANT: Clark, Samuel A. APPLICANT: Thigpen, Anice E.
                    31,278-03
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICATION NUMBER: US/08/589.028
FILING DATE: CONCULTENTLY HEREWILL
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STREET: P. C. Box 4433
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Patent No. 6087129
REGISTRATION NUMBER: 34,276
REFERENCE/POCKET NUMBER: 31.
TELECOMMUNICATION INFORMATION:
TELEDHONE: 201-831-3247
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
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Kruse, Fred
                                                                    TELEFAX: 201-841-3505
INFCRMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 194 amino acids
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Best Local Similarity 98.9%;
Matches 90; Conservative (
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INFORMATION FOR SEQ ID NO: 10:
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amino acid
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                                                                                                                                                                                      ; MOLECULE TYPE: protein US-08-459-906-4
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MEDIUM TYPE: Floppy
                                                                                                                                                    TYPE: amino acid
TOPOLOGY: linear
                                                                                                                                                                        linear
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US-08-589 028-10
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APPLICANT:
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Length 217;

DB 3;

97.9%; Score 460;

Query Match

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                                                       2 FPTIPLSRLFONAMLRAHRLHQLAFDTYGEFEERYIPKEQKYSFLGNPQTSLSFSESIPT 61
                                                                                2 FPTIPLSRLFDNAMLRAHRLHQLAFDTYQEFEEAYIPKEQKYSFLUNPQTSLSFSFSIPT 61
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                     Gaps
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Pred. No. 7.1e-51;
0; Mismatches 1; Indels
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SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/784,582
FILING DATE: Concurrently Herewith
                                                                                                                                 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                          Halban, Philippe A.
No. 6119257mington, Karl
Clark, Samue: A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/028,427
FILING DATE: 15-0CT-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US U8/589,028
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICATION NUMBER: US U8/589,028
FILING DATE: 19-JAN-1996
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NAME: Highlander, Steven L.
REGISTRATION NUMBER: 37,642
REFERENCE/DOCKET NUMBER: UTSD:514
TELECOMMUNICATION INPORMATION:
                                                                                                                                                                                                                                                                                                                  GENERAL INFORMATION:
APPLICANT: Newsard, Christopler B.
                                                                                                                                                                                                                                                                              Sequence 13, Application US/08784582
Patent No. 6116707
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-
                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: Quadde, Christian
                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: Thigpen, Anice E.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: McGarry, Dennis
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Best Local Similarity 98.9%
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INFORMATION FOR SEQ ID NO:
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CITY: Houston
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ADDRESSEE: Arnold, W
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
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APPLICANT: Rock, Fernando L. APPLICANT: Bazan, J. Fernando APPLICANT: Bazan, J. Fernando APPLICANT: Kastelein, Robert A. APPLICANT: Kastelein, Robert A. NUMBER OF SRQUENES: 11 CORRESPONDENCE ADDRESS: 11 CORRESPONDENCE ADDRESS: ADDRESSE: DNAX Research institute GTREET: 901 California Avenue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 217;
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CTHER INFORMATION: /note: "The peptides above are corner in Figure 1"
US-08-759-628-11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-005/MS-DOS
SOFTWARE: Patentin Helease #1.0, Version #1.30
CUBRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       97.9%; Score 460; DB 3; 98.9%; Pred. No. 7.1e-51;
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FILLING DATE: 05-7E: 1996
PLASSIFICATION: 445
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRIOR APPLICATION DATA: APPLICATION NUMBER: US 60/008.574 FILING DATE: 06-DEC 1995 ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NAME: Ching, Edwin P.
REGISTRATION NUMBER: 34,C ±
REFERENCE/DOCKET NUMBER: 1x05520
TELECOMMUNICATION 1NFORMATION:
TELEPHONE: 415-852-9196
TELEFRAX: 415-496-1200
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INFORMATION FOR SEQ ID NO: 11:
SEQUENCE CHARACTERISTICS:
LENGTH: 217 amino acids
TYPE: amino acids
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
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Best Local Similarity 96.7-
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STRANDEDNESS: single
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133..153
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32..53
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94..115
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LOCATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                   COUNTRY:
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US-09-284-878-1
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APPLICANT: Newgard, Christopher B.
APPLICANT: Newgard, Christopher B.
APPLICANT: New 194176minqton, Karl D.
APPLICANT: Clark, Samuel A.
APPLICANT: Clark, Samuel A.
APPLICANT: Cuade, Christian
APPLICANT: Thigpen, Anice E.
APPLICANT: Wruse, Fred
TITLE OF INVENTION: RECEMBINANT EXPRESSION OF PROFFINS FROM
TITLE OF INVENTION: SECRETORY CELL: INES
NUMBER OF SECURIORS: SE
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tive 0: Mismatches 1; Indels
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COMPUTER: 1BM PC COMPALIBLE
OPERATING SYSTEM: PC-FOS/MS-FXS
SOFTMARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
FILING DATE: Concurrently Herewith
CLASSIFICATION: 435
    62 PSNREETQQKSNLELLRISLLLIQSWLEPVC 92
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P.O. Box 4433
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                                                                                                                                                                                                                                                                                                         Sequence 10, Application US/08785271
Patent No. 6:94176
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Matches 90: Conservative
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MEDIUM TYPE: Floppy
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GENERAL INFORMATION:
APPLICANT: Sato, Seiji
APPLICANT: Hoparantion:
APPLICANT: Hoparantanian and Applicant: Hoparantanian and Applicant: Hoparantanian and Applicant: Hoparantanian and Applicant: Kebanguak Applicant: Kebanguak Applicant: Kebanguak Encoding New Fusion Professor Portificant: Norwition: Dass Encoding New Fusion Preferation of THE TITLE OF INVENTION: DASS TITLE OF INVENTION: DASS TITLE OF INVENTION: DASS TITLE OF INVENTION: DASS TITLE OF INVENTION: HUMBER: US/09/280,030A
CURRENT APPLICATION JMER: US/09/280,030A
CURRENT FILING DATE: 1999-03-26
EARLIER APPLICATION JMER: JPIG-87339/1998
EARLIER PILING DATE: 1998-03-31
NUMBER OF SEQ ID MSS: 66
  2 FPTIPLSRLFUNAMLRAHRLHQLAFDTYQEFEEAYIPKEQKYSFLONPGTSLSFSESIPT 61
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TITLE OF INVENTION: RECOMBINANT EXPRESSION OF PROTEINS FROM
TITLE OF INVENTION: SECRETORY CELL LINES
NUMBER OF SEQUENCES: 79
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         97.9%; Score 460; DB 4; Length 245;
98.9%; Pred. No. 8.4e<sup>.</sup>51;
tive 0; Mismatches 1; Indels
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                                                                                                                      111 PSNREETQQKSNLELLRISLLLIQSWLEPVQ 141
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APPLICANT: Habban, Philippe A.
APPLICANT: No. 610707mington, Karl D.
APPLICANT: Clark, Samuel A.
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Patent No. 6110707
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APPLICANT: Thigpen, Anice E.
APPLICANT: Quade, christian
APPLICANT: Kruse, Fred
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STREET:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FEATURE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RESULT 12
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         APPLICANT: Salvado, Jose Maria Viader
TITLE OF INVENTION: Genetically Modified Methylotrophic P. pastoris Yeast for the
TITLE OF INVENTION: Genetically Modified Methylotrophic P. pastoris Yeast for the
TITLE OF INVENTION: Production and Secretion of the Human Growth Hormone
FILE REFERENCE: 1829.0010000
CURRENT APPLICATION NUMBER: US/09/284,878
CURRENT FILING DATE: 1999.07-21
PRIOR APPLICATION NUMBER: POT/MX97/00033
PRIOR FILING DATE: 1997-10-24
NUMBER OF SEQ ID NOS: 9
SOFTWARE: Patentin Ver. 2.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEONG, Baik-Lin
TITLE OF INVENTION: Process for prejuring recombinant professing highly
efficient expression vector from Sach romyces cerevisiae
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                                                                                                                                                                                                                                                                                                                                                                                               Ouery Match
Best Locui Simularity 98.9%; Pred. No. 7.16-51;
Matches 90; Conservative 0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 460; DB 4; Length 241;
Pred. No. 8.2e-51;
0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COUNTRY: U.S.A.
ZIP: 06510-2802
CHMOTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.5 inch, 1.44 Mb storage
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CORRESPONDENCE ADDRESS:
ADDRESSEE: BACHMAN & LAPOINTE, P.C.
STREET: Suite 1201, 900 Chapel Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: HANIL SYNTHETIC FIBER CO., LTD.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              62 PSNREETOOKSNLELLRISHLINGSWIEPV 92
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CURRENT APPLICATION DATA:
APPLICATION DOMBER: US/09/424,620B
FILING DATE: 24-ND. 6391545 1999
INFORMATION FOR SEQ ID NG: 25:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER: IBM
OPERATING SYSTEM: WINDOWS 95/98
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MOLECULE TYPE: PROTEIN
SEQUENCE DESCRIPTION: SEQ ID NO: 25:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       US-09-424 6208-25

: Sequence 25, Application US/094246208

: Patent No. 6391585

: GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LENGTH: 241 amino acids TYPE: amino acid
Saldana, Hugo Barrera
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MOON, Jae-Woong
HAE, Cheon-Soon
YANG, Doo-Suk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Ki-Ryong
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   97.98;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE CHARACTERISTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LEE, Jee-Won
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CITY: New Haven
STATE: Connecticut
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SOFTWARE: MS WORD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Ouery Match
Best Local Similarity 98.9
Matches 90: Conservative
                                                                                                                                                                                                                                                                                                                             ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  JANG.
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                                                                                                                                                                                                                                                                                LENGTH: 217
                                                                                                                                                                                                                                                                                                                                                   US-09-284 878-1
                                                                                                                                                                                                                                                     SEQ ID NO 1
                                                                                                                                                                                                                                                                                                       TYPE: PRT
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O
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APPLICANT: Halban, Philippe A.
APPLICANT: No. 6110707mington, Karl B.
APPLICANT: Clark, Samuel A.
APPLICANT: Thiqpen, Anice E.
APPLICANT: Clark, Samuel A.
APPLICANT: Winse, Fred
APPLICANT: Moderny, Dennis
APPLICANT: Kruse, Fred
APPLICANT: Kruse, Fred
APPLICANT: Kruse, Fred
APPLICANT: McGarry, Dennis
APPLICANT: McGarry, Pennis
APPLICANT: McGarry, Pennis
APPLICANT: McGarry, SECRETORY CELI. LINES
NUMBER OF ESQUENCES: 79
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            97.9%; Score 460; DB 3; Length 274; 98.9%; Pred; No. 9.9e 51;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       : Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDIUM TYPE: Floppy disk
COMPUTER: 18H PC compatible
OPERATING SYSTEM: PC-000/ANS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
                                                                                         on #1.30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             0; Mismatches
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC Compartible
COMPUTER: BW PC COMPATION
CHERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN Release #1.0, Ver. on
CHERENT APPLICATION DATA:
APPLICATION NUMBER: US/08/784,582
FILING DATE: CONCULTERLIY HETEWITH
CLASSIFICATION: 435
                                                                                                                                                                                  PRIOR APPLICATION: 433
PRIOR APPLICATION NUMBER: US 60/028,427
FILING DATE: 15-0CT-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/589,028
FILING DATE: 19-JAN-1996
ATTOKNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                          NAME: Highlander, Stever I.
REGISTATION NUMBER: 37.642
REFERENCACKET NUMBER: 17.51 9.14
TELEPHONE: 512/418-3000
TELEPHONE: 512/418-3000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     5: Arnold, White & Durkee
P.O. Box 4433
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICATION NUMBER: US/08/784,582
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        US-08-784-582 73
; Sequence 73, Application US/08784582
; Patent No. 6110707
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     INFORMATION FOR SEQ ID NO: 71: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 274 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Ouery Match
Best Local Similarity 98,9%
warehos 90; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CURRENT APPLICATION DATA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Houston
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Texas
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           77210
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                US-08-784-582 71
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STREET:
CITY: HO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COUNTRY:
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GENERAL INFORMATION:
APPLICANT: CHAPPEL, SCOTT
APPLICANT: CHAPPEL, SCOTT
TILLE OF INVENTION: after hematopoietic stem cell transplantation in humans
FILLE DETERBRUE: CHAPPELLE.
CURRENT APPLICATION NUMBER: 05/09/465,461
CURRENT FILING DATE: 1999-12-17
PRIOR APPLICATION NUMBER: 60/712,668
PRIOR FILING DATE: 1999-12-17
PRIOR FILING DATE: 1999-12-17
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       2 FPTIPLSRLFDNAMLRAHRIHQLAFDTYQEFFEAYIPKEQKYSFLQNPOTSLSFSESIPT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              .
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              l; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Ouery Match 97.9%; Score 460; DB 3; Bost Local Similarity 98.9%; Pred. No. 1.4e 50; Matches 90; Conservative 0; Mismatches 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  62 PSNREETQQKSNLELLRISLLLIQSWLEPVQ 92
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             62 PSNREETQQKSNI,ELLRISI,LLIQSWLEPVO 92
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    61 PSNREETQQKSNLELLRISLLLIQSWLEPVQ 91
             CLASSIFICATION 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
ELING DATE: 15-OCT-1996
PRIOR APPLICATION DATA:
APPLICATION DATE: 08/589,028
FILING DATE: 19-JAN-1996
ATYORNEY/AGENT INFORMATION:
NAME: Highlander, Steven I.
REGISTRATION NUMBER: 37,642
Concurrently Herewith
                                                                                                                                                                                                           REGISTRATION NUMBER: 37,642
REFERENCE/DOCKET NUMBER: UTSD:514
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ; Sequence 4, Application US/08187756C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 1, Application US/09465461
Patent No. 6348444
                                                                                                                                                                                                                                                                           TELEPHONE: $12/418-3000
TELEFAX: $12/474-757
INFORMATION FOR SEC 10 NO 73:
SEQUENCE CHARACTERISTICS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SOFTWARE: Patentin version 3.1
                                                                                                                                                                                                                                                                                                                                                                        360 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Ouery Match
Best Local Similarity 97.8%
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ORGANISM: homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                        amino anid
                                                                                                                                                                                                                                                                                                                                                                                                                                      linear
                                                                                                                                                                                                                                                                                                                                                                                                          STRANDEDNESS
                                                                                                                                                                                                                                                                                                                                                                                                                                      ;
US-08-784-582-73
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              US-08-187-756C-4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LENGTH: 191
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              US-09-465-461-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         09-465-461-1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RESULT 14
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Ouery Match 96.5%; Score 454; UB 1; Length 217; Best Local Similarity 97.8%; Pred. No. 4.2e-50; Matches 89; Conservative 0; Mismatches 2; Indels 0; Gaps
Patent No. 5597709
GENERAL INFORMATION:
APPLICANT: ROSEM:
1TILLE OF INVENTION: Human Growth Hormone
NUMHER OF SROUENCES: 7
CORRESSORDENCE ADDRESS: 7
CORRESSORDENCE ADDRESS: 7
AUDRESSE: CECCHI, STEWART & OLSTEIN
SIREET: 6 BECKER FARM ROAD
CITY: HOSELAND
STATE: NEW JERSEY
COUNTRY: USA
ZIP: 0706M:
                                                                                                                                                                                                                                                                                                                                   COMPUTER: IRM ESCA
SOFTWARE: WAS FERD.
SOFTWARE: WAS FERD.
SOFTWARE: WAS FERD.
SOFTWARE: WAS FERD.
APPLICATION NUMBER: US/UB/197,75437
CLASSIFICATION: 435
PRIOR APPLICATION 435
PRIOR APPLICATION A35
PRIOR APPLICATION OFTA:
FILING DATE:
FILING DATE:
FILING SATE:
FILING SATE:
FERRAROY GREGORY D.
RESISTRATION NUMBER: 325800-55
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TELEFAX: 201-994-1744
INFORMATION POR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
FENGTH: 217 AMINO ACHOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TOPOLOGY: LINEAR
MAULECULE TYPE: PROTEIN
US-08-187-7560-4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TYPE: AMINO ACID
STRANDEDNESS:
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62 PSNREETQQKSNLELLRISHLIJQSWLEPVQ 92

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Search completed: September 15, 2003, 12:05:31 Job time: 22,1039 secs

GenCore version 5.1.6 Copyright (c) 1993 - 2003 Compugen Ltd.

OM protein - protein search, using sw model

September 15, 2003, 12:03:35; Search time 38.5805 Seconds Run on:

(without alignments) 347.945 Million cell updates/sec

3.7

US-09-423-100-2 470

1 MEPTIPLSRLFDNAMLRAHR.......NLELLRISLLIOSWLEPVO Title: Perfect score: Sequence:

Gapop 10.0 , Gapext 0.5 HLCSUM62 Scoring table:

541935 seqs. 145917426 residnes Searched:

Total masker of hits satisfying chosen parameters:

Minimum OB seq length; 0 Maximum OB seq length; 2000000000

Post-processing: Minimum Match 0% Maximum Match 100%

Listing first 45 summaries

Database :

/cgn2_6/ptodata/1/pubpaa/US09_NEW_PUB.pep: •
/cgn2_6/ptodata/1/pubpaa/US10A_PUBCOMB.pep: •
/cgn2_6/ptodata/1/pubpaa/US10C_PUBCOMB.pep: •
/cgn2_6/ptodata/1/pubpaa/US10C_PUBCOMB.pep: •

/cqn2_6/ptodata/1/pubpaa/US10_NEW_PUB.pep:*/cqn2_6/ptodata/1/pubpaa/US60_NEW_PUB.pep:* /cgn2_6/ptodata/1/pubpaa/US60_PUBCOMB.pep:* Pred. No. is the number of results predicted by chance to have a score areafor than or egoal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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Result No.	Score	Ouery Match	Duery Match Length DB	03	10	Description
-	470	100.0	6.	7	US-10-054-8 \ \cdot 2	Sequence 2, Appli
~	470	100.0	150	14	US-10-054 8.3-7	Sequence 7, Appli
**	460	97.9	191		US-09:984-010-23	Sequence 23, Appl
4	460	97.9	191	12	US-10-153 207-1	Sequence 1, Appli
٧	460	97.9	191	12	US-10-400-377-1	_
9	460	97.9	191	12	US-10-400-708-1	
7	460	97.9	214	12	US-10-153-207-6	9
œ	460	97.8	217	6	US-09-929-918-9	Sequence 9, Appli
5	460	97.9	245	6	US-09-280-030-66	Sequence 56, Appl
10	454	96.6	217	σ	US-09-853-688-2	Sequence 2, Appli
11	454	9.96	217	12	US-09-969-748C-4	Sequence 4, Appli
12	45.	96.4	217	10	US-09-804-409A-16	Sequence 16, Appl
13	447	95.1	217	6	US-09-853-688-4	Sequence 4, Appli
14	444	94.5	191	12	US-09-824-200-12	Sequence 12, Appl
15	396	84.3	217	6	US-09-850-887-3	Sequence 3, Appli

LENGTH: 92 amino acids

TYPE: amino acid

SEQUENCE CHARACTERISTICS

Sequence 3.0, App Sequence 2, Appli Sequence 411, App Sequence 18, Appl Sequence 18, Appl		Sequence 2, Appli Sequence 14, Appl Sequence 32, Appl Sequence 33, Appl Sequence 33, Appl Sequence 26, Appl	sequence 27, Appl sequence 21, Appl sequence 22, Appl sequence 21, Appl sequence 25, Appl sequence 2, Appl sequence 27, Appl	Sequence 24, Appl Sequence 18, Appl Sequence 15, Appl Sequence 13, Appl Sequence 1, Appl Sequence 20, Appl
5 US-10-043-487-350 2 US-10-353-207-2 5 US-10-103-313-411 5 US-10-188-246-18	4 US-10-054-873-1 4 US-10-054-873-6 5 US-10-191-879-19 10-10-191-879-10 5 US-10-043-467-337	0 US-09-887-569A-2 2 US-10-122-746-4 1 US-09-876-478-14 5 US-10-140-293-33 5 US-10-140-293-33	5 0S-10-140-243-27 5 0S-10-140-243-22 5 0S-10-140-243-22 5 0S-15-140-24-21 4 0S-10-0-0-6-969-2 4 0S-10-19-1	5 18-10-140-293-24 5 18-10-140-293-18 5 18-10-140-293-19 5 18-10-140-293-13 2 08-10-140-293-13 2 08-10-140-293-20
	444444	355 388 388 198 198 199		1999 1 1999 1 1997 1 197 1 1999 1
81.1 81.1 79.4 73.4	885.38 87.78 84.11 86.11	8 8 8 8 8 8 8 8 8 8 8 8 8 8 8 8 8 8 8	2	25.3 25.1 24.7 24.7 24.7
381 381 373 345	260 260 174.5 174.5	161. 161. 142. 131. 126.	125 124 124 121 121 121 131 151	119 118 117 116 116
16 17 18 19	2 2 2 2 2 2 3 5 4 5 5 5 5 5 5 5 5 5 5 5 5 5 5 5 5 5	26 28 28 30 30 31 30 31	(C) ** ** # # # # # # # # # # # # # # # #	2 4 4 4 4 4 4 5 5 5 5 5 5 5 5 5 5 5 5 5

ALIGNMENTS

Sequence 2, Application US/10054873
Publication No. US20020164712Ai
GENERAL INFORMATION:
APPLICANT: Gan. Zhong Ru
TITLE OF INVENTION: Chimeric Protein Containing an
Intramolecular Chaperone-Like Sequence COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
OPERATING SYSTEM: P. LOSS/MS-123S
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/054.873
FILING DATE: 22-Jan-2002
CLASSIFICATION: <unknown> ADDRESSEE: Townsend and Townsend and Crew LLP STREET: Two Embarcadero Center, Eiglich Floor NAME: Mycroft, Frank J REGISTRATION NUMBER: 46,946 RFFERENCE/DOCKET NUMBER: G20167-000130US APPLICATION NUMBER: WO PCT/CN98/00052 FILING DATE: 31-MAR-1998 APPLICATION NUMBER: US 09/423,100 FILING DATE: 11-DEC-2000 COUNTRY: USA
ZIP: 94111-1834
COMPUTER READABLE FORM:
MEDIUM IYPE: Floppy disk ATTORNEY/AGENT INFORMATION: CITY: San Francisco STATE: California PRICE APPLICATION DATA: CORRESPONDENCE ADDRESS: INFORMATION FOR SEQ ID NO. NUMBER OF SEQUENCES: RESULT 1 US-10-054-873-2

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61 TPSNREETQOKSNLELLARISLLLIQSWLEPVQ 92
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Matches 90; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TITLE OF INVENTION: Chimeric Protein Containing an Intramolecular Chaperone-Like Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 150;
                                                                                                                                                                                                                               100.0%; Score 470; DB 14; Length 92; 100.0%; Pred. No. 2.2e-45; tive 0; Mismatches 0; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew LLP
STREET: TWO Embarcadero Center, Eighth Floor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  REFERENCE/DOCKET NUMBER: 020167 0601300S
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FILING DATE: 31-AMR-11994
APPLICATION NUMBER: US 09/423,100
FILING DATE: 11-DEC-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 + 1111 | + 1111 | + 1111 | + 1111 | + 1111 | + 1111 | + 1111 | + 1111 | + 1111 | + 1111 | + 1111 | + 1111 | + 1111 | + 1111 | + 1111 | + 1111 | + 1111 | + 1111 | + 1111 | + 1111 | + 1111 | + 1111 | + 1111 | + 1111 | + 1111 | + 1111 | + 1111 | + 1111 | + 1111 | + 1111 | + 1111 | + 1111 | + 1111 | + 1111 | + 1111 | + 1111 | + 1111 | + 1111 | + 1111 | + 1111 | + 1111 | + 1111 | + 1111 | + 1111 | + 1111 | + 1111 | + 1111 | + 1111 | + 1111 | + 1111 | + 1111 | + 1111 | + 1111 | + 1111 | + 1111 | + 1111 | + 1111 | + 1111 | + 1111 | + 1111 | + 1111 | + 1111 | + 1111 | + 1111 | + 1111 | + 1111 | + 1111 | + 1111 | + 1111 | + 1111 | + 1111 | + 1111 | + 1111 | + 1111 | + 1111 | + 1111 | + 1111 | + 1111 | + 1111 | + 1111 | + 1111 | + 1111 | + 1111 | + 1111 | + 1111 | + 1111 | + 1111 | + 1111 | + 1111 | + 1111 | + 1111 | + 1111 | + 1111 | + 1111 | + 1111 | + 1111 | + 1111 | + 1111 | + 1111 | + 1111 | + 1111 | + 1111 | + 1111 | + 1111 | + 1111 | + 1111 | + 1111 | + 1111 | + 1111 | + 1111 | + 1111 | + 1111 | + 1111 | + 1111 | + 1111 | + 1111 | + 1111 | + 1111 | + 1111 | + 1111 | + 1111 | + 1111 | + 1111 | + 1111 | + 1111 | + 1111 | + 1111 | + 1111 | + 1111 | + 1111 | + 1111 | + 1111 | + 1111 | + 1111 | + 1111 | + 1111 | + 1111 | + 1111 | + 1111 | + 1111 | + 1111 | + 1111 | + 1111 | + 1111 | + 1111 | + 1111 | + 1111 | + 1111 | + 1111 | + 1111 | + 1111 | + 1111 | + 1111 | + 1111 | + 1111 | + 1111 | + 1111 | + 1111 | + 1111 | + 1111 | + 1111 | + 1111 | + 1111 | + 1111 | + 1111 | + 1111 | + 1111 | + 1111 | + 1111 | + 1111 | + 1111 | + 1111 | + 1111 | + 1111 | + 1111 | + 1111 | + 1111 | + 1111 | + 1111 | + 1111 | + 1111 | + 1111 | + 1111 | + 1111 | + 1111 | + 1111 | + 1111 | + 1111 | + 1111 | + 1111 | + 1111 | + 1111 | + 1111 | + 1111 | + 1111 | + 1111 | + 1111 | + 1111 | + 1111 | + 1111 | + 1111 | + 1111 | + 1111 | + 1111 | + 1111 | + 1111 | + 1111 | + 1111 | + 1111 | + 1111 | + 1111 | + 1111 | + 1111 | + 1111 | + 1111 | + 1111 | + 1111 | + 1111 | + 1111 | + 1111 | + 1111 | + 1111 | + 1111 | + 1111 | + 1111 | + 1111 | + 1111 | + 1
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APPLICATION NUMBER: US/10/054,873
FILING DATE: 22-Jan-2002
CLASSIFICATION: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         OPERATING SYSTEM: PC-DOS/MS-EXIS
                                                                                                                  SEQUENCE DESCRIPTION: SEQ ID NO: 2:
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SEQUENCE DESCRIPTION: SEQ ID NO: 7;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER: IBM PC compatible
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REGISTRATION NUMBER: 46,946
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDIUM TYPE: Floppy disk
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STRANDEDNESS: <Unknown>
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APPLICANT: Gan, Zhong Ru
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                                    TOPOLOGY: linear MOLECULE TYPE: protein
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                                                                                                                                                                                                                                                                                                             92; Conservative
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ZIP: 94111-3834
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Best Loral Similarity
                                                                                                                                                                                                                                    Query Match
Best Local Similarity
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61 TPSNREETQOKSNLELLRISLLLIQSWLEPVQ 92

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CORRESPONDENČE ADDRESS:
ADDRESSEE: FINNEGAN, HENDERSON, FARABOW, GARRETT & DUNNER, LLP
                                                                 APPLICANT: Ballance, David James
TITLE OF INVENTION: RECOMBINANT FUSION PROTEINS TO GROWTH HORMONE
AND SERUM ALHOMIN
                                                                                                                                                                                                                                                                                                                                                                    COMPUTER: 1BM PC compatible
OPERATING SYSTEM: PC-NOS/MS-LV-S
SOFTWARE: Patentin Release #1.0, Version #1.30 (EPU)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 191
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       97.9%; Score 460; DB 11;
ilarity 98.9%; Pred. No. 7.8e-45;
Conservative 0; Mismatches 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        62 PSNREETQQKSNLHLIRRISLLLLUSWLEPVU 92
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FILING DATE: 19-DEC:1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICATION NUMBER: US/09/984,010
FILING DATE: 21-May-2002
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICATION NUMBER: US 09/091.873
FILING DATE: 25-JUN-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: Brian C. Cumingham
TITLE OF INVENTION: OROWTH HORM NE VARIANIS
FILE REFERENCE: 669.12-05-07
CURRENT APPLICATION NUMBER: US/10/153,207
CURRENT FILLING DATE: 2002-05-22
PRIOR APPLICATION NUMBER: 08/479,884
PRIOR FILING DATE: 1995-06-07
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE DESCRIPTION: SEQ ID NO: 24:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FILING DATE: 1994-02-02
APPLICATION NUMBER: 07/960,227
Sequence 23, Application US/09984010
Publication No. US20030104578A1
                                                                                                                                                                                                                                                                                        ZTP: 20.85-5415
CARUTER READABLE FORM;
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICATION NUMBER: 08/190,723
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      INFORMATION FOR SEQ 1D NO: 23:
SEQUENCE CHARACTERISTICS:
LENGTH: 191 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 1, Application US/1015:207
Publication No. US20030153003A1
GENERAL INFORMATION:
APPLICANT: James A. Wells
APPLICANT: Brian C. Cunningham
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STRANDEDNESS: < Unknown>
                                                                                                                                                                                                         STREET: 1300 : Street,
CITY: Washington
         GENERAL INFORMATION:
                                                                                                                                          NUMBER OF SEQUENCES: 26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TOPOLOGY: linear MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TYPE: amino acid
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Query Match
Best Local Similarity 98.9 
Matches 90, Conservative
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US-10-153-207-6
                                                                                                                                                                                                      LENGTH: 191
TYPE: PRT
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US-09-929-918-9
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APPLICANT: COX 11. George N
APPLICANT: COX 11. George N
APPLICANT: Bolder Biotechnology, Inc.
11TTE OF INVENTION: George N
FILE REFERENCE: 4152-1-PUS
CURRENT APPLICATION NUMBER: US/10/400,377
CURRENT FILLING DATE: 2003-03-26
PRINK APPLICATION NUMBER: US/02/462,941
PRINK FILLING DATE: 1097-07-14
PRINK FILLING DATE: 1997-07-14
SPRINK FILLING DATE: 1997-07-14
NUMBER: GF SEQ IE NGS: 41
SOFTWARE: PALENTIN VOINGER: 60/052,516
SEQ ID NO 1
LENSTH: 191
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APPLICANT: Bolder Biotechnology, Inc.
TITLE OF INVENTION: Derivatives of Growth Hormone and Related Proteins
FILE REFERENCE: 4152-1-PUS
                                                                                                                                                                                                                                                                                                                              97.4%; Shorry 450; TR 12; Tongth 191; 98.4%; Pred. No. 7.86 45;
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97.9%; Score 460; DB 12; Length 191;
Best Local Similarity 98.9%; Pred. No. 7.8e 45;
Matches 90; Conservative 0; Mismatches 1; Indels
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PRIOR FILING DATE: 1992-10-13
PRIOR APPLICATION NUMBER: 07/875,204
PRIOR FILING DATE: 1992-04-27
PRIOR FILING DATE: 1992-04-27
PRIOR APPLICATION NUMBER: 07/428,065
PRIOR APPLICATION NUMBER: 07/264,611
PRIOR APPLICATION NUMBER: 07/264,611
PRIOR FILING DATE: 1988-10-28
NUMBER OF SED IO NOS: 20
SOFTWARE: FUSICE ION WINGOWS VERSION 4.0
SED ID NO 1
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; Publication No. US20030166865A1
; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     : Sequence 1, Application US/10490377
: Publication No. US20630162949A1
                                                                                                                                                                                                                                                                                                                                                    Best Local Similarity 98.4
Matches 90: Conservative
                                                                                                                                                                                                                                          TYPE: PKT
ORGANISM: Homo Sapiens
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ORGANISM: Homo sapiens
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: James A. Well's
APPLICANT: Brian C. Cunningham
TITE OF INVENTION: GROWTH HORMONE VARIANTS
FILE REFERENCE: 669-12-US-7
CURRENT APPLICATION NUMBER: US/10/153,207
CURRENT FILING DATE: 2002-05-22
PRIOR APPLICATION NUMBER: 08/479,884
PRIOR FILING DATE: 1955-06-07
PRIOR FILING DATE: 1954-02-02
PRIOR FILING DATE: 1954-04-27
PRIOR FILING DATE: 1962-04-27
PRIOR FILING DATE: 1989: 10-28
PRIOR FILING DATE: 1989: 10-28
PRIOR FILING DATE: 1989: 10-28
NUMBER OF SEQ 1D NOS: 20
SOFTWARE: FASTERQ for Windows Version 4.0
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: CURRENT APPLICATION NUMBER: US/10/40C,708
: CURRENT FILING DATE: 2003-03-26
: PRIOR APPLICATION NUMBER: US/09/462,941
: PRIOR FILING DATE: 2000-01-14
: PRIOR FILING DATE: 1997-07-14
: PRIOR FILING DATE: 1997-07-14
: NUMBER OF SEQ ID NOS: 41
: SEQ ID NO 1
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Publication No. US/0030153003A1
GENERAL INFORMATION:
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115 PSNREETQQKSNLELLRISLLLIQSWLEPVQ 145
                                                                                                                               Sequence 2. Application US/09853688
Patent No. US20020081605A1
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97.88;
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Matches 89, Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              : ORGANISM: Homo sapiens
US-09-853-688-2
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Best Local Similarity
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                                                                                   RESULT 10
US-09-853-688-2
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Fatent No. US20010021515A1
GENERAL: INFURMATION: Saij
APPLICANT: Higashikuni, Nachiko
APPLICANT: Higashikuni, Nachiko
APPLICANT: Higashikuni, Nachiko
APPLICANT: Kudo, Toshiyuki
APPLICANT: Kondo, Masaaki
TITLE OF INVENTION: DANS ENCOLING NEW FUS) & TROUGH EXPRESSION OF THE
TITLE OF INVENTION: DANS
FILE KEFERRECE: 382.1025
CURRENT APPLICATION NUMBER: US/09/280,030A
CURRENT FILING DATE: 1999-03-26
EARLIEK APPLICATION NUMBER: JP10-87339/1998
EARLIEK FILING DATE: 1998-03-31
NUMBER OF SEQ ID NOS: 66
SOOTWAKE OF SEQ ID NOS: 66
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Sequence 9, Application US/09929918
Patent No. US20020096678A1
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Roadyum, Vitaliy A.
APPLICANT: Slavehenko, Iryna Yu.
APPLICANT: Slavehenko, Iryna Yu.
APPLICANT: Slavehenko, Iryna Yu.
TITLE OF INVENTION: PRAGE-DEPENDENT SUPER PRODUCTION OF
TITLE OF INVENTION: BIOLOGICALLY ACTIVE PROTEIN AND PEPTIDES
FILE HEFERENCE: PHAGE-DEPENDENT SUPER PROTEIN AND PEPTIDES
CURRENT APPLICATION NUMBER: US/09/929,918
CURRENT FILING DATE: 2001-08-15
PRICK APPLICATION NUMBER: 09/318,288
PRICK APPLICATION NUMBER: 09/318,288
PRICK FILING DATE: 1999-05-25
NUMBER OF SEQ ID NOS: 11
SOFTWAKE: FastisEQ for Windows Version 4.23
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Pred. No. 9.26-45;
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tive 0; Mismatches 1; Indels
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Best Local Similarity 98.91
Matches 90; Conservative
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Best Local Similarity 98.9
Matches 90; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                              TYPE: PR1
ORGANISM: Nome Sapiens
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LENGTH: 245
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Sequence 4, Application US/09969748C
Publication No. US2003016180941
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: HOUSTON, Lou, L.
APPLICANT: SHEERIDAN, Pailip, J.
APPLICANT: HAWLEY, Stephen
APPLICANT: GLYNN, Jacquelline, M.
APPLICANT: CHAPIN, Steven
APPLICANT: CHAPIN, Steven
APPLICANT: GLYNN, JAcquelline, M.
APPLICANT: GLYNN, JAcquelline, M.
APPLICANT: GLYNN, JAcquelline, M.
APPLICANT: GLYNN, GOMPOSITIONS AND METHERS FOR THE TRANSPORT OF BIOLOGICALLY ACTION COMPOSITIONS ACROSS CELLILLAR BARRIERS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             0; Gaps
GENERAL INFORMATION:
APPLICANT: COOPER, DAVID N.
APPLICANT: COOPER, DAVID N.
APPLICANT: PROCTER, ANNIE M.
APPLICANT: GREGORY, JOHN S.
TITLE OF INVENTION: METHOD FOR DETECTING GROWTH HORMONE VARIATIONS IN
TITLE OF INVENTION: HUMANS, THE VARIATIONS AND THEIR USES
FILE REFERENCE: WCM78
CURRENT APPLICATION NUMBER: US/09/853,684
CURRENT FILING DAIR: 2010 05 14
NUMBER OF SEO ID NOS: 66
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   96.5%; Score 454; DB 9; Length 217; 97.8%; Pred. No. 4.5e 44; Live 0; Mismatches 2; Indels
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Pred. No. 4.5e-44;
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CURRENT APPLICATION NUMBER: US/09/969,748C
CURRENT FILING DATE: 2002-12-10
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PRIOR FILING DATE: 2000-11-14
PRIOR FILING DATE: 2000-11-14
PRIOR FILING DATE: 2000-11-13
PRIOR PLICATION NUMBER: US 60/248,478
PRIOR FILING DATE: 2000-10-02
NUMBER OF SEQ 1D NOS: 115
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PRIOR FILING DATE: 2001-62-09
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US-09-850-887-4
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                               2 FPTIPLSRLFDNAMLRAHRLHULAFDTYQEFEEAYIPKEQKYSFLQNPQTSLSFSESIPT 61
                                               2 FPTIPLSRLFDNAMLRAHRLHQLAFDTYQEFEEAYIPKEQKYSFLQNPQTSLSFSESIPT 61
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      2 FPTIPLSRLFUNAMLRAHRLHQLAFUTYQEFEEAYIPKEQKYSFLQNPQTSLSFSESIPT 6;
     Gaps
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APPLICANT: PROCIEE, ANNIE M.
APPLICANT: GREGORY, JOHN
APPLICANT: MILLAR, DAVID S.
ITTLE OF INVENTION: METHOD FOR DETECTING POWTH HORMONE VARIATIONS IN TITLE OF INVENTION: HOMANS, THE VARIATIONS AND THEIR USES
FILE REFERENCE: WOM78
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 Indels
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                                                                                                                  62 PSNREETQOKSNLELLRISLILLQSWLFPVQ 92
 0; Mismatc: s
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APPLICANT: CHENCA ANTHONY T.
TITLE OF INVENTION: COMPOSITIONS AND METER-
TITLE OF INVENTION: EXPRESSION IN SUI
FILE REFERENCE: 029996/027 8721
COURTENT APPLICATION NUMBER: US/09/804,409A
COURTENT FILING DATE: 2001-03-12
NUMBER OF SEQ ID NOS: 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CURRENT AFFICATION NUMBER: US/09/853,588 CURRENT FILING DATE: 2001-05-14 NUMBER OF SEQ ID NOS: 66
                                                                                                                                                                                                  US-09-804-409A-16
- Sequence-16. Application US/09804409A
- Patent No. US20020155100A1
- GENEWAL INFORMATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 4, Application US/09853688
Patent No. US20020081605Al
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                      SOFTWARE: Patentin Ver. 2.1
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SEO 10 No. 4
 89; Conservative
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TYPE: PRT
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LENSTH: 217
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2 PPTIPLSKLFUNAMLRAHK GOLAFUTYGEFEEAYIPKEQKYSFLQNPQTSLSFSESIPT 61
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TITLE OF INVENTION: POLYPEDILDES FROM PLANTS
FILE REFERENCE: 15712-0.03.
CURRENT APPLICAL: 1001-0.4 0.4
CURRENT APPLICAL: 2001-0.4 0.4
PRICE APPLICATION DATE: 2001-0.4 0.4
NUMBER OF SEQ ID NOS: 14
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Corley, Neil C.
Corror, Gina
TITLE OF INVENTION: THYROLD AND FITULIARY MEMBRANE PROTEIN
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 191:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SOFTWARE: Word Perfect 6.1 for Windows/MS-DUS 6.2 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/850,887
FILING DATE: 07 May-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 444; DB 12;
Pred, No. 5.3e-43;
0; Mismatches 3;
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                       PSNREETOOKSNLELLRISLLLJOSWLEPVQ 117
35
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC DOS/MS:DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRIOR APPLICATION DATA: APPLICATION NUMBER: 09/087,678
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NAME: CERRONE, MICHAEL C. REGISTRATION NUMBER: 39,132
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STREET: 3174 PORTER DRIVE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CLASSIFICATION: <Unknown>
                                                                                                                                 US-09-824-200-12
; Sequence 12, Application US/09824200
; Publication No. US20030167531A1
; GENERAL FURORNATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence % Application US/0985G887
Patent No. US20020009778A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FILING DATE: <Unknown> ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        94.5%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STATE: CALIFORNIA COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                   Patentin Ver. 2.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  88; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      : ORGANISM: Homo sapiens
US-09-824-260 12
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Bost Local Similarity
Matches 88; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GENERAL INFORMATION:
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Query Morth 84.3%; Smite (%) 1805, Tenath 287, Best Local Similarity 84.6%; Pred. Mo. 1905 C. Mandels Matches 77; Conservative 6; Mismatches 8; Undels
REFERNCE/DOCKET NUMBER: PF-0535 US
TELECOMMUNICATION INFORMATION:
TELEPAX: (560) 845-4166
TELEFAX: (560) 845-4166
INF.HMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 217 amino acid
STRANDENESS: single
TYPE: amino acid
STRANDENESS: single
TOPOLOCY: linear
TOPOLOCY:
LIBRARY: GenBank
LIBRARY: GenBank
SEQUENCE: 9406987
US-09-8*C-867 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             62 PSNREETOOKSNLELLRISILLIOSWLEPVO 92
17:11111: 11111 | 111111111 | 1
87 PSNKEETOOKSNLELLRISILLIOSWLEPVO 117
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Search completed: September 15, 2003, 12:24:35 Job Lime - 38,5806 secs

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GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.
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OM protein : protein search, using sw model

September 15, 2003, 11:56:45; Search time 15,1685 Seconds (without alignments) 583.264 Million cell updates/sec Run on

Title: Perfect score: Sequence:

US-09-423-100-2 470 1 MFPTIPLSRLFDNAMLRAHR.........NLFILKISI.LLIGSWI.EPVQ 92

BLOSGM62 Gapop 10 0 , Gapext O.f Scoring table:

284308 seqs, 99158687 res. Les Searcind

283408 Total number of hits satisfying chosen parameters:

length: 2000000000 Minimum DB seq length: 6 Maximum DB seq length: 20 Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

pirl:* pir2:* pir3:* PIR_76:*
1: pir1:*
2: pir2:*
4: pir3:* Database

pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

KIES	Description	end I display to the sound to the sound of the sound to t		~	~		ma:	chorionic somatoma	chorionic somatoma	chariomamnotropin	chor tomammot ropin	choriomammotropin	somatctropin - dol	somatotropin - sei	somatotropin precu	somatotrofin - hor	ā	somatotropin predu	somatotropin - Afr	somatotropin precu	somatotropin precu	somatotropin precu	somatotropin precu	somatotropin - alp	somatotropin - Arc	somatotropin precu		somatotropin precu		Some of contraction
SUMMARIES	91	STHU	167410	STHUV	STHUV2	167411	167409	167408	153267	LCHUC	E32435	A26449	B49159	PN0140	STMS	STHO	STRT	S49483	JKC219	STPG	146145	JC4632	A37782	A61584	JS0429	STBO	STSH	STGT	532682	101514
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	Length	217	217	217	256	217	217	212	217	217	217	215	216	150	216	190	216	216	190	216	216	216	216	190	190	217	217	217	217	216
œ	Vuery Match	97.9	97.6	8.68	8.68	85.5	84.5	84.3	84.3	81.1	81	76.5	66.1	65.4	64.8	64.4	64.4	64.4	64.1	64.1	64.1	64.1	63.7		65.8	61.6	61.6	61.6	61.6	59.3
	Score	460	460	422	422	402	197	356	336	181	381	359.5	310.5	307.5	5.409	302.5	102.5	302.5	301.5	101.5	301.5	301.5	5.667	297.5	295.5	289.5			289.5	278.5
	Result. No.		7	æ	4	S	e)	7	œ	s S	10	=	12	13	14	15	16	17	18	19	20	21	22	23	24	25	56	27	28	59

A: Residues: 1-21. AROS.

A: Note: 35-Pro was also found

B: Note: 35-Pro was also found

A: Note: 35-Pro was also found

B: Science 205, 602-607, 1979

A: Title: Human growth hormone: complementary DNA cloning and expression in bacteria

A: Reference number: A94247

A: Molecule type: mRNA

A: Residues: 1-217 < AMAN

A: Title: Human pituitary growth b. rmone. XIX. The primary structure of the hormone. A; Roference number: A90048; MUD: 9289202; PMID:5810834

A: Contents: annotation

R: Li C. H.: Dixon, J.S.

Arch: Biochem. Biophys: 146, 233-236, 1971

A: Title: Human pituitary growth hormone. XXXII. The primary structure of the hormone A; Reference number: A90051; MUD: 72143935; PMID:5144027

A: Molecule type: protein

somatotropin precu	somatotropin - gre	somatotropin precu	somatotropin - Rus	somatotropin - bul	somatotropin - bul	somatotropin precu	choriomammetropin-	somatotropin - bow	somatotropin - blu	EST/beta-Gal mutan	somatotropin I pre	somatotropin - sei	somatotropin - com	somatotropin - nob	somatotropin - sil
A60509	A60625	S04929	521750	A56816	151188	.150037	B32435	151250	A60623	167761	310483	JN0387	JC5682	150763	538351
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216	191	216	190	140	215	215	66:	3.65	183	87	209	163	190	210	710
58.6	57.1	55.5	54.8	52.7	50.7	50.5	8.5	49.7	48.0	43.8	37.1	36.4	35.2	35.2	35.2
		.7	. ک	5	8.5	7.5	234	33.5	25.5	206	74.5	171	5.5	S.	ۍ ن
275.5	258.5	7	257	247	23	23		~	~				Ë	=	-

ALLENMENTS

RESULT 1 STHU
somatotropin precursor [validated] - human N/Alternate names: growth hormone l; hGH-N; pitcitary somatotropin
N.Contains: growth hormone 5K peptide: somatotropin 1, long form; somatotropin 1, s
c.species: Homo sapiens (man) C.Date: 24.Apr-1984 #sequence_revision 10.Feb-1995 #text_change 08-Dec-2000
C.Accession: A93731; A32435; A91694; A94247; A90651; A93397; A93778; A91764; A90217
KiDeNoto, F.M.; Moore, D.D.; Goodman, H.M. Nucleic Acids Res (9, 3719-3730, 1981
A)Title: Human growth hormone DNA sequence and mkNA structure: possible alternative
A;Reference number: A93731; MUID:82014939; PMID:6259091
A: Accession: A93731
A;Molecule type: DNA
A; Residues: 1-217 <den></den>
A;Cross-references: GB:V60520
A; Note: the 20K short form somatotropin lacks residues 58-72 (32-46 in the active h
R.Chen, E.Y.; Liao, Y.C.; Smith, D.H.; Barrera-Saldana, H.A.; Gelinas, R.E.; Seebur
Genomics 4, 479-497, 1989
A;Title: The human growth hormone locus: mucleotide sequence, biology, and evolutio
A; Reference number: A32435; Millo:89307277; PMID:2744760
A:Accession: A32435
A:Molecule type: DNA
A;Residues: 1-217 <che></che>
A:Cross-references: GB::03071; NID:q183148; PIUN:AAA52549.1; PH::g183149
R;Roskam, W.; Rougeon, F.
Nucleic Acids Res. 7, 305-320, 1979
A;Title: Molecular cloning and nucleotide sequence of the human growth hormone stru
A; Reference number: A93654; MUID: <0034477; PMID: 846281
A: Accession: A93694
A:Molecule Type: mrna
A:Residues: 1-217 <ros></ros>

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Rigolos, T.G.; Durning, M.; Fisher, J.M.; Fowler, P.D.
Endocrinology 133, 1744-1752, 1993
Affitle: Cloning of four growth hormone/chorionic somatomammotropin-related compleme
                   C:Comment: The gene for this hormone is transcribed only in somatotrophic cells of C:Comment: About 90% of somatotropin is the 22K long form.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             0
                                                                                                                                                                                                                                                                  C; Superfamily: prolactin
C; Keywords: alternative splicing; normone; pituitary
F;1-25/Domain: signal sequence #status predicted <SIG>
F;27-21/7/Product: somatotropin 1, long form #status experimental <SOL>
F;27-69/Product: growth hormone 5K peptide #status experimental <5KP>
F;27-57,73-317/Product: somatotropin 1, short form #status experimental <SOS>
F;79-191,208-215/Disuifide bonds: *status *xperimental
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         2 FPTIPLSRLFUNAMLRAHRIHQLAFDTYGEFEBAYIPKEQKYSFLÖNPQTSLSFSESIPT 61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       27 FPTIPLSRLFDNAMLRAHRLHQLAFDTYQEFFERAYIPKEQKYSFLCNPQTSLCFSESIPT 86
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           2 FPTIPLSRLFUNAMLRAHKLHQLAFDTYQEFEEAYIPKEQKYSFLQNPQTSLSFSESIPT 61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   N.Alternate .:ames: growth hormone
C.Species: Macaca mulatta (Thesus maraque)
C.Date: 31:May-1996 #sequesch_revision 31:May-1996 #text_change 16:Jul-1999
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A:Contents: annotation: identification of source organism
C:Superfamily: prolactin
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98.5%; Pred. No. 4.46-42;
tive 0; Mismatches 1; Indels
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A:Residues: 27-99, 'Q',101-178,'D',180-217 <LIC>
A:Note: the monkey species is not identified in the reference
R:Raben, M.S.
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Arch. Biochem. Biophys. 245, 287-291, 1986
                                                                                                                                                                    GDB:119982; OMIM:139250
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                                                                                                                                                                                                   A:Map position: 17q23.1-17q23.3
A:Introns: 4/1: 57/3: 97/3: 152/3
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Matches 90: Conservative
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Best Local Similarity 98.9%
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A; Residues: 1-217 <RES>
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J. Biol. Chem. 256, 2395-2401, 1981
A. Paritter: The 20,000 molecular weight variant of human growth hormone. Preparation and sc. A. Reference number: A92311; MuID:81117361; PMID:7462247
A. Contents: Somatotropin, 20K short variant
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A;Residues: 27.34, %, 36-47 <ROB»
A;Residues: 27.34, %, 36-47 <ROB»
A;Red Vos. A.M.; Ultsch, M.; Kossiakoff, A.A.
Science 255, 306-312, 1992
A;Title: Human growth Hormone and extracellular domain of its recreptor: crystal structur
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R.Bewley, T.A.; Dixon, J.S.; Li, C.H.
Int. J. Pept. Protein Res. 4, 281-287, 1972
A.Title: Sequence comparison of human pituitary growth hormone, human chorionic somatoma A.Reference number: A91764; MUID:73092028; PMIV:4675454
A.Accession: A91764
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A:Title: Periplasmic production of correctly processed human growth hormone in Escherich A;Reference number: 141126; MUID:86137393; PMID:3912261

A;Accession: 184549
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A;Molecule type: protein
A;Molecule type: Drotein
A;Residues: 27-51 cMIA>
B;Niall. H.D.: Hogan, M.L.: Sauer, R.: Rosenblum, I.Y.: Greenwood, F.C.
Proc. Natl. Acad. Sci. U.S.A. 68, 866-869, 1971
Proc. Natl. Acad. Sci. U.S.A. 68, 866-869, 1971
A;Title: Sequences of pituitary and placental lactogenic and growth hormones: evolution A;Reference number: A93778; MUID:71153968; PMID:5279528
A;Accession: A93778
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A:Residues: 27-217 <HEW>
A:Residues: 27-217 <HEW>
B:Lewis, 1.5.1 Honewald, L.F.; Lewis, L.J.
Biochem. Biophys. Res. Commun. 92, 511-516, 1980
A:Title: The 26,000-dalton variant of human growth hormone: local: .. of the amino acid A:Reference number: A90217; MUID:80130196; PMID:7356479
A:Contents: somitoiropin, 20K short variant.
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A; Contents: annotation; X-ray crystallography, 2.8 angstroms
A; Note: the structure of the complex with growth hormone receptor is described R:Gray, G.L.; Baldridge, J.S.; McKeown, K.S.; Heyneker, H.L.; Chang, C.N.
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A.Mediculo type: protein
A.Mediculo type: 27-57:73-79 cCHA>
R.Singh, R.N.P.: Sravey, B.K.: Lewis, L.J.: Lewis, U.J.
J. Protein Chem. 2, 425-436, 1983
A.Title: Human growth hormone peptide 1 43: isolation from pituitary glands.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               in Prolactin and Carcipouphesis, Proc. Fourth Francis Workshop Presentin.
Affile: The chemistry of the human factorence horizones.
A;Reference number: A94422
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                                                                          Nature New Biol. 230, 90-91, 1971
A.Title: Revised primary structure for human growth hormone.
A.Reference number: A93397; MUID:71139765; PMID:5279046
A.Accession: A93397
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*Molecule Uype: mRNA
A:Residues: 1-26 <RES>
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A;Residues: 119-120;157-159 <NI2>
R;Niall, H.D.
A;Residues: 27-94;96-217 <LIC>R;Niall, H.D.
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A;Residues: 46-57;73-80 <LEW>
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R.Cooke, N.E.; Ray, J.; Emery, J.G.; Liebhaber, S.A.
J. Biol. Chem. 263, 9001-9006, 1988

A.; Ille: Two distinct species of human growth hormone-variant mRNA in the human plan A.; Reference number: A92725; MUID:88243769; PMID:3379057

A.; Reference number: A92725; MUID:88243769; PMID:3379057
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C:Date: 30-Sep-1989 #sequence_revision 10-Feb-1995 #text_change 02-Sep-1997
                                                                                                                  somatotropin 2 precursor, splice form 2 - human
N:Alternate names: growth hormone variant-2; placental somatotropin form 2
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A;Rosiduos: 1-217 «RES»
A:Cross-references: GB:Ll6555; NID:g293116; PIDN:AAA20180.1; PID:g293117
C;Superfamily: prolactin
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C.Keywords: alternative splicing; hormone; placenta
F:1-25/Domain: signal sequence #status predicted <SIG>
F:27-256/Product: somatotropin 2 splice form 2 #status predicted <MAI>
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A:Residues: 1-256 <COO>
A:Residues: 1-256 <COO>
A:Rotte: an alternative splice junction for intron 4 is used
C:Genetics:
A:Genetics:
A:Genetics: A:Genetics: GDB::119943; GMIM.:139240
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85.7%; Pred; No. 7.86-85;
wiematches 7;
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92.3%; Pred. No. 6.7e-38;
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A:Status: preliminary; translated from GB/EMBL/JubbJ
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A:Introns: 4/1: 57/3: 97/3: 152/3
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Best Local Similarity
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                                    N.Alternate names: growth hormone 2; growth hormone variant; höif-V; placental somatotroph N.Contains: somatotropin 2, long splice form; somatotropin 2, short splice form N.Contains: somatotropin 2, long splice form; somatotropin 2, short splice form C.Species: Homo sapiens (man) (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A.Cross-references: GB.J03071; NID:q183148; PIDN:AAA52552.1; PID:g184152
KCOOKe, N.E.; Ray, J.; Emery, J.G.; Licbhaher, S.A.
J. BJOJ. Chem. 253, 9031-9005, 1906.
A.Title: Two distinct Species of Johann qrowth Porecore variant EPNA in the common placenta.
A.Reference number: A92725; Mullichart 4759; PMID: 8478-52.
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R:Residues: 1-217 <000>
R:Residues: 1-217 <000>
R:Residues: 1-217 <000>
R:Residues: 1-217 <000>
R:Residues: 1-219-249, 1982

DNA 1, 239-249, 1982

DNA 1, 239-249, 1982

NATILIE: The futuata growth hormone gene family: nucleotide sequences show recent divergent A:Reference number: A01511; MUID:83182010; PMID:7169009

A:Accession: A01511
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A; Residues: 1-217 <1GO>
A; Residues: 1-217 <1GO>
A; Residues: 1-217 <1GO>
A; Crass-references: GB:M38451; NID:9183179; U. N:AAA35891.1; PID:9183180
B; Frankence, F.: Scippo, M.L.; Van Beeumen, U.: Igout, A.; Hennen, G.
J. Glin, Endocrinol, Metab. 71, 15-18, 1990
A; Title: Identification of placental human growth hormone as the growth: hormone-V gene
A; Reference number: A60711; MUID:90317018; PMID:2196278
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F:166/Binding site: carbohydrate (Asn) (covalent) Estatus predicted
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A; Residues: 1 34,7P',36-217 <SEE>
R: Joout, A.: Scrippo, M.L.; Frankenne, F.; Honden, G.
Arch. Int. Physiol. Blochim, 96, 63-67, 1988
A:Title: Cloning and nucleotide sequence of placental hGH-V CDNA.
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Pred. No. 5.5e-38;
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A;Status: preliminary; translated from GB/EMBL/DDBJ
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A;Introns: 4/1; 57/3; 97/3; 152/3
C;Superfamily: prolactin
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somatotropin 2 precursor - human
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Best Local Similarity 92.33
Matches 84; Conservative
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A:Residues: 27-44;46-57 <FRA>
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A. Molecule type: mRNA
A. Residues: 1-3 < TANA
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A. Residues: 1-3 < TANA
A. Cross references: UR. M. SA 19; NID: 9506#32
A. Cross references: UR. M. S. Steeller, J. By Service of the procursor to human
A. Reference number: A93833: MUID: 80034970; PM: D: 291643
A. Recession: A93833: MUID: 80034970; PM: D: 291643
A. Recession: A93833: MUID: 80034970; PM: D: 291643
A. Residues: 1.3 - 26 < SHE>
A. Res
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Cysperies: Home sapices (mar)
Cyste: 23 oct 1981 #sequece revision 25-(-1-1981 #text_change 68-Der-2000
Cyste: 23 oct 1981 #sequece revision 25-(-1-1981 #text_change 68-Der-2000
Cyste: 23.435, 494422; i52342. A93833. A93192, A99054; A94427, A61283; i52229;
Rochen, E.Y.; Lido, Y.C.; Sauth, D.H.; Barrera Saldana, H.A.; Gellnas, R.E.; Seeburg,
Genomics 4, 479-497, 1989
Arrite: The human growth hormone locus: nucleotide sequence, thology, and evolution
A.Reference number: A32435, MulD:89307277; PMID:2744760
A.Recession: C32435
A.Rocession: C32436
A.Residues: 1-217 ACHE>
A.Rocession: C32436
A.Rocession: 
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A:Reference number: A94422
A:Reference number: A94422
A:Molecule type: mkNA
A:Residues: 1-217 <GGO>
B:Indaka, M.: Masuaha, M.: Yamakawa, M.: Shimizu, K.: Nagai, J.: Nakash: Biochem. Int. 16, 287-292, 1988
A:Itle: cDNA cioning of human chorionic somatomammotropin-1 mRNA whose transcription A:Reference number: 152342, MUID:88209696; FMID:2835050
A:Recession: 152342
A:Recession: 152342
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A; Accession: A93192
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Fourth Tenovus Workshop Prolactin, Griffiths, A;Title: The chemistry of the human lactogenic hormones.
A;Reference number: A94427
A;Accession: A94427
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N:Alternate names: chorionic somatomammetratic 1: placental Jactogen
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A:Residues: 50-217 <SH1>
A:Experimental source: placenta
R:Li, C:H.: Dixon, J:S.; Chung, D.
A:Tc, Bicochem Biophys: 155, 95-110, 1973
A:Title: Amino acid sequence of human chorionic somatomamotropin.
A:Reference number: A90054; MUID:7320:971; PMID:4712450
                                                                                                                                           Length 217;
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88 SNLEETQQKSNLELLRISLLLIOSWLEPVQ 117
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                                                                                                                                           84.3%;
82.2%;
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                                                                                                                                   Query Match
Best Local Similarity 82.2%
Matches 74; Conservative
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C:Species: Macaca mulatta (rhesus macaque)
C:Date: 31-May-1996 #sequence_revision 31-May-19** *text_change 16-Jul-1999
C:Accession: 167409
C:Accession: 167409
C:Accession: 167409
C:Accession: 167409
C:Accession: 167409
A:Title: Cloning of four growth hormone/chorionic somatomammotropic-related complementary A:Title: Cloning of four growth hormone/chorionic somatomammotropic-related complementary A:Accession: 167409
A:Status: preliminary: translated from GB/EMBL/DDBJ
A:Accession: 167409
A:Status: preliminary: translated from GB/EMBL/DDBJ
A:Residues: 1-217 <RES-
A:Coss-references: GB:L16554; NID:q293112; PIDN:AAA18841.1; PID:q293113
C:Superfamily: prolactin
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C:Species: Macaca mulatta (rhesus macaque)
C:Date: 31 May 1966 *sequence_revision 31 May 1966 *text_change 16-Jul-1999
C:Accession: 164408
R:Golos, T.G.: Durning, M.: Fisher, J.M.: Fowler, P.D.
R:Golos, T.G.: Durning, M.: Fisher, J.M.: Fowler, P.D.
A:Title: Cloning of four growth hormone/chorionic somatomammotropin-related complementar
A:Reference number: 153267; MUID:94008724; PMID:8404617
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C.Species: Macaca mulaita (rhesus macaque)
C.Date: 17 May-1996 Esequence_revision 31-May-1996 Etext_change 16-Jul-1999
C.Accession: 153267
R.Golos, T.G.: Durning, M.: Fisher, J.M.: Fowler, P.D.
Endocrinology 133, 1744-1752, 1993
A.Title: Cloning of four growth hormone/chorionic somatomammotropin-related complementar A:Reference number: 153267; MUID:94008724; PMID:8404617
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            28 PSVFLSFLFULL LEED FILLE FIL
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A.Residues: 1-212 (RES>
A.Cross-references: GB:L16553: NID:9293110: PIDN:AAA18840.1: PID:q293111.
C.Superfamily: prolactin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         :Cross-references: GB:L16552; NID:g293108; PIDN:AAA18839.1; PID:g293109
:Superfamily: prolactin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Lenath 217;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       84.5%; Score 397; DB 2; Denath 217
83.3%; Pred. No. 2 70 35;
Uye - B: Missarches - 7; Indets
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A:Status: preliminary; translated from CB/FMBL/DDBJ

A; Accession: 167408

63 SNREETOOKSNLELLRISLLLIQSWLEPVQ 43

Ouery Match Best Local Similarity 83.3 Matches 75, Conservative

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RESULT 7 167408

11 | HILLHHILLHILLHILLHILLHILLISWIEPVO 112

chorionic somatomammotropin-1 - rhesus macaque

RESULT 6

63 SNREETQQKSNLELLRISLLLIQSWLEPVQ 92

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Best Local Similarity 82.2 Matches 74; Conservative

A:Status: preliminary: translated from GB/EMBL/DDBJ A:Molecule type: mRNA A:Residues: 1-217 <RES>

us-09-423-100-2.rpr

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C.Accession: E32435
R.Chen, E.Y.; Lido, Y.C.; Smith, D.H.; Barrera-Saldana, H.A.; Gelinas, R.E.; Seeburg Genomics 4, 479-497, 1989
A.STILLE: The human growth hormone locus: nucleotide sequence, biology, and evolution A; Reference number: A32435, MUD:89307277; PMID:2744760
A; Ascession: E32435
A; Status: preliminary
A; Molecule type: DNA
A; Residues: 1-217 <CHE>
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R;Southard, J.N.; Sanchez-Jimenez, F.; Campbell, G.T.; Talamantes, F.
Endocrinology 129, 2965-2971, 1991
A;Title: Sequence and expression of hamster projactin and growth hormone messenger HA:Reference number: A49159; MUID:92063850: PMID:1954881
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    R:HIrt, H.: Kimelman, J.: Birnbaum, M.J.: Chen, E.Y.: Seeburg, P.H.: Eberhardt, N.L. DNA 6, 59-70, 1987
A.Title: The human growth hormone yene locus: Structure, evolution, and allelic variance anomore: A26449: MUID:87161235; PMID:3030680
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C;Date: 29·Dec-1989 *sequence_revision 29·Dec-1989 *text_change 16-Jul-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      C;Species: Homo sapiens (man)
C;Date: 30-Jun-1988 *sequence_revision 30-Jun-1988 #text_change 28-Jul-1995
C;Accession: A26449
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C;Species: Mesocricetus auratus (golden hamster)
C;Date: 19-Dec-1993 #sequence_revision 18-Nov-1994 #text_change 21.Jnl-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              4 TIPLSRIFONAMERAHREHQLAFDTYQEFEEAYIPKEQKYSFIQNPQISLSFSESIPTPS
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C;Superfamily: prolactin
F;1-26/Domain: Signal sequence #status predicted <SIG>
F;27-215/Product: choriomammotropin, hCS-3 allele #status predicted <MAT>
                                                                                                                                                                                                                                                                                                                                                                                                     A;Cross-references: GB;JC3071; NID:g183148; PiDN:AAA52553.1; PID:g183153
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Pred. No. 1.46 53;
8; Mismatches 8;
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80.5%; tred. No. 2.9e-31;
ive 8; Mismatches 8;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      choriomammotropin precursor (allele ECS-3) - human
N, Alternate names: chorionic somatomammotropin 2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A.Cross-reterences: GDB.119813; GMIM:11882)
A.Map posttion: 1792z 179z4
C.Superfamily: profaction
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Matches 70; Conservative
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Matches 73; Conservative
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B49159
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**Sherwood, L.W.; Handwerger, S.; McLauera, W.E.; Lanner, M.

**Raterwood, L.W.; Handwerger, S.; McLauera, W.E.; Lanner, M.

**Asteference number: 454, 497, 497, 485  

**Schoelders: annotation

**Astille: Identitication of the interchain disulfide bonds of dimeric human placental lad Astille: Identitication of the interchain disulfide bonds of dimeric human placental lad Astille: Identitication of the interchain disulfide bonds of dimeric human placental lad Astille: Identitication of the interchain disulfide bonds of dimeric human placental lad Astille: Asternary annotation; diseric disulfide bonds

**Reference number: As: Baxter, J.D.; Bell, G.L.; Eberhardt, N.L.

**J. Biol. Chem. 259, 1313-13139, 1984

**Asteference number: 155229; MJID:85030426; PMID:6208192
                                                                                                                                                                                                                                                                                                                  A;Note: choriomammotropin apparently copurified with placental catechol-O-mothyltransfer R;Sherwood, L.M.; Handworger, S.; McLaurin, W.D.; Lanner, M. R;Arerwood, L.M.; Handworger, S.; McLaurin, W.D.; Lanner, M. A;Title: New Bioi. 233, 59-61, 1971
A;Title: New Bioi. 234, 59-61, 1971
A;Title: Amino-acid Sequence of human placental lactogen.
A;Reference number: A93401; Muid:72016313; PMID:5286363
                                                                               R;Nic A Bhaird. N.; Tipton, K.F.
Blochem. Soc. Trans. 19, 208, 1991
A;Title: Calcehol-O-metnyltransferase from human placenta: purification and some propert
A;Reference number: A61283; MUID:91244006; PMID:2037148
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A.Introns: 4/1: 57/3: 97/3: 152/4
C.Seywords: hormone: racenta
F.1-26/Ixomain: signal sequence *status experimental sperimentalF.37-217/Product: choriomammotropin A *status experimental syntamidide bonds: *status experimentalF.37-19/1/Ixomain: signalide bonds: (in monomeric form) *status experimental
F:208/Disulfide bonds: interchain (to 215 in dimeric form) *status experimentalF:215/Disulfide bonds: interchain (to 208 in dimeric form) *status experimental
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A.Title: Nucleotide sequence of a human gene c ding for a polypeptide hormone. A.Reference number: 159658; MUID:78160787; PHI::611657
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A;Residues: 150-217 <RE2>
A;Cross references: GB:M25118; N;D:q181124: PFFFEAAA$5721.1; P!D:q181125
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A;Cross references: GDB:119084; UMIM:150260
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A.Status: translated from GB/EMBL/DDBJ
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              A;Residues: 27-217 <NIA>
A;Experimental source: placenta
                                                                                                                                                                                                                 A; Accession: A61283
A; Molecule type: protein
A; Residues: 27-46 <NIC>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A; Molecule type: DNA
A; Residues: 1 217 <RES>
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Gaps

choriomammotropin B precursor - human

RESULT 10 E32435

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Gaps

63

Superfamily: prolactin

A; Molecule type: mRNA A; Residues: 1-216 <50U> A;Status: preliminary A; Accession: B49159

1: :1: TELETE: THE FITHER HE HE HE HE HE HE HE PTGKEEAQQKSDMELLKESI LIIQSWLGFVG 116 62 PSNREETQQKSNLELLRISLLLIQSWLEPVQ 92

δ qq RESULT 13

us-09-423-100-2.rpr

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Cyber 13-10-1981 ksequence_revision 13-0-1982 flext_change_23-Aug-1996
Cyberession Avi72. Avi 445. A5184: Av0240: Avi514
Krakin, M.M.; Foscus, E. Guigetta, A.A.; Fortura, P.: Santome, O.A.; Dellacha, O.M.;
Int., J. Pejat, Protein Pes E. 435-444; 1976
Artitle: Primary structure of equipe qrowth hormone.
Askedence number: Avi722 Nulb:77065410; PMiD:966551
A.Redence number: Avi722 Nulb:77065410; PMiD:966551
A.Redence number: Avi722 Nulb:77065410; PMiD:966551
A.Redence number: Avi722 Nulb:77065410; PMiD:9706510
A.Redence of protein
A.Redence of capine growth hormone.
A.Title: The amino acid sequence of equipe growth hormone.
A.Reference number: Apj395
A.Reference number: Apj395; AujD:74020362; PMID:4747849
A.Reference number: Apj395
A.Reference
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A.Title: Adino acid sequences around the cystice residues in equine growth hormone. A.Title: Adino acid sequences around the cystice residues in equine growth hormone. A.Reference number: A91383
A.Accession: A91383
A.Molecule type: protein
A.Molecule type: protein
A.Molecule type: protein
B.Oliver, L., Hartree, A.S.
B.Oliver, L., Hartree, A.S.
A.Title: Adino acid sequences around the cystice residues in horse growth hormone. A.Reference number: A9240; MGID:69368390; PMID:4876100
A.Accession: A9240; MGID:69368390; PMID:4876100
A.Molecule type: protein
A.Molecule type: protein
A.Molecule type: protein
A.Molecule type: protein
B.Residues: 176-190 coll:
C.Superfamily: protactin
C.Superfamily: protactin
C.Superfamily: protactin
C.Suberfamily: protactin
C.Suberfamily: protactin
C.Suberfamily: protactin
C.Suberfamily: protactin
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                                                                                                                                                                                                                                                  2 FPTIPLSRLFDNAMLRAHRLHQLAFDTYÖRFERAYIPKROKYSFLQNPQTSLSFSESIPT
                                                                                                             Gaps
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         Length 216;
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                                                                                                   17; Indels
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         DH 1;
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Keywords: hormone; pitultary
52-163,180-188/Disulfide bunds: #status experimental
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            17;
Ouery Match 64.8%; Score 304-5; DB L
Best Local Similarity 64.8%; Pred. No. 2.4e-25;
Matches 59; Conservative 14; Mismatches 17.
                                                                                                                                                                                                                                                                                                                                                                                                                           1: :II | I::::I-II | EI:IIII | III | EB PTGKEEAQORTOMELLRESLLLIQSWLGPVQ 116
                                                                                                                                                                                                                                                                                                                                                                              62 PSNREETOOKSNLELLRISLLIUSWLEPVO 92
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Job time : 16.1685 secs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    N.Alternate names: growth hormone
C.Species: Eggus cabailus (domestic horse)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 59; Conservative
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Matches 59, Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 somatotropin - horse
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C:Species: Mus muserulus (house mouse)
C:Dacession: B21911
R:Librarer, U.B.1.H.: Inalmantes, F.
B:Librarer, U.B.1.H.: Inalmantes, F.
A:Title: Nucleotide sequence of mouse prolactin and growth hormone mRNAs and expression
A:Reference number: A92548: MUD:85261358; PMIC:2991252
A:Accession: B23911
A:Moleoule type: mRNA
A:Residues: 1.216 < LIN>
A:Residues: 1.216 < LIN>
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A:Residues: 1.216 < LIN>
C:Supertamily: prolactin
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C:Supertamily: prolactin
C:Supertamily: prolactin
C:Supertamily: prolactin
C:Reywords: anterior pluulary: growth factor: hormone
F:1.26/Domain: signal sequence istatus predicted <SIG>
F:27-216/Product: somatotropin #status predicted
S:78-189,206-214/Disulfide bonds: #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Foreign Section 1. Set whate National Section 1. Set whate Naternate names: attemth hormone Naternate names: attemth hormone Naternate names: attemth hormone C.Speckes: Balaenchetera borealis (set whate) C.Speckes: Balaenchetera borealis (set whate) C.Speckes: Balaenchetera borealis (set whate) N. A.; Pankov, Y.A.; Bulatov, A.A.; Osipova, T.A. Biokhimia 47, 1059-1069, 1982
A.Title: Amino acid sequence of setwhate somatotropin.
A.Reference number: PNO140; MUID:83000569; PMID:7115818
A.Accession: PNO140; MUID:83000569; PMID:7115818
A.Molecule type: protein
A.Mole: article in Russian with English abstract.
C.Superfamily: prolactin
C.Keywords: growth factor; hormone
F:52-163,180-188/Disulfide bonds: *status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           2 FPTIPLSRLFONAML, RAHRLHGLAFDTYQEFEEAYIPKEQKYSFLONPOTSLSFSESIP; 61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  11 :111 11 11:111 11:111 11:111 11:1:1
27 FPAMPLSSIFANAVLRAGHAHOLAADTYKEFERAYIPEGGKYS-1GNAGTAFFFSFIIFA 85
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  2 FPT1FF.SKLEDNAMLRAHRLHOLAFDTYQEFEEAYIPKEQKYSFLQNPUFSLSFSFSIFF 61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TEPAMPLSSLEANAVLRACHLHELAADTYKEFERAYIPEGGRY-FLQNAGSTGTESEVIPT 59
                                                                                                                                                                                                                                                                                               Ouery Match

66.1%; Score 310.5; DB 2; Length 2:6;
Best Local Similarity 67.0%; Pred. No. 5.5e-26;
Matches 61; Conservative 13; Mismatches 16; Indels 1; daps
                                                                                                   A: Cross-references: GB:S66299; NID:q239355; PIDN:AAB2G368.1; PID:g239346
A: Note: sequence extracted from NCBI backbone (NCBIN:66299; NCBIP:66300)
C:Superfamily: prolactin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   -:
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Length 190;

14; Mismatches 15; Indels

6.2 PSNREETOOKSNLELLRISHLINGSWLEPVC 9.2

q ô q somatotropia precursor - mouse

RESULT 14 STMS

65.4%; Score 307.5; DB 2; 67.0%; Pred. No. 9.8e-26;

Best Local Similarity 67.00 Matches 61; Conservative

Query Match

GenCore version 5.1.6 Copyright (c) 1993 - 2003 Compugen Ltd.

OM protein - protein search, using sw model

September 15, 2003, 11:54:00; Search time 8:57348 Seconds (without alignments) 504:633 Million ceil updates/sec Run on:

US-09-423-100-2 Title: Perfect score:

.....NLELLRISHLANDSWLEPVQ 1 MFPT1PLSRLFDNAMLRAHE. Sequence:

3

BLOSUM62 Gapor 10.0 / Gapixt 0 f Scoring table:

12786 * seqs, 47.26705 res has

Searched

Total number of mits satisfying chosen parameters:

12786.1

Minimum DB seq length: 0 Maximum DB seq length: 2000000000

Post-processing: Minimum Match U% Maximum Match 1998

Listing first 45 summaries

SwissProt_41:* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

		æ			NEI EN FERNON	
Result		Overy				
<u>Q</u>	Score	Match	Length I	DR	a:	Description
-	460	97.9	217	-	SOMA, HUMAN	P01241 homo sapien
7	460		217	_	SOMA_MACMU	
~	460	47.9	217		SUMA PANTE	
4	4 4 4 4	92.1	217	-	SOMA SAIBB	
s.	4 3 2	91.3	217		SOMA_CALJA	
9	4 30	91.5	217	_	SOM2_PANTR	
7	775	86.8	217	_	SOM2_HUMAN	
æ	396	84.3	217	-	SOM2_MACMU	macac
6	383	81.1	217	-	PLI_HUMAN	P01243 homo sapien
10	310.5	66.1	216		SOMA_MESAU	_
1.1	307.5	65.4	190	-	SOMA_BALRO	P33092 balaenopter
12	304.5	64.8	216	-	SOMA_MOUSE	_
13	302.5	4.4	216	_	SOMA_HORSE	P01245 equus cabal
14	302.5	₹. ₹.	716	_	SCMA_RABIT	P46467 oryctolagus
15	302.5	64.4	216	_	SOMA_KAT	P01244 rattus norv
16	302.5	64.4	217	,	SOMA_GALSE	Oggkal galago sene
17	302.5	64.4	217	_	SOMA_NYCPY	Ogab2 nyet teebus
81	301.5	64.1	1.50	~	SOMA_LOXAF	220392 lexodonta a
<u>5</u>	3.11.5	64.1	216	~	SOMA_CANFA	P34711 canis tamil
70	301.5	64.1	216	-	SOMA_FELCA	P46404 felis silve
21	401.5	64.1	216	_	SOMA_PIG	P01248 sus sereta
77	299.5	63.7	216		SOMA_MUSVI	219795 mustela vis
5.7	2.242.5		190	-	SOMA_LAMPA	
24	245.5	6.2.9	190		SOMA_VULVU	
52	291.5	62.0	215	_	SOMA_MONDO	_
56	291.5	62.0	215	-	SOMA_TRIVU	O62754 trichosurus
7.7	5.887		217	~	SOMA_BOVIN	
58	289.5		217	_	SOMA_CEREI,	P56437 cervus elap
5.7	289.5	61.6	217	-	SOMA_SHEEP	-
30		60.1	217	~	SOMA_BUBBU	
3.			216	-	SOMA_MELGA	
32	275.5	58.6	216	_	SOMA_CHICK	_
33	274.5	58.4	217	-	SOMA_STRCA	O9pwg3 struthio ca

crocodylus	chelonia my	ands platyr	acipenser q	acipenser q	lepisosteus	xenopus lac	rana catesb	bufo marinu	prionace ql	xenopus lae	protopterus
P55755	P34005	P11228	P26773	P26774	P79885	P12855	P10813	073849	P34006	P12856	073848
SOMA_CRONG	SOMA_CHEMY	SOMA_ANAPI.	SOM1_ACIGU	SOM2_ACIGU	SOMA_LEPOS	SOMA_XENLA	SOMA_RANCA	SOMA_BUFMA	SOMA_PRIGI.	SOMB_XENLA	SOMA_PROAN
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58.0	57.	55.	54	'n	S	S	٠,	•		_	7
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ALIGNMENTS

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POIZAL: 014455 | 016641; 09HKA1; 09HMA7; QHUNLS; 21-JUL-1986 (Rel. 01, Created) | 01-MR-1992 (Rel. 01, Created) | 01-MR-1992 (Rel. 21, last sequence update) | 15-SEP-2003 (Rel. 4); last annotation update) | Somatopropin precur: r (Growth hormone) (GH-N) (Pitaltary growth hormone) (Growth hormone) (GH-N) (Pitaltary growth
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDIINE-89307277; PubMed-2744760; Chen E.Y., Liao Y.C., Smith D.H., Barrera-Suidana H.A., Gelinas R.E., Seeburg P.H.; The human growth hormone locus: nucleotide sequence, biology, and evolution ".
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       =
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A. (ISOFORM 1), AND POSSIBLE ALTERNATIVE SPLICING. BEDLINE-SEQUENCY SPORMED. ADDITION BOOLD SPORMED BOOLD F.M., MOOTE D.D., GOODWAN H.M.; "Human growth bormone DNA sequence and mRNA structure: possible
                                                                                                                                                                                                                                                                                                                                                                                           Eukaryota, Metazoa, Chordata, Craniata, Verrebrata, Euteleostomi, Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Romo.
NCBL_TaxID=9606,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       "The human growth hormone gene lamily: nucleotide sequences show recent divergence and predict a new polypoptide hormone"; DNA 1:239-249(1982).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Martial J.A., Hallewell R.A., Baxter J.D., Goodman H.M.:
"Human growth Bormone: complementary BNA closing and expression
bacterial";
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Gu J., Huang O.-H., Li N., Xu S.-H., Han Z. G., Fu G., Chen Z.;
An ovel gene expressed in human pituitary.";
Submitted (SEP-1999) to the EMBL/GenBank/DDRJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Roskam W., Rouqeon F.: "Molecular cloning and nucleotide sequence of the human growth hormone structural gene.": Nucleic Acids Res. 7:305-320(1979).
                                                                            217 AA
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Nucleic Acids Res. 9:3719:3730(1981).
                                                                            . L. H. J.
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SEQUENCE FROM N.A.
MEDLINE-83182010; PubMed=7169009;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             [2]
SEQUENCE FROM N.A. (1SOFORM 1).
MEDLINE-79203293; PibMed-377496.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A. (ISCFCKM 1).
MEDLINE-80034477; Pubmed-386281;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Science 205:662-607(1979)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Genomics 4:479-497(1989).
                                                                            STANDARIO
                                                                                                                                                                                                                                                                                                                                                             Homo sapiens (Human)
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Hu R.-M., Han Z.-G., Song H.-D., Peng Y.-)., Huang Q.-H., Ren S. X., Gu Y.-J., Huang C.-H., Li Y.-B., Jiang C. L., Fu G., Zhang Q.-H., Ku Gu B.-W., Dai M., Mao Y.-F., Gao G.-F., Kung R., Ye M., Zhou J., Xu S.-H., Gu J., Shi J.-X., Jin W.-R., Zhang C.-K., Wu T.-M., Huang G.-Y., Wu T.-M., Chen Z., Chen M.-D., Chen J.-L., Gree expression profilling in the human hypothalamus-pituitary-adrenal axis and full-length cDNA cloning."
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MEDLINE-80130196; PubMed-7356479;
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Li C.H., Utxon J.S.;
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28-FEB-2003 (Rel. 41, Last annotation update)
Somatotropin precursor (Growth hormone) (CT) (GH-N) (Pitaltary growth
                                       Gaps
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Li C.H., Chung D., Lahm H.W., Stein S.;
The primary structure of monkey pituitary growth hormone.";
Arch. Biochem. Biophys. 245:287-291(1986)
I FUNCTION: Plays an important role in growth control. Its major role in stimulating body growth is to stimulate the liver and other tissues to secrete IGF-1. It stimulates both the
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   Score 460; DR 1; Length 217;
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Mammalia, Eutheria, Primates, Catarrhin
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Independent duplication of the growth hormone gene in three
Anthropoidean lineages.";
Submitted (ARR-2001) to the EMBL/GenBank/DDBJ databases.
I FUNCTION: Plays ac important role in growth control. Its major role in stimulating body growth is to stimulate the liver and other tissues to secrete IGF-1. It stimulates both the differentiation and proliferation of myoblasts. It also stimulates amnino acid uptake and protein synthesis in muscle and other issues (By similarity).
I Subschioliarity. Eccarious Secreted.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            28-FEB-2003 (Rel. 41, last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Somatotropin precursor (Growth hormone) (GH) (GH:N) (Pitultary growth
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           2 FPTIPLSRLFDNAMLRAHRLHQLAFDTYQEFERAYIPKEQKYSFLQNPQTSLSFSFSIPT
                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
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Mammalia: Eutheria, Primates, Catarrhini, Hominidae, Pan.
NCBL_TaxID=9598;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ..
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                                                                                         DB 1; Length 217; 8.8e-41;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DB 1; Length 217;
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N >> D (IN REF, 2).
2C5180341EEC46D0 CRC64;
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                                                                                                                                                                                                                                                                                                                                                                           62 PSNREETOOKSNLELLRISLLLIQSWLEPVO 92
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                                                                                                                                                       0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SOMATOTROPIN.
BY SIMILARITY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 0; Mismatches
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                                                                                                Score 460;
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PROSITE; PS00266; SOMATOTROPIN_1: 1.
PROSITE; PS00338; SCMATOTROPIN_2: 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EMBL; AF374232; AAL72284.1; -.
InterPro: IPR001400; Somatotropin.
Pfam; PF00103; hormone; 1.
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                                24913 MW;
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                                                                                             94.08;
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                                                                                                                          98.98;
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                                                                                                                                                       Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STANDARD
                                217 AA;
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                                                                                                                             Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
                                                                                                                                                       90;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SOMA PANTE
P587563
   CONFLICT
                            SEQUENCE
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                                                                                             Query Mat.ch
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Saimiri boliviensis boliviensis (Bolivian squirrel monkoy).
Eukaryota: Metazoa: Chordata: Craniata: Vertebtata; Eureleostomi;
Mammalia: Eutberia; Primates: Platyritini: Petidao: Moninae; Sarriti.
                                                                                                                                                                                                                                                                                                                                                                            tissues (By similarity).
SUBCELLUIAR LAXATION: Secreted.
SIMILARITY: BELONGS TO THE SOMATOTROPIN/PROLACTIN FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 217;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   BY SIMILARI.
BY SIMILARII.
951528999, 152997 CRU64:
                                                                                                         28 FEB-2003 (Rel. 41, Created)
28-FEB-2003 (Rel 41, Last Sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
             217 AA
62 PSNREETQQKSNLELLRISLLLIQSWLEPVQ
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                                                                                                                                                    Somatotropin precursor (Growth hormone).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PROSITE; PSOUZ66; SOMATOTROPIN_1; 1. PROSITE; PSOUJ338; SOMATOTROPIN_2; 1. Hormone; Pituitary; Signal.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             InterPro; IPR001400; Somatotropin.
Pfam; PF00103; hormone; 1.
PRINTS; PR00836; SOMATOTROPIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           208 215 E
217 AA; 24864 MW;
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                                                                                       STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Best Local Similarity
                                                                                                                                                                                                              NCB1_, Lax : 1. - 3.54 <2.;
                                                                                    SOMA_SAIBB
P58343;
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                                                                                                                                                                                                              **Mallis O.C., Wallis M.; **Cloning and characterisation of a patative growth hormone encoding **Cloning and characterisation of a patative growth hormone encoding gene from the marmoset (Callithrix jacchab) databases.

Sobmitted (AUG-2000) to the EMBL/GenBank/Dibl databases.

FUNCTION: Plays an important role in growth control. its major rele in stimulation body growth is to stimulate the liver and other lissues to secrete (DF-1). It stimulates both the dileterialism and proliferation of myollasts. It also stimulates amino acid uptake and protein synthesis in muscle and other
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28-FEB-2003 (Rel. 41, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Growth hormone variant precursor (GH-V) (Placenta-specific growth hormone) (Growth hormone 2).
                                                                                                             Eukaryota: Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Platyrrhini; Callitrichidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Pan.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       .,
                                                                                                                                                                                                                                                                                                                                                                                                                   -! - SIMILARITY: BELONGS TO THE SOMATOTROPIN/PROLACTIN FAMILY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 217;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 432; DB 1; Length 21:
Pred, No. 7.2e 38;
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BY SIMILARITY.
E102151A12CE4192 GRC64:
28-FEB-2003 (Rel. 41, Created)
28-FEB-2003 (Rel. 41, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    91.9%; Score 432; DB 91.2%; Pred. No. 7.2e
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       5; Mismatches
                                                       Somatotropin precursor (Growth hormone)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Pfam; PF00103; hormo:e; 1.
PROSITE; PS00266; SOMATOTROPIN_1: 1.
PROSITE; PS00338; SOMATOTROPIN_2: 1.
                                                                                         Callithrix jacchus (Common marmoset)
                                                                                                                                                                                                                                                                                                                                                                                 tissues (By similarity).
*!* SUBCELLULAR LOCATION: Secreted.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    InterPro, IPR001400; Somatotropin.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Pan troglodytes (Chimpanzee).
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Best Local Similarity 91.28
Matches 83, Conservative
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                                                                                                                                                                                                     SEQUENCE FROM N.A.
                                                                                                                                                              NCBI_TaxID=9483;
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P58757;
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DISULFID
SEQUENCE
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NCBI_TaxID-9598;

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Gaps .;

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Baumann G.:
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or send an email to licenseelish-sib.eh).
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                                                                                             Submitted (APR-2001) to the EMBL/GenBank/DDBJ databases.

FUNCTION: Plays an important role in growth control. Its major role in stimulating body growth is to stimulate the liver and other tissues to secrete [GF-1]. It stimulates both the differentiation and proliferation of myoblasts. It also stimulates amino acid uptake and protein synthesis in muscie and other
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Growth hormone variant precursor (GH-V) (Placenta-specific growth
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Eukaryota, Metazoa: Chordata, Craniata; V-rtebrata, Eutoleostomi;
Mammalia: Eutheria: Primates; Catarrhin; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               "The human growth hormone gene family: nucleotide sequences show recent divergence and predict a new polypeptide hormone.";
                                                                                                                                                                                                                           tissues.
-!- SUBCELLULAR LOCATION: Secreted.
-!- TISSUE SPECIFICITY: Expressed in the placenta.
-!- SIMILARITY: BELONGS TO THE SOMATOTROPIN/PROLACTIN FAMILY.
                                     Revol A., Esquivol D., Santiago D., Barrera-Saldana H., *Independent duplication of the growth hormone gene in three Anthropoidean lineages.*;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         91.5%; Score 430; DH 1; Length 217; 93.4%; Pred. No. 1.2e-37;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GROWTH HORMONE VARIANT.
BY SIMILARITY.
BY SIMILARITY.
1592A429075677DE GRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           P01242: P09587;
21 JUL-1986 (Rel. 01, Created)
28-FEB-2003 (Rel. 41, Last Sequence ::pdate)
15-SEP-2003 (Rel. 42, Last arnotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 62 PSNREETQUKSNLELLRISLLLIQSWLEPVQ 92
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           217 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Hormone, Placenta, Signal, Glycoprotein, Signal, 26 BY SIMILARITY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      3; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A. (ISOFORMS 1 AND 2).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PROSITE: PS00266; SOMATOTROPIN_1; 1.
PROSITE: PS00338; SOMATOTROPIN_2; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDLINE-88243769; PubMed-3379057
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A. (ISOFORM 1)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Ptam: PF00103; hormone;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Ouery Match
Rest Local Similarity
Thos 85; Conserva
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Homo sapiens (Human)
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79 1
208 2
217 AA;
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                   SEQUENCE FROM N.A.
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*** Strong March 1980 | Purmed 12477932;

*** STROLINE-2286822.** Purmed 12477932;

*** Strougher Floor Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,

*** Altschul S.F., Zeeherg B., Burtow K.H., Schaefer C.F., Bhat N.K.,

*** Altschul S.F., Zeeherg B., Burtow K.H., Schaefer C.F., Bhat N.K.,

*** Altschul S.F., Zeeherg B., Burtow K.H., Schaefer C.F., Bhat N.K.,

*** Altschul S.F., Zeeherg B., Burtow K.H., Schaefer C.F., Bhat N.K.,

*** Appkins R.F., Jordan H., Moor T., Max S.I., Mang J., Hsieh F.,

*** Appkins R.F., Jordan H., Booters M.F., Casavant T.L., Scheetz T.E.,

*** Rabia S.S., Loquellano N.A., Helers G.J., Abramson R.D., Millahy S.J.,

*** Rabia S.S., Morley K.C., Halers G.J., Abramson R.D., Millahy S.J.,

*** Rechards S., Worley K.C., Hale S., Carcia A.M., Gay L.J., Hulyk S.W.,

*** Villaloc U.K., Muzny D.M., Sodergen E.J., Ju. X., Gibbs R.A.,

*** Richards S., Worley K.C., Hale S., Carcia A.M., Gay L.J., Hulyk S.W.,

*** Whiting M., Madan A., Young A.C., Schechenko Y., Boutfard G.G.,

*** Riakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,

*** Rabia S.A., Gilmwood J., Schmitz J., Myerrs R.M.,

*** Reneration and Jihtial analysis of more than 15,000 full-length

*** Furman and mount analysis of more than 15,000 full-length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    This SWISS-PROT entry is copyright. It is produced through a collaboration
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 between the Swiss institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           It also stimulates
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SUBUNIT: Monomer, dimer, rimer, tetramer and pontamer, disulfide-
linked or non-covalently associated, in homopolymeric and
linked or non-covalently associated, in homopolymeric and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            heteropolymeric combinations. Can also form a complex either with
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          "The human growth hormone locus: nucleotide sequence, biology, and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                "Growth hormone heterogeneity in human pituitary and plasma.":
Horm. Res. 51 Suppl. 1:2-6(1999).
-!- FUNCTION: Plays an important role in growth control. Its major
Cooke N.E., Ray J., Emery J.G., Liebhaber S.A.; "Two distinct species of human growth hormone-variant mRNA in the human placenta predict the expression of novel growth hormone proteins.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  role in stimulating body growth is to stimulate the liver and other tissues to secrete IGF-1. It stimulates both the differentiation and proliferation of myoblasts. It also stimul
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        amino acid uptake and protein synthesis in muscle and other
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-!- TISSUE SPECIFICITY: Expressed in the placenta.
-!- SIMILARITY: BELONGS TO THE SOMATOTROPIN/PROLACTIN FAMILY.
                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A. (ISOFORM 1).
MEDLINE.89024984: PubMed-2466050;
Jout A., Scippo M.L., Frankenne F., Hennen G.;
"Cloning and nucleotide sequence of placental hGH-V cDNA.";
Arch. Int. Physiol. Biochim. 96:63-67(1988).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDLINE-89307277; PubMed-2744760;
Chen E.Y., Liao Y.C., Smith D.H., Barrera-Saldana H.A.
Gelinas R.E., Sceburg P.H.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Nat1, Acad. Sci. U.S.A. 99:16899-16903(2002)
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SUBCELLUIAR LOCATION: Secreted.
ALTERNATIVE PRODUCTS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Event-Alternative splicing: Named isotorms=2;
Name=1; Synonyms=GH-V1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Name-2; Synonyms-GH-V2;
Isold=P01242-2; Sequence-VSP_006203;
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                                                                                                                                                                                        . Biol. Chem. 263:9001-9006(1988).
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Local Similarity
es 77; Conserv
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   TISSUE-Placenta
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CONFLICT
SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for connecrain entities requires a license agreement (Sec http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                        N-LINKED (GECNAC, ...) (POTENTIAL).
RLEDGSPRIGGIFNGSYSKFDIKSHNDDALLKNYGGI YGFR
KIMDKVETFIRIVGGKSVEGSGGF > VRVAPGIPNPGAP
                                                                                                                                                                                                                                                                                                                      LASRDWGEKHCO: FSSQALTQENSPYSSFPLVNPPGLSIQ
POGEGGKWMNERGREGESOPSAWPLLLFLHFARAGREWQPPDWA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Macaca mulatta (Rhesus macaque).
Eukaryota, Metazoa: Chordata; Craniata: Vertebrata; Euteleostomi:
Mammalia: Eutheria: Primates; Catarrhini: Cercopithecidae;
                                                                                                                                                                                                                        Hormone, Placenta: Signal: Clycoprofein: Alternative sp.icing;
                                                                                                                                                                                                                                                                                                                                                                                                                 89.8%; Score 422; DB 1; Length 217; 92.3%; Pred. No. 7.8e-37;
                                                                                                                                                                                                                                                                                                                                                                                                                                       4; Indels
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                                                                                                                                                                                                                                                                                                                                                                      /FIId-VAR_014591.
1 -> T (IN REF. 2).
789324698E822F96 CRC64;
                                                                                                                                                                                                                                                                                                                                          DLOSVLOUV (in i.oform 2).
/FTId-VSP_096263.
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3; Mismatches
                                                                                                                                                                                                                                                                 HY SIMILARITY.
BY SIMILARITY.
                                                                                                                                                                  GG: GG:GG0514G; F:poptide Lermanne; IAS,
InterPro: IPPC(1400; Semanoti-pin,
Pram: PF001 9; heimener; 1,
PROSITE: PS0024G; S-MATCTROPIN, 2: 1,
PROSITE: PS003449; S-MATCTROPIN, 2: 1,
                                                EMBL; K00470; AAA98619.1; --
EMBL; J03356; AAB59547.1; --
EMBL; W1875; AAB59548.1; --
EMBL; W18451; AAA55891.1; --
EMBL; J03071; AAA52552.1; --
EMBL; BCU20760; AAH20760.1;
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217
191
215
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166
                                                                                                                PIR: A28072; STHUV2.
PIR: D32435; STHUV.
HSSP; P01241; 1A22.
Genew: HGNC:4262; GH2.
                                                                                                                                                                                                                                                                                                                                                                                          217 AA;
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Best Local Similarity
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166
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                                                                                                                                                                                                                                Polymorphism.
SIGNAL
                                                                                                                                                Genew: HGNC:
MIM: 139240;
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CARBOHYD
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                                                                                                                                                                                                                                      Toke in stimulating body growth is to stimulate the liver and other tissues to secrete 10Fr. It stimulates both the differentiation and profiteration of myoblasts. It also stimulates amino acid uptake and protein synthesis in muscle and other
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            27 FPTIFLSWJENTAVERAHHLAKJAFDTYPKILEEAYIPKEGKYSFLKNPQTSLCFSESIPT
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01-APR-1988 (Rel. 07, tast sequence update)
15-SEP-2009 (Rel. 42, Last annotation update)
Lactogen precursor (Chorlomammotrupin) (Chorlonic somatomamotrupin).
CSH1 AND CSH2.
Homo sapiens (Human).
                        Golos T.G., Burning M., Fisher J.M., Fowler P.D.,
"Cloning of four growth hormone-chorionic somatomammotropin related complementary decaytibonucleic acids differentially expressed during pregiouncy in the rhesus monkey placenta.";
Endocrinology 133:1744-1752(1993).
... FUNCTION: Plays an important role in growth control. Its major
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Mammalia, Eutheria, Primates, Talarrhini, Hominidae, Homo.
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MEDLINE-85030426; Pubmed-6208192:
Selby M.J., Barta A., Baxter J.D., Bell G.I., Eberhardt N.L.;
                                                                                                                                                                                                                                                                                                                                                                                                                              -: TISSUE SPECIFICITY: EXPRESSED in the placents.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              84.3%; Score 396; DB 1; Length 217;
84.6%; Pred. No. 3.9e 34;
Live 6; Mismatches 8; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         8DB116CBC24EA090 CRC64;
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GROWTH HORMONE VARIANT.
                                                                                                                                                                                                                                                                                                                                                                                                        !- SUBCELLULAR LOCATION: Secreted (By similarity).
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BY SIMILARITY.
L >> F (IN REF. 2).
E -> G (IN REF. 2).
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| 1:1111-1111-11 | 11-111-1111
| PSNREFTQOKSNLEDALISDALIOSMLEPVO 117
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DiterPro; 1PR001460; Somatotropin.
Pfam. PF00103; hormone: 1
PRINTS; PR00846; SOMATOTROPIN.
PROSITE; PS00266; SOMATOTROPIN.
PROSITE; PS00338; SOMATOTROPIN.
MEDLINE-94008724; Pubmed-8404617;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 26 HY
27 217 GRN
79 1917 BY
208 215 BX
208 215 L
152 52 L
217 AA; 25221 MW;
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HSSP: P01241; 1HGU.
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XX MEDLINE-22388257; PubMed-12477932;

XA Klausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,

XA Klausher R.D., Collins F.S., Wagner L., Shemmen C.M., Schuler G.D.,

A Altschul S.F., Zeeberg B., Buetow K.H., Schaeter C.F., Bhat N.K.,

A Hopkins K.F., Jordan H., Moore T., Wang J., Hasher F.D.,

A Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,

Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Schectz T.E.,

A Browstein M.J., Usdin T.B., Toshlyuki S., Carrinor P., Pranqe C.,

Raha S.S., Loquellano N.A., Peters G.J., Atramson R.D., Mullahy S.J.,

Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratre P.H.,

Richards S. Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

VIII John D.K., Muzny V.M., Sodergren E.J., Lu X., Gibbs R.A.,

Raha S.S., Worley K.C., Shevcenko Y., Routfard G.G.,

Rahaksley R.W., Touchman J.M., Green E.D., Lickson M.C.,

Rodriguez A.C., Grimwood J., Schmutz J., Myers R.W.,

Butterfield Y.S.N., Krzywinski M.T., Skalska U., Smailus D.E.,

"Generation and initial analysis of more than 15,000 full-length."

In human and mouse Colba Sequences."
*Analysis of a major human chorionic somatomammotropin gene. Evidence for two functional promoter elements.";
J. Biol. Chem. 259:13131-13138(1984).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDLINE-89307277; Pithmed-2744760; Chen E.Y., Lido Y.C., Smith D.\mathrm{H.}, Barreru Caldana H.A., Swiisas R.E.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           The human growth hormone locus: nucleofide sequence, biology, and
                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
MEDIJNE-83160916: PubMed-6300056;
Marrera-Saldana H.A., Seebirg P.H., Saunders G.F.,
"Two structurally different genes produce the same serreted human placeful lactonen formone.";
J. Brol. Chem. 258.3787 429 (1983).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       "The human growth hormone gene tamily: nucly lide sequences show recent divergence and predict a new polypeptide hormone.":
DNA 1:239-249(1982).
                                                                                                                                     Hirt H., Kimelman J., Birnbaum M.J., Cher E.Y., Seeburg P.H., Eberhardt N.L., Barta A.:
The human growth hormone gene locus: structure, evolution, and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  JI C.H., Dixon J.S., Chung D.; Amino acid sequence of human chorionic somatomamotropin.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Proc. Natl. Acad. Sci. U.S.A. 99:16899 16963(2002)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A. (GENES CSHI AND USHZ).
                                                                                           SEQUENCE FROM N.A. (GENE CSH2).
MEDLINE-87161235; PubMed*3030680;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Nature 270:494-499(1977).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Genomics 4:479-497(1989).
                                                                                                                                                                                                               variations.";
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                                                                                                                                                                                                                                   DNA 6:59-70(1987).
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Construction and
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    evolution.
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MEDLINE-72016313; PubMed-5286363;

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                                                                                                                                                                            INTERCHAIN (WITH C-215 IN A DIMER).
[INTERCHAIN (WITH C-208 IN A DIMER).
P -> A (IN CSH2).
/FIId-VAR_007166.
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                                                                                                   Sherwood L.M., Handwerger S., McLaurin W.D., Lanner M.;
Nature New Biol. 235:64-64(1972).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SDD -> BBS (IN REF. 9).
235B0DC7A713F431 CRC64;
Sherwood L.M., Handwerger S., McLaurin W.D., Lann
"Amino-acid sequence of human placental lactogen.
Nature New Biol. 233:59-61(1971).
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MISSING (IN REF. 9).
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/FTId-VAR_007167.
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PROSITE; PS00266; SOMATUTKOPIN_1: 1.
PROSITE; PS00338; SOMATOTKOPIN_2: 1.
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EMBL; J00289; AAA52115.1; ...
EMBL; M15844; AAA52115.1; ...
EMBL; J03071; AAA5255.1; ...
EMBL; J00118; AAA9862.1; ...
EMBL; BC002921; AAH02717.1; ...
EMBL; BC005921; AAH05271.1; ...
EMBL; BC005921; AAH05071.1; ...
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Genew, HGNC:2441; CSH2.
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215
208
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116
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PIR; C32435; LCHUC.
HSSP; P01241; 1A22.
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217 AA:
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Matches 73; Conserv
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VARIANT
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61: Conservative
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HSSP; P01241; 1AXI.
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                                                                                                                                             NCBI_TaxID 9768;
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P06880;
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                                                                                                                                                                                                                                                                                                                                                                                                         role in stimulating body growth is to stimulate the liver and
other tissues to secrete [GF-1. It stimulates both the
differentiation and proliferation of myobiasts it also stimulates
amino acid uptake and protein synthesis in muscle and other
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                           messenger RNAS.";
Endocrinology 129:2965-2971(1991).
                                                                                                                                                                                                                  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteieostomi;
Mammalia; Eutheria; Rodentia; Sclurognathi; Muridae; Cricetinae;
Mesocricetus.
                                                                                                                                                                                                                                                                                                          MEDIJINE-92063850, Putmed-1954881;
Southard J.N., Sanchez-Jimenez F., Campbe ; G.F., Talamantes F.;
"Sequence and expression of hamster prolactin and growth hormone
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SIMILARITY: BELONGS TO THE SOMATOTROPIN/PROLACTIN FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     3B69CE32AB6F1. + CRC64;
                                                                                                               01-07T-1994 (Rel. 30, Created)
01-07T-1994 (Rel. 30, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
GMI OR GH.
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BY SIMILARITY
                                                                                                                                                                                                    Mesocricetus auratus (Golden hamster).
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Piam: PPR0103; hormone: 1.
PROSITE; PS00246; SOMATOTROPIN_1: 1
PROSITE; PS00338; SOMATOTROPIN_2: 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SUBCELLULAR LOCATION: Secreted.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PIR; B49159, H49159.
HSSP, P01246; 1BST.
InterPro; 1PR001400; Somatotropin.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   24690 MW:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EMBL: $56299: AAB20368.1; -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Hormone: Pituitary: Signal.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Similarity 67.08 61, Conservative
                                                                                          STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     216 AA;
                                                                                                                                                                                                                                                                                                SEQUENCE PROMINIAL
                                                                                                                                                                                                                                                                  NCBI_TaxID:10036;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         t issues.
                                                                                          SOMA_MESAU
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SOMA_BALBO
P33092;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DISULFID
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61
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Structural Studies of 1199 ic peptions from sarge ryan sec bromide "Structural Studies of 1199 ic peptions from sarge ryan sec bromide fragments of sei Whale (Baialgoptera Baicotts) somatofrogin."; Bloong, Khim, 4:1589-1599 (5978).

-: FUNCTION: Plays an important role in growth control. its major role in stimulating body growth is to stimulate the liver and other tissues to secrete 16F1. It stimulates both the differentiation and proliferation of myobblasts. It also stimulates
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 2 FPTIPLSRLFDNAMIRAHRIMQLAFUTYQEFEEAYIPKEQKYSFLGNPQTSLSFSESIPT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
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MEDLINE-85261358; PubMed-2991252;
Linzer D.I.H., Talamantes F.;
"Nucleotide sequence of mouse prolactin and growth hormone mRNAs and
                                                                                                                                                                                                   Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Cetartiodactyla, Cetacea, Mysticeti,
Balaenopteridae, Balaenoptera.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciuroqnathi; Muridae; Murinae; Mus.
NCBL_TaxID-10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   in muscle and other
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      65.4%; Score 307.5; 08.1; Length 190; 67.0%; Pred. No. 5.20.25;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   :- SIMILARITY: BELONGS TO THE SOMATOTROPIN/PROLATIN FAMILY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             BY SIMILARITY.
BY SIMILARITY.
09FBFF6DR14A7506 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                   Yudaev N.A., Pankov Y.A., Bulatov A.A., Osipova T.A., "Amino acid sequence of seiwhale somatotropin.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ...
01-OCT-1993 (Rel. 27, Created)
01-OCT-1993 (Rel. 27, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             01-JAN-1988 (Rel. 06, Crealed)
01-JAN-1988 (Rel. 06, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Somatchropin precursor (Growth hormone)
GHI OR GH.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           expression of these mRNAs during pregnancy ";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      amino acid uptake and protein synthesis
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60 PANKDEAQORSDVELLRESLILLIOSWLGPV0 90
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               InterPro: IPR001400; Sumatotropin.
Pfam: PF00103; hormone: 1.
PROSITE: PS00266; SOMATOTROPIN_1: 1.
PROSITE; PS00338: SOMATOTROPIN_2: 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1. SUBCELLULAR LOCATION: Secreted
                                                                                                                                                                   Balaenoptera borealis (Sei whale)
                                                                                                                                                                                                                                                                                                                                                                                                   MEDLINE-83000569; PubMed-7115813;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             190 AA; 21835 MW;
                                                                                                       Somatotropin (Growth hormone)
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us-09-423-100-2.rsp

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hormone.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       InterPro;
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                                                                                                                                                                                                                     hormone.
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                                                                                                                                                                                      This SWISS PROT entry is copyright; is treduced through a collaboration between the SWISS Institute of Buoinform. Cs. and the EMBL outstation the Buropean Bioinformatics Institute. It relates no restrictions in its most by non-profit institutions as long as its confent is it no way modified and this statement is not remove. Usage by and for connectial entities requires a license agreement (Se http://www.isb-sib.ch/announce/or send as email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gene 169:209-213(1996).

-!- FUNCTION: Plays an important role in growth control. Its major role in stimulating body growth is to slimulate the liver and other Lissues to secrete IGF-1. It stimulates both the differentiat.on and proliferation of myoblasts. It also stimulates amino acid uptake and protein synthesis in muscle and other
                             STRAIN-FZTDD; TISSUE-Liver;
MEDLINE-96194803; Pubmed-8647448;
Das P., Meyer L., Seyfert H.-M., Brockmann G., Schwerin M.:
"Structure of the growth hormone-encoding gene and its promoter in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Eukaryota: Metazoa: Chordata; Craniata: W. Lebrata; Exteleoslumi:
Mammalia: Eutheria: Perissodactyla; Equiu...; Equus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DB 1; Length 216;
                                                                                                                                                                 -1- SUBCELLULAR LOCATION: Secreted.
-1- SIMILARITY: BELGNGS TO THE SCHATOTROPIN/PROLACTIN FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1.2e-24;
thes 17; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                        98666A3AE25D65FC CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    21-JUL-1986 (Rel. 01, Created)
01-NoV-1995 (Rel. 32, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TISSUE-Pituitary;
MEDLINE-94266171; PubMed-8206392;
Ascacio-Martinez J.A., Barrera-Saldana H.A.;
                                                                                                                                                                                                                                                                                                                                                                                                                     SOMATOTROPIN.
BY SIMILARITY.
BY SIMILARITY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       : Pred. No. 1.26
14; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                           BY SIMILARITY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            64,8%; Score 304.5;
64,8%; Pred. No. 1.2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Somatotropin precursor (Growth hormone)
                                                                                                                                                                                                                                                                                                                                                                       PROSITE; PSG0266; SOMATOTROPIN_1: 1.
PRUSITE; PS00338; SOMATOTROPIN_2: 1.
Biol. Chem. 260:9574-9579(1985)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRT:
                                                                                                                                                                                                                                                                                                                                                  InterPro, 1PR001400; Somatotropin.
                                                                                                                                                                                                                                                                                                                                                                                                                                                        24716 MW;
                                                                                                                                                                                                                                                                                            EMBL; X02891; CAA26650.1; -. EMBL; Z46563; CAA86658.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                 Hormone: Pituitary; Signal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STANDARD;
                                                                                                                                                                                                                                                                                                                                                              Pfam; PF00103; hormone;
                                                                                                                                                                                                                                                                                                                                                                                                                      216
189
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                                                                                                                                                                                                                                                                                                                                                                                                                               78 1
206 2
216 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                 PIR: B23911; STMS.
HSSP; P01246; 1BST.
MGD; MGI:95707; Gh.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
                    SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                          SIGNAL
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the Lucpean Bloinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license afterement (See http://www.isb.sib.ch/announce/or send an email to license*isb.sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Zakin M.M., Poskus E., hellacha J.M., Paladini A.C., Santome J.A., "Amino acid sequences around the cystine residues in equine growth
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Oliver L., Hartree A.S.; Amino acid sequences around the cystine residues in horse growth
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Santome J.A.
                                                                                                                                                                                                                                                                           Zakin M.M., Poskus E., Langton A.A., Ferrara P., Santome J.A.,
Dellacha J.M., Paladini A.C.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    64.4%; Score 302.5; DB 1; Length 216;
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Best Local Similarity 64.8%; Pred. No. 2e-24;
Matches 59; Conservative 14; Mismatches 17; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDLINE-74020362; PubMed-4747849;
Zakin M.M., Poskus E., Dellacha J.M., Paladini A.C.,
"The amino acid sequence of equine growt; hormone.";
"Sequence of a cDNA encoding horse growth hormone.";
Gene 143:299-300(1994).
                                                                                                                                                                                                                                                                                                                                                                                      "Primary structure of equine growth harmone.";
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Pfam: PF00103; hormone: 1.
PROSITE; PS00266; SOMATOTROPIN_1: 1.
PROSITE; PS00338; SOMAIOTRCPIN_2: 1.
Hormone: Pituitary: Signal
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                                                                                                                                                                                                                            MEDLINE-77005410; PubMed-965151;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FEBS Lett. 34:353-355(1973).
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189
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78 1
206 2
216 AA:
                                                                                                                                                                SEQUENCE OF 27-216.
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SOMA_RABIT

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norvegicus (Rat)
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             This SWISS PROT entry is copyright. It is produced through a collaboration between the SWISS Institute of Rioinformatics and the EMBL outstation the European Bloinformatics Institute. There are no restrictions on its use by non-profit institutions as ion as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license attemment (See Tite://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                 STRAIN-New Zealand white;
MEDLINE-96011643; PubMed-7590276;
Wallis O.C., Wailis M.;
"Cioning and characterisation of the rabbit growth hormone encoding
                                                                                                                                         Oryctolagus cuniculus (Rabbit).
Eukaryota; Metazoa; Chordata; Craniata; VerLebrata; Euteleostomi;
Mammalia; Eutheria: Lagomorpha; Leporidae; Oryctolagus.
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                                     01-NOV-1995 (Rel. 32, Created)
01-NOV-1995 (Rel. 32, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  21.JUL.1986 (Rel. 01, Created)
21.JUL.1986 (Rel. 01, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
GMI OR GH.
    216 AA
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                                                                                                  Somatotropin precursor (Growth hormone).
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PRINTS: PR00836; SOMATOTROPIN.
PROSITE: PS00266; SOMATOTROPIN.
1: IPROSITE: PS00338; SOMATOTROPIN.
2: 1.
    PRT;
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SUBCELLULAR LOCATION: Secreted.
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HSSP: P01246; 1BST.
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  STANDARD;
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es 59; Conserv
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SEQUENCE FROM N.A.
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SOMA_RABIT
P46407;
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-! FUNCTION: Plays an important role in growth control. Its major role in stimulating hody growth is to stimulate the liver and other tissues to secrete IGF-1. It stimulates both the differentiation and proliferation of myobiasts. It also stimulates amino acid uptake and protein synthesis in muscle and other
                                                                                                                                                                                                                                                                                                                                                                                                               Seeburg P.H., Shine J., Martial J.A., Baxter J.D., Goodman B.M.;
"Nucledide sequence and amplification in bacteria of structural gene
Informat prowth homose."
                                                                                                                                          MEDLINE-82059526; PubMed-6272224;
Page G.S., Smith S., Goodman H.M.:
"DNA sequence of the rat growth hormone gene: location of the 5'
Letminus of the growth hormone mRNA and identification of an internal transposon-like element.";
Eukaryota: Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Barta A., Richards R.I., Baxter J.D., Shine J.;
"Primary structure and evolution of rat growth hormone gene.":
Proc. Natl. Acad. Sci. U.S.A. 78:4867-4871(1981).
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1. SIMILARITY: BELONGS TO THE SOMATOTROPIN/PROLACTIN FAMILY.
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F -> L (IN REF. 2 AND 4).
CABF49DC0B2A226C CRC64;
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Pfam: PF00103; hormone: 1.
PROSITE: P500266; SOMATOTROPIN_1: 1.
PROSITE: PS00338: SOMATOTROPIN_2: 1.
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MEDLINE~96056604; Pubmed~85211 ;;
Rohn W.M., Weigent D.A.;
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MEDLINE-82060155; Pubmed=6946433;
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24656 MW;
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HSSP; P01246; IBST
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                                                        NCBI_TaxID=10116;
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Search completed: September 15, 2003, 12:01:29 Job time : 8.57348 secs

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GenCore version 5.1.6
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OM protein - protein search, using sw model

September 15, 2003, 11:54:30 ; Search time 35.9427 Seconds (without alignments) 660.520 Million cell updates/sec Run on:

US-09-423-100-2 Title: Perfect score:

1 MFPT1PLSRLFDNAMLRAHR......NLFLLRISLALIQSWLEPVQ 92

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table: Sequence:

830525 segs, 25#U52664 cosidnes Searched:

8.345.25 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match U%
Maximum Match 100%
Listing first 45 summaries

Database :

sp_archea:*
sp_bacteria:*
sp_fungi:*
sp_human:*
sp_human:* sp_unclassified:* sp_vertebrate:* sp_rvirus:*
sp_bacteriap:* sp_organelle:* sp_phage:* sp_rodent:* sp_mammal:* sp_mhc:* sp_plant:* sp_virus:* SPTREMBL_23:* Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

sp_archeap:*

Description	Q8wne0 ateles geof	Ol4644 homo sapien	Q07369 macaca mula	Q07368 macaca mula	007367 macaca mula	Q14407 homo sapien	Q8wnd9 ateles geof	Ol4643 homo sapien	O8mi74 callithrix	070615 spalax leuc	Q8mi73 delphinus d	Q8hye5 ailuropoda	Q9r2c3 mus musculu	Q95205 ovis aries	09jkm4 cavia porce	Q8mi75 callithrix
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	24	283.5	09			Q95MJ6	
	25	280.5	59.			028957	
	56	265.5	56.5			095240	
	27	255.5	54.4			09PU72	Q9pu72 cynops pyrr
	28	242.5	51.6			09BDR4	O9bdr4 qalago cras
	58	234	49.8			014406	014406 homo sapien
	30	233.5	49.7	195		091386	Q91386 amia calva
	31	186.5	39.7			0	
	32	177.5	37.8				
	3.5	167.5	35.6		Ť		
	34	156.5	£.				090283 carassius a
	35	165.5	5.	2 187			
	95	165.5	. 5.				
	3.7	165.5	35.				Q8qqjl heteropneus
	38	165.5	35				
	39	365.5	35.5				Q90201 mylopharyng
	0	165.5	35				091056 hypophthalm
	41	265.5	35.2		13		Q8uvc8 megalobrama
	42	164.5	35.(C8av82 silurus aso
	43	163.5	34.8				carassius
	44	162.5	34.6				Q8axs5 carassius a
	45		34.4			Q98SR7	098sr7 cyprinus ca
						ALIGNMENTS	
33	RESULT 1						
08%	OBWNE						
QI.	OBWNEO	NEO	PRE	PRELIMINARY		PRT; 217 AA.	
AC	08W	OBWNEO;					
TO	01-	MAR-2002		(TrEMBLrel.	20,	Created)	
DŢ	01-	01-MAR-2002		(TremBLrel.		Last	
IJŢ	01-	01-MAR-2003		(TrEMBLrel.	23,		te)
DE	Gro	Growth hormone	one.				
Z U	GH-N.	ž					
so	Ate	les geof	froy	i (Black	-han	Ateles geoffroyi (Black-handed spider monkey).	
8	Ruk	aryota;	Meta	coa; Cho	rdat	Bukaryota; Metazoa; Chordata; Craniata; Vertebrata;	Euteleosto
						7.4.5	

Mammalia; Eutheria; Primates; Platyrrhini; Cebidae; Atelinae; Ateles. Gaps .; 0 Revol A., Esquivel D., Santiago D., Barrera-Saldana H.:
Revol A., Esquivel D., Santiago D., Barrera-Saldana H.:
"Independent duplication of the growth hormone gene in three
Arthropoidean lineages.";
Submitted (APR-2001) to the EMBL/GenBank/DDh.! databases.
EMBL. AF374234; AAL72286.1;
PINEST PREODIOS: hormone: 1.
PROSTE, PSO20266; SOMATOTROPIN.]: 1.
PROSTE, PSO338; SOMATOTROPIN.]: 1.
SEQUENCE 217 AA; 24894 MW; 425829F41EEAAE6 CRC64: 92.6%; Score 435; DB 6; Length 217; 92.3%; Pred. No. 3.5e-41; Indels 4; Mismatches 84; Conservative Query Match Best Local Similarity NCBI_TaxID-9509 Matches SON REPRESENTANT SON CONTRACT TO SON CONTRACT

us-09-423-100-2.rspt

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TISSUE-Midpregnancy placenta;
               Ouery Match
Best Local Similarity 83.3%
These 75; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRELIMINARY;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   212 AA;
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01-MAR-2003
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Macaca mulatta (Rhesus macaque).
Eukaryota: Metazoa: Chordata; Craniata; Vertebrata: Eureleostomi:
Mammalia: Eutheria: Primates; Catarrini: Cercopithecidae;
                                                                                                                                                                                                                                                                                               Eukaryota; Metazoa: Chordata; Craniata; Verrebrata; Euteleostomi;
Mammalia; Eutheria: Primates; Catarrhini; Hominidae; Homo.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       89.8%; Score 422; H 4; Length 24: 92.3%; Pred. No. 1.25-39; Live 3; Mismatches 4; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    26 POTENTIAL.
27101 MW: 14CC7F8CD3 (91C8 CRC64)
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Pfam: PF00103; hormone: 1.
PR0SITE: PS00256; SOMATOTROPIN_1: 1.
PROSITE: PS00338; SOMATOTROPIN_2: 1.
SEQUENCE 217 AA; 24874 MM; FIEB6AFDBBAIB185 CRC64;
                                                                                                                                                  01-JAN-1998 (TrEMBirel. 05, Last sequence update)
01-DEC-2001 (TrEMBirel. 19, Last annotation update)
Placental growth hormone isoform hGH-V3 precursor.
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01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-MAR-2003 (TrEMBLrel. 2), Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     J. Clin. Endocrinol. Metab. 83.2878.2885(1998).
EMBE: AF006061; AAB71829.1; -.
HSSP: P01241; 1A22.
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                                                               245 AA
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                                                                                                               01-JAN-1998 (TrEMBLrel, 05, Created)
01-JAN-1998 (TrEMBLrel, 05, Last seq
01-DEC-2001 (TrEMBLrel, 19, Last ann
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Pfam; PF06103; hormone; 1, PROSITE; PS00266; SOMATOTROPIN_1; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRT;
                                                            PRT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              InterPro, IPR001400; Somatotropin.
                                                                                                                                                                                                                                                                                                                                                                                                                                               TISSUE-Term placenta;
MEDLINE-9837373; PubMed-9709963;
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MEDLINE-94008724; Pubmed-8404617;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Chorionic somatomammotropin-3.
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Matches 84: Conservative
                                                         PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRELIMINARY;
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NCBL_TaxID=9544;
                                                                                                                                                                                                                                                                  Homo sapiens (Human)
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RESULT 2
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                                                                                                                                    28 PSVPLSKLFDNIMMQAHRLHGLAFDTYQEFEKTYIPKEKKHSLMGNPQASFCFSESIPTP 87
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"Cloning of four growth hormone/choritonic somatomammotropin-related complementary decayribonucleic acids differentially expressed during pregnancy in the rhesus monkey placenta.";
Endocrinology 133:244-1752(1993).
Endocrinology 133:244-1752(1993).
HSSP: PO1241: IAXI.
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Cl-MAK-2003 (TrEMELrel, 2), Last annotation update)
Somatchropin 2 precursor (Growth hormone 2) (Fragment).
Badcaca mulatta (Rhesus macaque).
Eukaryota, Metazoa; Chordata; Craniata; Verrebrata; Euteleustomi; Mammalla; Eutheria: Primates; Calarrhini; Cercoplithecidae;
NCBI Taxinsoca.
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Mammalia, Eutheria: Primates, Catarrhini, Cercopithecidae,
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     Length 217;
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Best Local Similarity 82.2%; Pred. No. 8 7e+77;
Matches 74; Conservative II; Mismatches 5; Indels
84.5%; Score 397; DB 6; Length 21
63.3%; Pred. No. 6.9e-37;
ive 8; Mismatches 7; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    24525 MW: 27BC91:0625656F5 CRC64;
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Pfam; PF00103; hormone: 1.
PROSITE: PS00338; SOMATOTROPIN_2: 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TISSUE-Placenta;
MEDLINE-94608724; Pubmed-8404617;
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3. PT LPL SPLEDNAMLPARREIGN AFT (YOBITERAY LOKROKY SPLONYOTS USERISTED 1) 1. 1.2.
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01-MAR-2003 (TremBLrel, 23, Last annotal, a update)
Chorionic somatomammotropia CS-2 (Chorionic somatomammotropia hormone
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEGUENCE FROM N.A.
MEDIJNE-89307277; PubMed-2744760;
Chen E.Y., Liao Y.C., Smith D.H., Barrer, Saldana H.A., Gelinas R.E.,
            Golos T.G., Durning M., Fisher J.M., Fowler P.D.,
"Cloning of four growth hormone/chorionic somatomammotropin-related complementary deoxythomucleic acids differentially expressed during pregnancy in the rhesus monkey placenta.",
EMBL: 116525, AAA18839.1;
HSSP: P01241: 1AXI.
InterPro. 1PR001400; Somatotropin.
Pfum: PF00103; hormone: 1.
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Monreak-Johnes C.L., Phillips J.A. [1].;
"Hot sports for growth bermone gene deletions in homologous regions
outside of Alu repeats.";
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Mammalia, Butheria, Primates, Catarrhin, Hominidae, Homo,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         "The human growth hormone locus: nucleotine sequence, blology, evolution.":
                                                                                                                                                                                                                                 Length 217;
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Submitted (JUL-2002) to the EMBL/GenBank/DDBJ databases
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                                                                                                                                                          PRINTS; PRO08'6; SOMATOTROPIN.
PROSITE; PSO0338; SOMATOTROPIN.2: 1.
SEQUENCE 217 AA; 24942 MW; FF5AA8915131F2BC CRC64;
                                                                                                                                                                                                                                 84.3%; Score 396; DB 6;
82.2%; Pred. No. 8.9e-37;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                2:7 AA
                                                                                                                                                                                                                                              Best Local Similarity 82.2%; Pred. No. 8.96
Matches 74: Conservative 11: Mismirches
                                                                                                                                                                                                                                                                                                                                                                                   63 SNREETOOKSNLELLRISLLLIQSWLEPVQ 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             01-NOV-1996 (TrEMBLrel. 01, Created)
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InterPro: IPR01400; Somatotropin.
Pfam. PF00103; hormone: 1.
PRINTS; PR00836; SOMATOTROPIN.
PROSITE: PS00266; SOMATOTROPIN_1: 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRT:
MEDLINE-94008724; PubMed-8404617;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EMBL: BC022044; AAH32044.1; -. EMBL: BC035965; AAH35965.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Science 250:1745-1748(1990)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRELIMINARY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Genomics 4:479-497(1989).
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Atelinae; Ateles.
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Mammalia; Eutheria: Primates; Catarrhini; Hominidae; Homo.
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Revol A., Esquivel D., Santiago D., Barrera-Saldana H.;

*Independent duplication of the growth hormone gene in three

Anthropoidean lineages.*;
                                                                                          81.1%; Score 381; DB 4; Length 217; 82.0%; Pred. No. 4.4e-35; Live 8; Mismatches 8; Indels
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EMBL: AR374235; AR372287.1; -.
InterPro; IFR001400; Somatotropin.
Pfam: PF00103; hormone; 1.
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PROSITE; PS00266; SCMAIOTRUPIN. 1; 1.
SEQUENCE: 217 AA; 25293 MW: 741745AIR75C053E CRC64;
                                 39FAACDDH6B2E951 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Ateles geoffroyi (Black-handed spider moukey).
Eukaryota: Metazoa; Chordata; Craniata; Vertebrata;
Mammulia: Eutheria; Primates; Platyrrhin: Cebidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     01-MAK-2002 (TrEMBLrel, 20, Last sequence update)
01-00T-2002 (TrEMBLrel, 22, Last annotation update)
Growth hormone.
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01-JAN-1998 (TrEMBLIR). 05, Last sequence update)
01-JUN-2002 (TrEMBLIR). 21, Last annotation update)
Placental growth hormone 20kba isoform precursor.
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PROSITE: PS00338; SOMATOTROPIN_2; 1. SEQUENCE 217 AA; 24994 MW; 39FAA
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MEDLINE-98373737; PubMed-9709963;
                                                                                                                           Best Local Similarity 82.0 Matches 73: Conservative
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Matches 69: Conservative
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                                                                                                 Query Match
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216 AA

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PRELIMINARY;
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Q8M173;
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Eukaryota: Metazoa: Chordata: Craniata: Vertobrata: Euteleostomi;
Mommalia: Eutheria: Primates: Platyrrhici; Callitrichidae; Callithrix.
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Boguszewski C.L., Svensson P.A., Jansson T., Clark R.,
Carlsson L.M.S., Carlsson B.;
"Cloning of two novel growth hormone transcripts expressed in human
placenta.":
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Wallis O.C., Wallis M.; "Characterisation of the GH gene cluster in a new-world monkey, the marmoset (Callithrix Jacchus)."; J. Mol. Endocrinol. 0:006(2002).
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202 AA: 23128 MW: 38B64D011A9197C6 CRC64;
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01-0cT-2002 (TrEMBLrel. 22, Last sequence update)
01-0cT-2003 (TrEMBLrel. 23, Last annotation update)
Growth hormone-like protein 5 precursor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          71.6%; Score 336.5; DB 4;
76.9%; Pred. No. 4.4e-30;
tive 3; Mismatches 3;
                                                                                                                                                                                                                   J. Clin. Endocrinol. Metab. 83:2878-2885(1998).
EMBL: AF006060. AAB71828.1;
TASP: POL241: 1A22.
InterPro. IPRO01406; Somatotropin.
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PROSITE: PSU0338; SOMATOTROPIN_2: 1.
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PROSITE; PS00266; SOMATOTROPIN_1; 1.
PROSITE; PS00338; SOMATOTROPIN_2; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRT;
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InterPro; IPR001400; Somatotropin,
Pram; PF00103; hormone; 1.
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                                                                                                                                                                                                                                                                                                                                                                                                        Pfam: PF00103; hormone;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              217
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es 70; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 85
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Eukaryota, Metazoa: Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Cetacea; Odontoceti; Delphinidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  11 :111 1: 11:11 1: 11:11 11:11 11:11 11:11 : 11:11 : 11:11 27 FPAMPLSNLFANAVLRAUHHQLAADTYKEFERAY:PEGGRYS-IQNAQAAFCFSETIPA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1; Gaps
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                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
MEDLINE 99124645; DELMEd=9924177;
MEDLINE 99124645; DELMEd=9924177;
Lioupis A., Mey E., Hallis M.;
"Clocing and characterisation of the gene encoding mole rat (Spalax ehrenbergi) growth hormone.";
L. M. Mol. Endocrinol. 22.29-36(1999).
EMBL: AJ005819; CAA06716.1;
HSSP: POLG47: 1AX:
HSSP: POLG47: 1AX:
PROSTINE: PROSTING: Somatotropin.
PROSTINE: PSOC386; SCMATOTR-PIN_: 1.
FROSTINE: PSOC386; SCMATOTR-PIN_: 1.
                                                                                                                Growth hormone precursor.
Spalax leucodon ehrenbergi (Ehrenberg's mole rat).
Eukaryota; Metazoa; Chordata; Craniata: Vertebrata; Eutelcostomi;
Mammaila: Eutheria: Rodentia: Schurognathi: Muridae; Spalacinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  65.2%; Score 306.5; DB 11; Length 216; 65.9%; Pred, No. 1.2e-26; ative 13; Mismatches 17; Indels 1;
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EMBL; AJ492191; CAD37292.1; -.
InterPro: IPR001400; Somatotropin.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        216 AA: 24627 MW. FEABBA523BA0ADFE CRC64;
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01-OcT-2002 (TrEMBLrel, 22, Last sequence update)
01-MAR-2003 (TrEMBLrel, 23, Last annotation update)
                              01-AUG-1998 (TEMBLIC). 07, Last sequence update)
01-MAR-2003 (TEMBLIC). 23, Last annotation update)
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01-AUG-1998 (TrEMBLrel. 07, Created)
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PRINTS; PR00836; SOMATOTROPIN.
PROSITE; PS00266; SOMATOTROPIN.
PROSITE; PS00338; SOMATOTROPIN...; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Conservative
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Best Local Similarity
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                                                                                                                                                                                                                                                                                 Nannospalax.
NCBI_fax1D-30637;
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Pfam: PF00103; hormone; 1.
PRINTS: PR00836; SOMATOTROPIN.
PROSITE: PS003266; SOMATOTROPIN_1; 1.
PROSITE: PS00338; SOMATOTROPIN_2; 1.
SEQUENCE: 216 AA: 24682 MW; FG2A06UA02535B18 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Pfam: PF00103; hormone: 1.
PRINTS: PR00836; SCMATOTROFIN.
PROSTE: PS00266; SCMATOTROPIN. 1: 1
PROSTE: PS00338: SCMATOTROFIN.2: 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDLINE-97050633; PubMed-8895361;
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Matches 59; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Bovidae: Caprinae; cvis.
NCBI_TaxID=9940;
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Q9JKM4
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                                                                                                                                                 2 FPTIPLSRLFDNAMLRAHRLHQLAFDTYQEFEEAYIPKEQKYSFLQNPQTSLSFSESIPT 61
                                                                                                                                                                               2 FPT:PL.SRLFDNAMLRAHRLHQLAFDTYQEF! :AYTPKEQKYSFLQNPQTSL.SFSES:PT 61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
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Eukaryota: Metazoa: Chordata: Craniata: Vertebrata: Eutrileostomi:
Mammalia: Eutheria: Rodentia: Sciuroquathi; Muridae: Murinae: Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Alluropoda melanojeuca (Giant panda).
Evkaryota: Metazoa: Chordata: Craniata: Vertebrata: Euteleostomi:
Mammalia: Eutheria: Carnivora: Fissipedia: Ursidae: Alluropoda.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Nguyen T.N.K., Liebhaber S.A.;
"Mouse Growth Hormone Locus: Nucleotide Sequence and Phylogenetic
                                                                                                      ;
                                                64.1%; Score 301.5; UB 6; Length 216; 64.8%; Pred. No. 4.3e-26; Live 14; Mismatches 17; Indels 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Liso M., Zhu M., Zhang A.;
"Cloning and expression of CDNA encoding growth hormone from
Alluropoda melanoleuca.";
Submitted (AGG-2002) to the EMBL/Gentank/DDR; databases.
EMBL, AF540936; AAN77228.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               64.1%; Score 301.5; DB 6; Length 216; 64.8%; Pred, No. 4.3e-26;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  i7; Indels
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24509 MW; 1EC467A84CCFEB02 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    44EC17EC44BCB056 CRC64;
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61 MAR-2603 (TrEMBLIE) 23, East sequence poure)
01-MAR-2003 (TrEMBLIE), 23, Last andotation update)
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01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
                                                                                                                                                                                                                                                                                   14; Mismatches
                                                                                                                                                                                                                                                        62 PSNKEETQÖKSNLELLKISLLLIQSWLEPVQ 92
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      POTENTIAL
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SEQUENCE 216 AA; 24383 MW;
                                                                   Best Local Similarity 64.8%
Matches 59: Conservative
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Matches 59, Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Growth hormone precursor.
                                                                                                                                                                                                                                                                                                                                                                                                                                     PEEL IMINARY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRELIMINARY;
216 AA;
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SEQUENCE
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"Expression of the growth hormone gene in ovine placenta: detection and cellular localization of the protein.";
Endocrinology 137:4886-4892(1996).
EMBL: U49063; AAC466F9-1; -.
HSSP: P01241; IAXI.
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Eukaryota: Metazoa: Chordata: Crania:a; Vortebrata: Euteleostomi;
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Eukaryota: Metazoa: Chordata: Craniata: Vertebrata: Euteleostomi:
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Owery Match 63.5%; Score 296.5; DB 11; Length 216; Best Local Similarity 63.7%; Pred. No. 9.4e-26; Matches 58; Conservative 14; Mismatches 18; Indels 1:
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64.8%; Pred. No. 1.1e+25;
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U-FEB-1997 (TFEMBLE31, G2, Last sequence update)
01-MAR-2003 (TFEMBL: 1, 23, Last annotation update)
Placental growth hormone (Fragment).
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01-0CT-2000 (TrEMBLrel. 15, Last sequence update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
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es 17;
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Mammalia; Butheria; Rodentia; Hystricognathi; Caviidae; Cavia. NCBI_TaxID~10141;

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Ouery Match
Best Local Similarity 64.2%; Prod. No. 1.20.2%;
Matches 58; Conservative 34; Mismatches 18; Indels 1; Gaps
                                                                        | [1] | SEQUENCE FROM N.A. | P. SEQUENCE FROM N.A. | P. SEQUENCE FROM N.A. | Oddrico D.M., Fuller P.J., Herington A.C.; Oddrico D.M., Fuller P.J., Herington A.C.; Oddrico D.M., Fuller P.J., Herington A.C.; Submitted (FEB-2000) to the EMBL/GenHank/ 'OBJ databases. I. Submitted (FEB-2000) to the EMBL/GenHank/ 'OBJ databases. I. Submitted (FEB-2000) to the EMBL/GenHank/ 'OBJ databases. I. H. SEPPO 1993, NATOROPIO. | P. PROSTIE; PRO00436; SOMATOTROPIN. | PROSTIE; PS000266; SOMATOTROPIN. | PROSTIE; PS000318; SOMATOTROPIN. | P. PROSTIE; PS000318; PROSTIE; PS000318; SOMATOTROPIN. | P. PROSTIE; PS000318; PROSTIE; PS000318
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27 216 GROWTH HARRONE,
216 AA: 24622 MV: 45950PFELL BORINGE CROSS.
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| SIDSI/gcddata/geneseqg-embl/AA1986.DdT:•
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| SIDSI/gcgdata/geneseqg-embl/AA2002.DdT:•
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1 FVNOHLCGSHIVEALYLVCG.....IVEQCCTSICSLYQLENYCN
                                  GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.
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Maximum Match 100%
Listing first 45 summaries
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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Result		_				
Q Z	Score		Match Length DB 1D	DB	Q1	Description
. ~	463	100.0	100.0 86 5	; ; ;	AAP40829	Sequence of human
2	463	100.0	86	17	AAR84061	Human insulin. Ho
~	463	100.0	98	20	AAY42858	Human insulin prec
4	463	100.0	86	21	AAB12770	Human proinsulin p
S	463	100.0	86	23	AAM48218	Human proinsulin.
Q	463	100.0	87	m	AAP20036	Human proinsulin
۲	463	100.0	87	2	AAP40217	Sequence of the 32
œ	463	100.0	87	9	AAP50127	Sequence of the 32
6	463	100.0	87	9	AAP50060	Synthetic proinsul

Sequence encoded by Proinsulin protein Modified human ins hpl. Homo sapiens Yeast alpha-factor Synthetic proinsul Human proinsulin Human proinsulin Human proinsulin posquence encoded by Sequence of preprosonants of preprosonation of preprosonants of preprosonat	Sequence of human human preproinsuli human preproinsuli human preproinsuli human insulin. Ho human insulin. Ho human proinsulin. Ho human proinsulin. Ho mare preproinsulin. Ho mare preproinsulin a human met. Arg prointum met. Arg prointum met. Arg prointum met. Arg prointum met. Human met. Pre prointum met. Human proinsulin met. Human preproinsulin met	liabetes; hormone. de y or enzymatically peptide residue*
AAP61090 AAR32567 AAR32567 AAR33855 AAP20467 0 AAP90102 0 AAY08004 S AAR68998 1 AAB12773 AAP10042 AAP10053 AAP10053 AAP10053	AAYOGGOB AAYOGGOB AAYOGGOB AAYOGGOB AAYOGGOB AAYOGGOB AANGGOB AANGGOB AANGGOB AANGGOB AANGBOB	86 AA. recursor. ny peptide: d in B nectiny pepti in A A2-K r a chemicall A residue or H
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663 1000. 663 1000. 663 1000. 663 1000. 663 1000.	44444444444444444444 64666666666666666	0829 stand 0829; MR-2003 (JG-1992 (ance of hu lin precur sapiens. on fied-site fied-bond fied-bond fied-site
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This sequence represents a human insulin precursor comprising insulin
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                                                                                                                                    DNA encoding human insulin precursors - which comprise B- and A-chains linked via amino acid chain contq. 1 or more glycosylation sites, for prepn. of insulin in tungal cells
                                                                                                                                                                                                                                       DNA sequences encoding insulin precursors of formula 8-Pg A, where I and A represent B - and A-chains of insulin respectively, and Pg represents a modified or any number of amino acids comprising at least one qlycosylation consensus site, can be inserted into expression vectors which in turn can be used to transform the insulin expression vectors which in turn can be used to another included host cells. The fondal cells are then cultured and the insulin expressed in such cells cin be narvested.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Insulin; precursor; growth hormone; chaperone; intramolecular; folding; conformation; chimeric protein; clasavabie; recombinant;
                                                                                                                                                                                                                                                                                                                                                                                                         100.0%; Score 463; DB-17; Lenath 86; 100.0%; Pred, No. 8.4e-44; ive 0; Mismatches 0; Indels (
                                                      Van DEN HONDEL CAMJJ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (TONG-) TONGHUA GANTECH BIOTECHNOLOGY LTD.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               61 SLOKRGIVEQUATSICSLYOLENYON 86
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                                                      Valinger R.
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 (MEST/) MESTRIC S.
(PLIV ) PLIVA PHARM & CHEM FAB.
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                                                                                     WPI; 1996-129917/14.
N-PSDB; AAT17830, AAT17831
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Best Local Similarity 100.
Matches 86: Conservative
                                                      Punt PJ,
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                                                      Mestric S,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        The inventors claim a method for the propo, of an insuffice provinced in which the Archain and Brchain are joined through a connecting peptide. The connecting peptide joines the Archain at the amino group of A-1 to the B-chain at the carboxyl group of B-30. The method is pref. for the propo. of human insulin precursor (see APAPA0829). The SOS of the connecting joptides of a number of species (Updated on 25-MAR-2003 to correct PA field.)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             0; Gaps
                                                                                                                                                                                                                                                                  Insulin precursor produ. From Linear S-sulphonate and mercaptan in single step without separate oxida.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 86;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     100.0%; Score 463; Db.5;
100.0%; Pred. No. 8.4e-43;
Live 0; Mismatches 0;
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/product= Insulin
                                                                                                                                                                                                                                                                                                                   Claim 17: Column 4: 8pp: English.
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                                                                                            82US-0349397.
80US-0134389.
80US-0210696.
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Conservative
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86: Conserv
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                                                                                            16-FEB-1982;
27-MAR-1980;
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                                                             16-FEB-1982;
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US4430266-A
                              07 - FFB - 1984
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Best Local Si
Matches 86
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precursor can be a component of chimeric proteins which additionally contains an Verminal fragment of chimeric proteins which additionally contains an Neterinal fragment of chimeric proteins which additionally contains an Neterinal fragment of the portion of the chimeric protein acts as an intramolecular chapero. (IMC) for the insulin of protein acts as an intramolecular chapero. (IMC) for the insulin of protein acts as an intramolecular chapero. (IMC) for the insulin of protein acts as an intramolecular chapero. (IMC) for the insulin contains a C-lerminal Arg residue which enables the high portion of the chimeric protein to be removed after folding has taken place. Production of the combinant human insulin via an NGH-proinsulin chimeric protein can provide human insulin with correctly linked cysteine bridges with forwer necessary procedural steps, and hence resulting in a higher yield of human insulin. The IMC sequences not only protect insulin sequences from intracclular degradation precursor, facilitate the solubility of the fusion protein and decrease the intermolecular intraactions among the fusion proteins, thus allowing folding of the fused insulin intermolecular intermolecular intermolecular intermolecular commercially useful high concentrations. The procedural steps of cyanogec bronnies cleavage, oxidative supplicitysis and related contentrations. The procedural steps of promitic purification steps can thus be climinated. Appropriate the size of high concentrations of mercaphas or the use or appropriate and celerated.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PEARDIGVOOVELGGGPGAGSLUPLALEG 60
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              100.0%; Score 46x; DB 20; Leaqth 86; 100.0%; Pred, No. 8 4e-43; Live 0; Mismai 2xx 0; Indels c
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Hes 86, Conservative
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The present invention describes an itsulin-like growth factor (16F)-1 variant (1), where an amine acid at position 3, 4, 5, 7, 10, 14, 17, 23, 24, 44 or 45, optionally in cumbination with an amino acid at position 12 and/or 16 of the hally cumbin 16F1 sequence, is replaced with an alanine, alycine, or a serine residue. The residue at position 7 may be replaced by any amino acid. (1) can have antidlabetic, cardiant, oneuroprotective, anorectic, tranqualliser, vulnerary, anorectic, cephrotropic, dermatological, antiHIV and antiviral activities. The 16F1 mutants are used in any methods where 16Fs or insulin are used, e.g. in treating hyperdycaemia, obesity-related, neurological, cardiac, renal, immunological, and anabolic disorders. These disorders include lung climents are used in any methods where 16Fs or insulin, are are 16Fs of include lung climents are used in a normal include lung climents of include lung climents and anabolic disorders. These disorders include lung climents of include lung climents and include lung climents of include lung included and include includes and tissue creations. Ridney disorders, and whole body growth disorders. They are an also be used for includers, and dissue events of biological active 16F or insulin a mammal. The 16F-1 mutants improve the native place process.
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                          Novel insulingly encourth factor (IGF) I mutants that selectively bind to IGF binding protein (IGFBP)-1 or (GFBP-3, used to improve the half-lives of IGF-1 and insuling
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100.0%; Pred. No. 8.4e-43;
3ve. 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           exemplification of the present invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  61 SLOKRGIVEOCCISICSI, POLENYON 85 HILL THILL THILL THILL THILL THILL THE BIS SLOKRGIVEOCCISICSI, POLENYON 86
                                                                                                                                                                         Disclosure; Page 44; 48pp; English.
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2000US - 248985P
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Best Local Similarity
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15-NOV-2000;
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Dubaquie Y, Filvaroff EH, Lowman HB;

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Gaps

Length 87; Indels

150,0%; Score 463; DP 3; 100,0%; Pred, No. 8,5e 43;

C; Mismarches

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The sequence comprises human proinsulin. (Updated on 25-MAR-2003 to correct Pk field.)
                                                                                                               Ouery Match
Best Local Similarity 100.0
Matches 86; Conservative
                                                                                   87 AA:
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C5-SEP 1984;
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12-FEB-1992
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                                                                                       Sequence
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Region
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                                                                                                                                                                                              The present invention relates to a method for treating cartilage disorders. The method comprises contacting cartilage with an active agent such as insulin-like growth factor (IGF 1) analog with a binding alfinity preference for GF binding protein-3 (IGFBP-3) over IGFBP-1, an IGF-1 analog with a binding affinity preference for IGFBP-1 over IGFBP-3, or a IGFBP displacer peptide that prevents the interaction of IGF with an IGF-B and does not bind to human IGF receptor. The method is useful for treating cartilage disorders (CD), including descentaive CD, urticalar CD such as themstoid arthritis and osteoarthitis. The present sequence is human proinsulin, which was used the illustrate the uncertion
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Treating cartilage disorders including cartilage damage by injury or degenerative cartilagenous disorders, by contacting cartilage with insuling like growth factor analog with altered affinity for ICF-binding.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    100.0%; Score 463, (38.23); Length 86; Harity 100.0%; Pred. No. 46-43; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Plasmid cloning vehicles - useful for transforming bacterial hosts to produce eukaryotic polypeptide.s).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               61 STUKRGIVEOCCISICSLYOLENYCN 86
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                                                                                                                                                             Disclosure: Fig 15; 136pp; English
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82US-0354287.
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(first entry)
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Matches 86: Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                               HE AA:
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02-JAN-1982;
03-MAR-1982;
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22 JUL - 1992
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2 FVNQHLJGSHLVEALYLVIGGERGFFYTPK TRREAEDLQVGOVELGGGFGAGSLQPLALEG 51
1 FVNOHLOGSHLVEALYLVCGERGFFYTPKTRHEAEDJOVGOVELGGGPGAGSLUPLALEG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               plasmid pTh alpha 1 was constructed by inserting a synthesised gene for thymosin alpha 1 (AAN40178) into plasmid pBR322. It is used for the construction of PTFp24. The inventors claim a method for protecting bacteria from phage infection - by transformation with cloning vector cong. seqment with restriction and modification activity. Produ. of plasmid pPR 26 or pPR27 which uses pTFp24; and produ. of plasmid pPR29 which uses a synthetic gene coding for the 32 N terminal AAS of proinsulin (see ANN40179).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Protecting bacteria from phage infection - by transformation with cloning vector contq. segment with restriction and modification
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence of the 32 N terminal AAs of proinsulin.
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                                                                                                              Location/Qualifiers
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/label- B-chin
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8405-0647338
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(tirst entry)
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LEGETHILLETT LELLEGET LEGETHILLET 
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      replication and on transcription generating polycistronic mrna
                                                 Score 463; DB 5; Lenath 87;
Pred. No. 8.5e-43;
0; Mismatches 0; Indeis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   with autonomous
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence of the 32 Noterminal AAs of projusulin.
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//abel- B chain
67..87
//abel- A chain
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                                                 100.0%;
100.0%;
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85CN-0101555.
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                                                                                    86: Conservative
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                                                                    Best Local Similarity
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          87 AA;
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16 APR 2182
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            Sequence
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                                                                                                                                                                                          Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               New selectable and autonomously replicating DNA expression vector useful in producing proteinaceous granules in cell transformants.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       comprising a runaway replicon and a transcriptional and translational activating sequence in the reading frame of the proinsulin coding sequence, the sequence contq. a translational stop signal. Host cells contq. the vector, which is sep- plasmid pC2103, are cultured, and proinsulin is produced as a highly homogeneous species of proteinaceous granule. The granule can be
                                                                                                                                                                                     0
                                                                                                                                      160.0%; Score 46%; DB 6; Length 87; 100.0%; Pred. No. 4.50-44;
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interferon and funds tissue plasminogen activator. (Updated on 16-AUG-2002 to add missing us field.) (Updated on 25-MAR-2603 to correct PA field.)
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                                                                                                                                                                                                                                                                                                                         61 SLOKKSLVEQCCISICSLYQLENYCN 86
111115-(11111-11111-11111-1
62 SLOKKSLVEQCCISICSLYQLENYCN 87
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/label=C chain.
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Zlabel*A chain.
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18-FER-1993
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                                                                                                                               1 FVNQHLCGSHLVEALYLVCGERGFFYTPKTRREAEDLQVGQVELGGGFGAGSLQFLALEG 60
                                                                                                                                           The inventors claim new recombinant plasmids contg. a DNA sequence encoding a polypeptide, which is forwign to E.coli, in reading phase with a DNA SQ, coding for at least one functional fragment derived from an outer membrane lipoprotein gene of E.coli. The foreign gene may be for human insulin. The lipoprotein gene functional fragment may be the promoter, the 5'-UTR, the 3'-UTR or the transcription termination signal provided that it includes at least the promoter.
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readily isolated from cell lysates and is stable on washing with urea or detergent solns, at low concns. The granule contains at least 50% of proinsulin and all isolation operations are
                                                                                                                                                                                                                                                                                                                           Recombinant plasmid; E.coli expression retor; secretion vector.
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                                                                                                                                                                                                                                                                                                        Sequence encoded by the structural gene for human proinsulin.
                                                                                             Lengt!, 87;
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                                       (Updated on 16-AUG-2002 to add missing OS field.) (Updated on 25-MAR-2003 to correct PA fiv.1d.)
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Best Local Similarity 100.0%;
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02-JAN-1981;
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Score 463; DB 7; Length 87; Pred. No. 8.5e-43;

1 FVNQHLCGSHLVEALYLVCGERGFFYTPKTRREAEDLQVGQVELGGGPGAGSLQPLALEG 60

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61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       This sequence represents human proinsulin and was decoded from the sequences given in AAQ3696-7001. The cDNA fragment ciding for proinsulin was inserted into plasmid vector pUC19 and disested with Kpn1 and HudIII. This resulted in the formation of the vector pPLNS. A fragment encoding amino acids 1-73 of CAI (see AAQ37002) was inserted into ppINS to give a plasmid which contained DNA sequences which coded for amino acids 1-73 of CAI, an 8 amino acid linker sequence and human proinsulin. This plasmid, p.C.CAI-proinsulin, could be used in the formation of insulin analogues which may be used in the treatment of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 FVNQHIGGSHLVEALYI,VCGERGFFYTPKTRREAEDI,QVGQVELGGGPGAGSI,QPLALEG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    New hepato selective and peripheral selective human insulin analogues - and their corresp. DNA, for treatment of type L and
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                                                                                                                                                                                                                                                                                                                                                                                                         Proinsulin protein sequence
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es 86; Conservative
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18-JUN-1993
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RESULT 13
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                                                                                                                                                                                                                                                                                                                                                                                                                                                 human profession connecting peptide and natural human insulin A-chain. Dipeptide removal is carefully controlled to obtain the desired prod. Without further degradation occurring, irrespective of whether the next dipeptide in the sequence defines a cathepsin
                                                                                                                                                                                                                                                                                                                                                                                                                 This modified human insulin precursor comprises an N-terminal initialing dipeptide, chosen from Met-Tyr or Met-Arg, which does not define a cathepsia C dipeptide removal stop point. This dipeptide is linked to the natural human insulin B-chain, natural
                                                                                                                                                                                                                                                                                                                                                                       Human insulin precursor - contg. Met-Tyr or Met-arg initiating dl:peptide for controlled removal by cathepsin C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 88;
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/label*native human msulin A-chain
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(Updated on 25-MAR-2003 to correct PA field.)
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Pred. No. 8.6e-43;
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                                                                                                                                                                                                                                                                                                                                    Mackellar WC,
                                                                                                        Human insulin precursor; cathepsin C.
                                                                                                                                             Location/Qualifiers
                AAR07682 standard; protein; 88 AA.
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                                                                                      Modified human insulin precursor.
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100.0%;
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                                                                                                                          Homo sapiens
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                                  AAR07682;
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RESULT 12
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    This sequence represents an analogue of native human proinsulin (hpI). The DNA encoding this sequence was used in the construction of the expression vector of the invention. The coding region of the hpI gene was synthesised and was cloned into the expression plasmid pCZR1265 (see also AAQ38107). Expression of this gene lead to the inclusion of an extra amino acid (Arg) in the second position from the N-terminal of mature hpI. The extra amino acid provides increased expression of levels of the protein and is then cleaved off to avoid undesirable immunological effects when used in humars. (Updated on 25-WAR-2003 to correct PN field.)
                                                                                                                                                                                                        Proinsuling hpl: native; pCZR126S; expression vector; E. coll; human; expression; immunological effect.
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100.0%; Pred. No. 8.6e 43;
.ive 0; Mismatches 6; Indels (
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AAR33855 standard; Protein; 88 AA
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                                                                                                                                                                                                                                                                               Homo sapiens
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21-APR-1992
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88EP 0312306 870S-5139687

"dibasic processing site"

/note-38...72 38, 39

/not.e-

"proinsulin chain C"

8..37 /note- "proinsulin chain B"

Location/Qualitiers

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The proinsulin is expressed in Saccharomyres rerevisiae AB163.1. It is encoded by a synthetic quae (see AAN96279). The 3 consecutive peptides are proinsulin chains B, C and A resp. The regions are
                                                                                                                                                                                                                                                                                                                                                         Expression and secretion of heterologous proteins in yeast - using truncated a-factor leader sequence confq. signal peptide and glycosylation site.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              dibasic processing sites.
(Updated on 25-MAR 2003 to correct P. (Teld.)
                                                                                                                                                                                                                                                                                                                                                                                                               Disclosure; fig 1; Z2pp; English
                                                                                                                                                                                                                                                                  CHEER ) CHIRON YER
                                                                                                                                                                                                                                                                                                                     1989-208260/29
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                      BCA-5; yeast preferred codons; post-translational processing; insulin; endopeptidase.
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Yeast alpha-factor signal-human proinsulin fusion product
                                                                                                      /note= "signal-proinsulin junction"
37..38
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                                                                                  Location/Qualifiers
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889S-0183252
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1 FVNQHLCGSHLVEALYLVCGERGFFYTPKTEREAEDLOVGOVELGGGPGAGSLOPLALEG 60

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STORRGIVEOCUSICSLYQLENYCN 92 61 SLOKKGIVEQCCTSICSLYQLENYCN 86

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AAP90102 standard; protein:

RESULT 15

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AAP90102;

Proinsulin: synthetic gene: yeast

Homo sapiens

Synthetic proinsulin.

(first entry)

01-NOV-1989 25-MAR-2003

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/cgn2_6/ptodata/1/iaa/6B_COMB.pep:*
/cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep:*
GenCore version 5.1.6
Copyright (c) 1993 - 2003 :cmpugen Ltd.
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ATTORNEY/AGENT INFCRMATION:
NAME: Leslie McDonell
RECISTRATION NUMBER: 34,872
REFERENCE/LOCKET NUMBER: 02481.160C GU005
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 408-4900
                                                                                                           61 SLOKRGIVEOCCTSICSLYQLENYCN 86
                                                                                                                            61 SLOKRGIVEGCCISICSLYGLENYON 86
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                                                                                                                                                                                                                            US-09-134-836-4
; Sequence 4, Application US/09134836
; Patent No. 5986048
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INFORMATION FOR SEO ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 96 aming acids
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Patent No. 6534281

GENERAL: Unbigariantion

APPLICANT: NFAMATION

APPLICANT: KTAJIMA, Sachiko

APPLICANT: NAKASUBO, Kaoru

APPLICANT: NAWASUBO, 1530

CURRENT APPLICATION NUMBER: US/09/878, 880

CORRENT FILING NATE: 2000-06-12

PRIOR FILING NATE: 2000-06-12

NUMBER: US/SOF UD NOS: 2

SOFTWARP: PARAMITIN NOSES. 2

SOFTWARP: PARAMITIN NOSES. 2
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TITLE CF INVENTION: PROTEIN VALIANTS
FILE REFERENCE: P.712R!
CORRENT APPLICATION NUMBER: US/09/723,891.
CURRENT FILING LATE: 2000-11-28
PRIOR PITING LATE: US/09/477,923
PRIOR PITING LATE: 2000-01 05
NUMBER OF SEQ. (0.NOS: 6
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Patent No. 6509443
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Query Match
Best Local Similarity 100.
Matches 86; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               86; Conservative
                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: Dubaquie, Yves
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TYPE: PRT
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Best Local Similarity
Matches 86; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Ouery Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                           GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                  US-09-723-896-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RESULT 4
US-09-878:380 1
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LENGTH: 86
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Type: par
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
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GENERAL INFORMATION:
APPLICANT: MUDFODEL FRADZ JOSEF
APPLICANT: Keller, Reinhold
TITLE OF INVENTION: Improved process for obtaining
TITLE OF INVENTION: insulin precursors having correctly backed cystine bridges
NOMBER OF SEGURDES: 7
CORRESPONDENCE ALORESS:
                                                                      1 FVNQHLCGSHLVEALYLVCGERGFFYTPKTRREAEDLQVGQVELGGGPGAGSLQPLALFG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Finngaas, Henderson, Farranow, Garrett &
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPEMATING SYSTEM: P1-DOS/MS-DAS
SOFTWARE: Patestin Release #1.6, Version #1.30
CURRENT APPLICATION (ATA:
  Mismatches
  .;
O
86: Conservative
  Matches
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1 FVNOHLGGSHI,VEALYLVCGERGFFYTPKTRREAEDLQVGQVELGGGGPGAGSLQPLALEG 60
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               100.0%; Score 463; DB 1; Length 97; 100.0%; Pred. No. 1.8e 47;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Indels
         Process For Obtaining Proinsulin
Possessing Correctly Linked
Cystine Bridges
                                                                                                                                                                                                                                                  COMPUTER READABLE FORM:
MEDIUM TYPE: DISKETTE, 3.5 INCH, 1.44 Mb STCRAGE
COMPUTER: 15M 386
                                                                                                               ADDRESSEE: Kenneth A. Genoni, Esq. STREET: Rt. 202-206 No. 5473049th/P.O. Box 2500 CITY: Somerville STATE: New Jersey COUNTRY: U.S.A. 21P: 08876-1258
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: 1BM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ for Windows Version 2.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NAME: Barbara V. Mauret, Esq.
REG:STRATION NUMBER: 31,287
REFERENCE/DOCKET NUMBER: HOE 92/F 384
TELECOMMUNICATION INFORMATION:
TELEPHONE: (908) 231-4079
TELEFAX: (908) 231-2255
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GENERAL INFORMATION:
APPLICANT: CONKlin, Darrell C.
APPLICANT: Lotton-Day, Catherine E.
APPLICANT: Lot, Si
APPLICANT: Jaspers, Stephen R.
ITLE OF INVENTION: INSULIN HOMOLOG
NUMBER OF SEQUENCES: 17
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         61 SLOKRGIVEOCCESICSLYQLENYON 86
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                                                                                                                                                                                                                                                                                                                                        SOFTWARE: WORDPERFECT 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/2,50,376A
FILING DATE: December 1, 1993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ADDRESSEE: ZymoGenetics, inc.
STREET: 1201 Eastlake Avenue East
CITY: Seattle
STATE: WA
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 11, Application US/08950720A Patent No. 6046028
                                                                                                                                                                                                                                                                                                                   OPERATING SYSTEM: WINDOWS 3.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FILING DATE: December 2, ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 97 Amino Acids
TYPE: Amino Acid (AA)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Best Local Similarity 100.0
Matches 86; Conservative
      TITLE OF INVENTION: Prod
TITLE OF INVENTION: POSS
TITLE OF INVENTION: CYSI
NUMBER OF SEQUENCES: 7
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                       FILING DATE: December
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPELICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   98102
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$-09-386.303A-4
Sequence 4, Application US/09386303A
Sequence 4, Application US/09386303A
Patent No. 6380355
GENERAL INFORMATION:
GENERAL INFORMATION: Franz-Josef
APPLICANT: Rubroder, Franz-Josef
TITLE OF INVENTION: Improved process for obtaining
Insulin precurs as having correctly bended cystine bridges
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      0
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                                                                                                                                                            NUMBER OF SEQUENCES: 7
CORRESPONDENCE ADDRESS:
ADDRESSEE: Finnegan, Henderson, Farrahow, Garrett
Dunner
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       100.0%; Score 463; DB 4; Length 96; 100.0%; Pred. No. 1.8e-47;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                        CPERATING SYSTEM: PC'D SZMS-14/S
SOFTWARE: Patentin Release #1.0, Version #1.40
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICATION NUMBER: 09/134.836
FILING DATE: «ORNOWN»
AITOMRY/AGENT INFORMATION:
NAME: Lestie McDonell
REGISTRATION NUMBER: 34,872
REFERENCE/DOCKET NUMBER: 02481 1600-00000
TELECOMMUNICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CURRENT APPLICATION DATA:
RAPLICATION NUMBER: US/US/186, 301A
FILLNO DATE: 31-Aug-1999
CLASSIFICATION: <URKNOWN>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LOCATION: 1..96
SEQUENCE DESCRIPTION: SEC ID NO: 4:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      61 SLUKRGIVEQCCTSICSLYQLENYON 86
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                                                                                                                                                                                                                                                                                                                          COUNTRY: USA
ZIP: Z0005-3315
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: 18M PC COMPAILED
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ORGANISM: Escherichia coli
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TELEPHONE: (202) 408-400
TELEFAX: (202) 408-4400
INFORMATION FOR SEQ ID NO: 4:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 4, Application US/08160376A Patent No. 5473649 GENERAL INFORMATION:
APPLICANT: Obermeler, Ranier APPLICANT: Get!, Martin APPLICANT: Ludwig, Jurgen APPLICANT: Sabel, Walter
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE CHARACTERISTICS:
LENGTH: 96 amino acids
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NAME/KEY: Protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TOPOLOGY: linear MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                          CITY: Washington STATE: D.C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TYPE: amino acid
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Matches 86; Conservative
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  US-09-386-303A-4
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APPLICANT: Thigpen, Anice E. APPLICANT: Quaade, Christian APPLICANT: Kruse, Fred
  TELEPHONE: (512) 418-3000
TELEFRAX: (512) 474-7577
INFORMATION FOR SEO 1D NO: 2:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Clark, Samuel A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TELEPHONE: 512/418-3000
TELEFAX: 512/474-7577
INFORMATION FOR SEQ ID NO: 2
SEQUENCE CHARACTERISTICS:
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                                                                                  110 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              110 amino acids
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CORRESPONDENCE ADDRESS:
ADDRESSEE: Arnold, W
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER READABLE FORM MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TYPE: amino acid STRANDEDNESS:
                                                                                                amino acid
                                                                                                                                          linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GENERAL INFORMATION:
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STATE: Texas
COUNTRY: USA
''USA 77210
                                                                                                                   STRANDEDNESS
                                                                                                                                          TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT:
                                                                                                                                                          US-08-589-028-2
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                                                                              LENGTH:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LENGTH:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STREET:
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CORRESPONSENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match 100.0%; Score 463; DB 3: Longth 116; Best Local Similarity 100.0%; Pred. No. 2.16-47; Matches 86; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER: IBM PC compatible OPERATING SYSTEM: PC DOS/MS:DOS SOFTWARE: Patentin Release #1.0. Version #1.30 CURENT APPLICATION DATA: APPLICATION NUMBER: US/08/589.028 FILING DATE: CONCURTENLY HEREWITH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ATTORNEY/AGENT INFORMATION:
NAME: Highlander, Steven L.
REGISTRATION NUMBER: 47,642
REFERENCE/DOCKET NUMBER: UTSD:426\HYL
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ### HITTH HITTH HITTH HITTH HITTH ### 85 SLOKRGIVEOCCTSICSL/VOLENYCN 11:0
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Clark, Samuel A.
Thigpen, Anice E.
Quaade, Christian
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          61 SLUKRGIVEQCCTSICSLYOLENYON 86
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/950,720A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AUDRESSEE: Arnold, White & Durkee STREET: P. O. Box 4433 CITY: Houston
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: Newgard, Christopher B.
APPLICANT: Halban, Philippe
                                                                                                                                                                                           60 - 96
                                                                                                                             ATTORNEY/AGENT INFORMATION:
NAME: Sawislak, Deborah A
REGISTRATION NUMBER: 37,438
REFRENCE/DOCKET NUMBER: 96-0'
TELECOMMUNICATION INFORMATION:
TELEPHONE: 206-442-6672
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         US-08-589-028-2
; Sequence 2, Application US/08589028
; Patent No. 6087129
                                                                                                                                                                                                                                                                                            INFORMATION FOR SEQ ID NO: 11:
                                                                                                                                                                                                                                                                                                                                                                                                            No. 6045. 380
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER READABLE FORM: MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                           SECUENCE CHARACTERISTICS:
LENGTH: 110 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                                   TELEFAX: 206-442-6678
                                                                                                                                                                                                                                                                                                                                                                  STRANDEDNESS: single
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                                                     CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
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COUNTRY: USA
77210-4433
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                                                                                                                                                                                                                                                                                                                                                                                                         MOLECULE TYPE:
                                                                                                                   FILING DATE:
                                     FILING DATE
                                                                                                                                                                                                                                                                                                                                                                                                                              US-08-950-720A 11
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APPLICANT:
APPLICANT:
APPLICANT:
APPLICANT:
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TELEFAX: (617)227-5941
INFORMATION FOR SEQ 1D NO: 2:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ATTORNEY/AGENT INFORMATION
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amino acid
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRIOR APPLICATION DATA:
APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                       Z1E: 02109 1875
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CLASSIFICATION: 435
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Best Local Similarity
Matches 86: Conserv
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                                                                                 RESULT 12
US-08-472-701-2
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                                                                                                           1 FVNQHLCGSHLVEALYLVCGERGFFYTPKTRREAEDLOVGOVFLGGGPGAGSLQPLALEG 60
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APPLICANT: Halban, Philippe A.
APPLICANT: Halban, Philippe A.
APPLICANT: Clark, Samuel A.
APPLICANT: Thippen, Anice E.
APPLICANT: Thippen, Anice E.
APPLICANT: Thippen, Anice E.
APPLICANT: Kruse, Fred
TITLE OF INVENTION: RECOMBINANT EXPRESSION OF PROTEINS FROM TITLE OF INVENTION: SECRETORY CFLL. LINES
NUMBER OF SEQUENCES: 56
                                            100.0%; Score 463; DB 3; Length 110; 100.0%; Pred. No. 2.1e-47; ive 0; Mismatches 0; Indels
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COMPUTER: IBM PC COMPATIBLE
SOPTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
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Pred. No. 2.1e-47;
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100.0%; Pred. No. 4.
... 0; Mismatches
                                                                                                                                                                         APPLICATION NUMBER: US/08/785,271
FILING DATE: CONCURRENTLY HEYEWICH
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/589,028
FILING DATE: 19-JAN-1996
ATTORNEY/AGENT INFORMATION:
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                                                                                                                                                                                                                                                                                         Sequence 2, Application US/08785273 Patent No. 6194176
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                                                                             86; Conservative
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Best Local Similarity
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TOPOLOGY:
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            US-08-784-582-2
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1 FVNQHICGSHLVEALYLVCGERGFFYTPKTRREAEDLGVGQVELGGGPGAGSLQPLALEG 60
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APPLICANT: Ramesh, Nagarajan
TILE OF INVENTION: Compositions and Methods for Treating Diabetes
FILE REFERENCE: P-UW 3264
CURRENT APPLICATION NUMBER: US/09/185,852
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Sequence 2, Application US/08472701
Patent No. 6509165
GENERAL INFORMATION:
APPLICANT: Griffin, Ann C.
APPLICANT: Hickey, William F.
TITLE OF INVENTION: Detection and Treatment Methods for TITLE OF INVENTION: 19pp I Diabetes
NUMBER OF SEQUENCES: 23
CORRESPONDENCE ADDRESS:
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100.0%; Pred. No. 2.1e-47;
Live 0; Mismatches 0;
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                                                                                                                                                                    STAFE: Masson
STAFE: Masson
STAFE: Masson
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HEGISTRATION NOMBER: 31,533
REFERENCE/DOCKET NUMBER: 10.1-092DV
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                        MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPENATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: ASCLI Text
CURRENT APPLICATION SATA:
APPLICATION NUMBER: US/08/472,701
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US-09-185-852-2
Sequence 2, Application US/09185852
Patent No. 6537806
GENERAL INFORMATION:
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Search completed: Septer
Job time : 20,7276 secs
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                                                                                                                                                                                                        Length 110;
                                                                                                                                                                                                                                           Indels
                                                                                                                                                                                                      Score 463; DB 4;
Pred, No. 2.1e-47;
                                                                                                                                                                                                                                         0; Mismatches
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
UPERATING SYSTEM: PC INS/MS-DGS
SOFTWARE: ASCII TEXE
CUPRENT APPLICATION DATA:
APPLICATION DATA:
APPLICATION DATA:
APPLICATION DATA:
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TITLE OF INVENTION: and Treating Type
NUMBER OF SEQUENCES: 23
CORRESPONDENCE ADDRESS:
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TELECOMMUNICATION INFORMATION:
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STREET: 60 State Street, suite 510
CURRENT FILING DATE: 1998-11-04
EARLIER APPLICATION NUMBER: 60/087,660
EARLIER FILING DATE: 1998-06-02
NUMBER OF SEQ 1D NOS: 11
SEQ ID NO: 2.0
SEQ ID NO: 2.0
LENGTH: 110
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ATTORNEY/AGENT INFORMATION:
AMME: Defont; Gluito A. Jr.
REGISTRATION NOMBER: 31,503
                                                                                                                                                                                                     100.0%;
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APPLICATION NUMBER: US 08,
FILING DATE: 08-JULY-1994
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TELEFAX: (617)227-5941
INFORMATION FOR SEQ ID NO: 2:
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                                                                                                                               ) TYPE: PRT
) ORGANISM: Homo sapiens
US-09-185-852-2
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Matches 86: Conserve
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Matches 86; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Boston
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APPLICANT: Higashkuni, Naohiko
APPLICANT: Higashkuni, Naohiko
APPLICANT: Kudo, Toshiyuki
APPLICANT: Kudo, Toshiyuki
APPLICANT: Kudo, Toshiyuki
APPLICANT: Kudo, Masaayiki
APPLICANT: Kudo, Masaayiki
APPLICANT: Kudo, Toshiyuki
TITLE OF INVENTION: DNAS ENCODING NEW FUSION PROTEINS AND PROCESSES FOR
TITLE OF INVENTION: PREPARING USEFUI, POLYPEPTIDES THROUGH EXPRESSION OF THE
TITLE OF INVENTION: DNAS
TITLE OF INVENTION: DNAS
TITLE OF INVENTION: DNAS
TITLE OF INVENTION: DNAS
TITLE OF INVENTION NEW BRITER APPLICATION NEW BRITES APPLICATION NEW BRITER APPLICATION NEW BRITES AP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             September 15, 2003, 12:05:32
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                                                                                                                            61 SLOKRGIVEQUOTSICSLYQLENYCH
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Patent No. 6506595
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September 15, 2003, 12:03:35 : Search time 36.0645 Seconds (without alignments) 347.945 Million cell updates/sec
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GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

/cgn2_6/ptcodata/1/pubp: //S10_NEW_PUB_pep: • /cgn2_6/ptcodata/1/pubpa_/US60_NEW_PUB.pep: • /cgn2_6/ptcodata/1/pubpa_/US60_PUBCOMB.pep: •

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	463	100.0	98	0.5	US-09-878-380-1	Sequence 1. Appli
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~	463	100.0	98	14	US-10-028 :15-2	-
4	463	100.0		14	US-10-05473-4	
5	4.6.3	100.0	96	7.0	US-09-947 (63-4	
ę	464	100.0		2	US-09-205-+ 8 125	Sequence 125, App
7	463	100.0	_	'n	US-09-815-229-3	Sequence 3, Appli
α¢	463	100.0	110	10	US-09-804-405A-9	Sequence 9, Appli
ۍ	464	100.0		12	US-09-969-148C-6	Sequence 6, Appli
0.1	463	100.0	_	15	US-10-038-686-1	Sequence 1, Appli
Ξ	463	100.0		15	US-10-328-813-2	Sequence 2, Appli
17	463	100.0		5	US-09-280-030-63	Sequence 63, Appl
1 3	463	100.0	•	σ	US-09-280-030-62	Sequence 62, Appl
14	457	98.7		10	US-09-947-563-5	Sequence 5, Appli
15	306	66.1		6	US-09-925-297-805	Sequence 805, App

Sequence 10, Appl Sequence 13, Appl Sequence 5, Appli Sequence 6, Appli Sequence 7, Appli	Sequence 5, Appli Sequence 3, Appli Sequence 18, Appl Sequence 19, Appl	3, A 12, A 10, A 3, Ap 12, A		Sequence 7, Appli Sequence 132, Appli Sequence 113, Appli Sequence 115, Appli Sequence 115, Appli Sequence 14, Appli Sequence 14, Appli Sequence 4, Appli
0 0 0 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1	11001	50 14 US-10-066-0948-3 124 9 US-09-736-611-12 125 9 US-09-736-611-16 147 9 US-09-736-611-8 124 9 US-09-740-359-12 124 10 US-09-894-711-12	2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2	146 10 0S-09 89-84, 711-5 146 10 0S-09 89-7711-7 46 9 0S-09-205-658-13 50 9 0S-09-205-658-13 46 9 0S-09-205-658-115 46 9 0S-09-205-658-115 32 9 0S-09-815-229-14 35 9 0S-09-947-563-6 46 9 0S-09-947-563-6 46 9 0S-09-815-229-4
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ALIGNMENTS

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APPLICANT: KITAJIMA, Sachiko
APPLICANT: KURANO, Yoshihiro
APPLICANT: KURANO, Yoshihiro
APPLICANT: KURANO, Yoshihiro
APPLICANT: MARATSUBO, Kaoru
APPLICANT: NISHIZUNO, 18 aoru
IIILE OF INVENTION: Inmunoassay For Measuring Human C-Peptide and Kit Therefor
FILLE REPERENCE: 0760-0291P
CURRENI PELING DATE: 2001-06-12
PRIOR APPLICATION NUMBER: JP 2000-174591
PRIOR APPLICATION NUMBER: JP 2000-174591
NUMBER OF SEO 10 NOS: 2
SOFTWAKE: Patentin version 3.1
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                      Sequence 1, Application US/09878380 Patent No. US20020160435Al GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity 100.
Matches 86; Conservative
                                                                                                       APPLICANT: Fujirebio Inc. APPLICANT: KITAJIMA, Sac
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US-09-878:380-1
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                                                                                                                                                                                                                                                    APPLICANT: Dubaquie, Yves
APPLICANT: Filvaroff, Ellen
APPLICANT: Lowman, Henry B.
TITLE OF INVENTION: METHOD FOR TREATING CARTILAGE DISORDERS
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TITLE OF INVENTION: PROTEIN VARIANTS
FILE REFERENCE: P172R1-1
CURRENT AFFLICATION NUMBER: US/10/026,416
CURRENT FILING OATE: 2001-12-15
PRIOR APPLICATION NUMBER: US/09/477.524
PRIOR APPLICATION NUMBER: US/09/477.524
PRIOR FILING CATE: 2000 61-05
SEQ 10 NO 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FILE REFERENCE: P1794R1
CURRENT APPLICATION NUMBER: US/09/658,9358
CURRENT FILINS DATE: 2002-37-02
PRICE FILING DATE: 2000-11-15
PRICE FILING DATE: 2000-11-15
PRICE REPLICATION NUMBER: US 60/204-450
PRICE FILING LATE: 2000-05-16
NUMBER OF SEQ 1D NOS: 153
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                                                                   Sequence 4, Application US/09858935B
Publication No. US20030069177A1
GENERAL INFORMATION:
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; Publication No. US/20020160955Al
; GENERAL INFORMATION:
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: Sequence 4, Application US/10054873
: Publication No. US20020164712A1
: GENERAL INFORMATION:
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Matches 86, conservative
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US 10-628-415 2
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insulin precursors having correctly bonded cystine brid
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APPLICANT: Gar, Zrong Ru
TITLE OF INVENTION: Chimeric Protein Containing an
Intramolecular Chaperone-Like Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match 100.0%; Score 464, DB 14; Length 86; Best Local Similarity 100.0%; Pred. No. 9.7e-45; Matches 86; Conservative 0; Mismatches 0; Indels 0
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                                                                                                                                                                                                                                                                    COMPUTER REAGASIE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IHM PC COMPUTER:
OPERATING SYSTEM: PC-NOS/MS-LUS
SOFTWARE: Patentin Release #1.0, Version #1.30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: Rubreder, Franz-Josef
Kejter, Reinhold
TITLE OF INVENTION: Improved process for obtaining
                                                                                                                           ADDRESSER: Townsend and Townsend and Grew LLP STREET: Two Embarcadero Center, Eighth Floor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NAMÉ: Mycrolt, Frank J
REGISTRATION NUMBER: 46,946
REFERENCE/DOXCKET K MBER: 020167-000130US
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRIOR APPLICATION DATA: MC PCT/CNS8/COOS2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FILLING DATE: 31-MAR-1998
APPLICATION NUMBER: US 69742+ 100
                                                                                                                                                                                                                                                                                                                                                                                       CURRENT APPLICATION DATA:
RAPILOKTION NUMBER: US/10/054.873
FILENG DATE: 22-543-2002
GLASSIFICATION: «UNKNOWN»
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE DESCRIPTION: SEQ ID NO. 4: 0S-10-054-873-4
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MEDIUM TYPE: Floppy disk
COMPUTER: 118M PC compatible
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FILING DATE: 11-DEV-2000
A FURNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 4, Application 05/09947563 Patent No. US20020156234A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STRANDEDNESS: <Unknown>
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                                                                                                                                                                     CITY: San Francisco
STATE: Cali:ornia
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                                                                                                 CORRESPONDENCE ADDRESS:
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ULE TYPE: protein
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STATE: D.C.
COUNTRY: USA
                                                                            NUMBER OF SEQUENCES: 7
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Sequence 3, Application US/09815229

Patent No. US20020058614A1

Patent No. US20020058614A1

Patent No. US20020058614A1

Patent No. US20020058614A1

APPLICANT: Filvaroff, Ellen H.

APPLICANT: Okumu, Franklin W.

TITLE OF INVENTION: USE OF INSULIN FOR THE TREATMENT OF CARTILAGENOUS DISORDERS
FILE BEFERNCE: P1786R1US

CURRENT APPLICATION NUMBER: US/07/415,229

PRIOR APPLICATION NUMBER: US/07/415,229

PRIOR APPLICATION NUMBER: US/05/1921/3

PRIOR APPLICATION NUMBER: US/05/1921/3

PRIOR APPLICATION NUMBER: US/05/1921/3
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                               1 FVNQHICGSHLVEALYLVCGERGFFYTPKTRRFAEDLQVGQVELGGGPGAGSLQPLALEG 60
                                                      1 FVNQHICGSHIVEALYLVCGERGFFYTPKTRREAEDLQVGQVELGGGPGAGSLQPLALEG 60
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APPLICANT: KIEFER, TIMOTHY J.
APPLICANT: CHEUNG, ANIHONY T.
APPLICANT: CHEUNG, ANIHONY T.
TITLE OF INVENTION: CAPACITIONS AND METHODS FOR REGULATED PROTEIN
TITLE OF INVENTION: EXPRESSION IN SUT
FILE REPERENCE: 0.9996/0.027 87.21
CURRENT APPLICATION NUMBER: US/09/804.4.05A
CURRENT FILING DATE: 2001-03-12
NUMBER OF SEQ ID NOS: 18
SOFTWARE: PATENTIN VEY. 2.1
SEQ ID NO 9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match 100.0%; Score 463; DB 9; Best Local Similarity 100.0%; Pred. No. 1.3e-44; Matches 86; Conservative 0; Mismatches 0;
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                                                                                                                                          ## S SLOKRGIVEOCCISICSLYQLENYCN 110
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                                                                                                                     61 SLQKRGIVEQCCTSICSLYQLENYCN 86
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US-09-815-229-3
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ORGANISM: Homo sapiens
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US-09-815-229-3
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Patent No. 1820010029617a1
GENERAL INFORMATION:
APPLICANT: RUNKWIN, GATY
APPLICANT: RUNKWIN, GATY
TITLE OF INVENTION: THERAPEUTIC AND DIAGN-SFIC TYOLS FOR
TITLE OF INVENTION: THERAPEUTIC AND DIAGN-SFIC TYOLS FOR
TITLE OF INVENTION: IMPAIRED GLUCOSE TOLERANCE CONDITIONS
FILE REFERENCE: 00786/351004
CURRENT APPLICATION NUMBER: 08/957,074
EARLIER FILING DATE: 1998-12-03
EARLIER FILING DATE: 1997-07-07
EARLIER FILING DATE: 1997-07-07
EARLIER FILING DATE: 1997-07-07
EARLIER FILING DATE: 1997-07-07
EARLIER FILING DATE: 1998-05-15
NUMBER OF SEO ID NOS: 328
SOFTWARE: RESULT NOS: 328
SOFTWARE: RESULT NOS: 328
SOFTWARE: RESULT NOS: 328
         CURRENT APPLICATION DATA:
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/947,563
FILING DATE: 07-Sep-2001
CLASSIFICATION: CURKOWN>
PRIOR APPLICATION: CURKOWN>
PRIOR APPLICATION NUMBER: 09/134,836
FILING DATE: CONKNOWN>
ATTORNEY/AGENT INFORMATION:
NAME: Leslie McDoncell
REGISTRATION NUMBER: 34,872
REFERENCE/DOCKET NUMBER: 34,872
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 2 SEQUENCE DESCRIPTION: SEQ 1D NO: 4 US-09-947-56.44
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                                                                                                                                                                                                                                                                                                                 TELEPHONE: (202) 408-4000
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
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                                                                                                                                                                                                                                                                                                                                                                                                            LENGTH: 96 amino acids
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                                                                                                                                                                                                                                                                                                                                                                                                                                    amine acid
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Moderniar TYPE: protess
ORIGINAL SOURCE:
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ORGANISM: Homo sapiens
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Matches 86; Conserva
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APPLICANT: Hasbhkuni, Nachiko
APPLICANT: Hasbhkuni, Nachiko
APPLICANT: Hugashikuni, Nachiko
APPLICANT: Hugashikuni, Nachiko
APPLICANT: Kudo, Toshiyuni
APPLICANT: Kondo, Masaaki
TITLE OF INVENTION: DINAS ENCODING NEW FUSTON PROTEINS AND PROCESSES FOR
TITLE OF INVENTION: DNAS
FILE REPERENCE: 382.1026
CURRENT APPLICATION NUMBER: US/99/280,030A
CURRENT FILING DATE: 1999-03-26
EARLIER PILING DATE: 1999-03-26
EARLIER FILING DATE: 1999-03-31
NUMBER OF SEQ ID NOS: 66
   1 FVNOHLCGSHLVEALYLVCGERGFFYTPKTRREAEDLOVGGVELGGGFGAGSLQPLALEG 60
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                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: Osborne, William R.A.
APPLICANT: Ramesh, Nagarajan
TITLE OF INVENTION: Compositions and Methods for Treating Diabetes
FILE REFERENCE: P-UW 3-244
CURRENT APPLICATION NUMBER: US/10/328.81*
PRIOR APPLICATION NUMBER: US/09/185.452
PRIOR FILING BATE: 19-4-1-64
PRIOR FILING BATE: 19-4-1-64
PRIOR APPLICATION NUMBER: US/09/185.452
PRIOR FILING BATE: 19-4-1-64
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                                                                                                                                61 SLOKRGIVEGCCTSICSLYOLENYCH
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; Patent No. US20010021515A1
; GENERAL INFORMATION:
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Publication No. US20030113305A1
GENERAL INFORMATION:
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ORGANISM: Artificia: Sequence
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NUMBER OF SEQ 1D NOS: 11
SOFTWARE: Patentin Ver. 2.0
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Matches 86; Conservative
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APPLICANT: SHERIDAN, Philip, J.
APPLICANT: SHERIDAN, Philip, J.
APPLICANT: SHERIDAN, Philip, J.
APPLICANT: GLAPIN, Jacqueline, M.
APPLICANT: GLAPIN, Jacqueline, M.
APPLICANT: GLAPIN, Steven
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE TRANSPORT OF BIOLOGICALLY ACTIVE
FILE OF INVENTION: AGENTS ACROSS CELLULAR BARRIERS
FILE OF INVENTION: AUGUST ACROSS COORTING
FILE OF INVENTION AUGUST ACROSS COORTING

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100.0%; Pred. No. 1.3e-44;
tive 0; Mismatches 0;
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TITLE OF INVENTION, AUTOANTIGEN VACCINE
FILE REFERENCE: 10276-067001
CURRENT APPLICATION NUMBER: US/13/038,686
CURRENT FILING DATE: 2002-05-31
PRICE APPLICATION NUMBER: 60/266,068
PRICE FILING DATE: 2001-01-05
NUMBER OF SEQ ID NOS: 6
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85 SLOKRGIVEQCCTSICSLYQLENYCN 110
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                                                                                                                                                                                                                                                APPLICANT: ARIZEKE PHARMACEUTICALS, INC
                                                                                                                                                       ; Sequence 6, Application US/09969748C; Publication No. US20030161809A1; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RESULT 10
US-10-638-686 i
Sequence 1, Application US/10038686
Publication No. US20030045467A1
GENERAL INFORMATION:
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Best Local Similarity 100.
Matches 86, Conservative
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Matches 86; Conserv
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LOCATION: (84) COTHER UPPERMATION: Xea equals any of the naturally occurring L-amino acids NAME/KEY: SITE
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IITLE 09 INVENTION Nucleic Acids, Proteins and Autibodies
IITLE 06 INVENTION NUCLEIC ACIDS, Proteins and Autibodies
CURRENT FELERENCE: PAIO5
CURRENT FILING DATE: 2001-08-10
PRIOR APPLICATION NUMBER: PCT/VUSUO/05989
PHIOR FILING DATE: 2000-03-08
                                                                                                OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
                                                                                                                                                                                                                                                                                                                                                                       REFERENCE/DOCKET NUMBER: 02481.1600-00000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      96.7%; Score 457; DB 10;
100.0%; Pred, No. 5.2e-44;
tive 0; Mismatches 0;
                                                                                                                                  CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/947,563
FILING DATE: 07-Sep-2001
CLASSIFICATION: <Unknown>
                                                                                                                                                                                                                                                   APPLICATION NOMBER: 09/134,835
FILLING DATE: <UNKNOWN:>
ALTORNEY/AGENT INFORMATION:
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Z1F: 20005-3315
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IMM PC compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LOCATION: 1..96
SEQUENCE DESCRIPTION: SEQ ID NO:
US-09-947-563-5
                                                                                                                                                                                                                                                                                                                         NAME: Lestie McDonell
REGISTRATION NUMHER: 34,872
                                                                                                                                                                                                                                                                                                                                                                                          TELECOMBUNICATION INFORMATION:
TELPHONE: (202) 408-4400
TELPHONE: (202) 408-4400
INF MMALLIN FOR SEQ LO NOS 5:
SEGUENTE CHARACTER+STIFS:
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: Patent No. US20020081659A1
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MOLECULE TYPE: protein
ORIGINAL SOURCE:
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Rest Local Similarity 150.09
Matches 85; Conservative
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SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 805
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ORGANISM: Homo sapiens
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Keller, Reinhold
TITLE OF INVENTION: Improved proce < for obtaining
insulin precursors having correctly bonded cystine bridges
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TITLE OF INVENTION: DNAS ENCOUNG NEW FLACON PROTEINS AND PROCESSES FOR TITLE OF INVENTION: PREPARING USEFUL POLYPEPTIDES THROUGH EXPRESSION OF THE TITLE OF INVENTION: DNAS
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                                                                                                                                    32 FVNQHLGGSHLVEALYLVGGERGFFYTPKTRREAEDLQVGQVELGGGPGAGSLQPLALEG 91
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larity 100.0%; Pred, No. 1,65-44;
Conservative 0; Mismatchins 0; Indels (
                          Length 117;
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ADDRESSEE: Finnegan, Henderson, Farrabow, Garrett
                                                                   0; Indels
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                        Score 463; DB 9;
Pred. No. 1.4e-44;
                                                                   0; Mismatches
                     100.0%; Score 463;
100.0%; Pred. No. 1
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CURRENT APPLICATION NUMBER: US/09/280, U
CURRENT FILING DATE: 1999-03-16
EARLIER APPLICATION NUMBER: JP10-87319/
EARLIER FILING DATE: 1998-03-11
NUMBER CF SEQ ID NOS: 66
SOFTWARE: Fatentin Ver. 2.0
                                                                                                                                                                                                   61 SLGKRGIVEQCCTSICSLYOLENYCN 86
[11111111111111111111111]
92 SLGKRGIVEQCCTSICSLYQLENYCN 117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            61 SLUKRGIVEQCCTSICSLYQLENYCN 86
                                                                                                                                                                                                                                                                                                                                     US-09 280-036-62
Sequence 62, Application US/09280030A
Fatent No. US200(0021515A1
GENERAL INFERMATION:
APPLICAN: Sato, Seiji
APPLICANI: Sato, Seiji
APPLICANI: Rudo, Toshiyuki
APPLICANI: Rudo, Toshiyuki
APPLICANI: Rudo, Masaaki
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                     Query Match
Best Local Similarity 100.0
Matches 86; Conservative
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Matches 86; Conserv
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US-09-947-563-5
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COTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids NAMEYER: SITE
COATION: (105)
COTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids NAMEYER: SITE
COATION: (124)
COTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids NAMEXEX: SITE
COATION: (132)
COTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids NAMEXEX: SITE
COATION: (144)
COTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids NAMEXEX: SITE
COATION: (145)
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COCATION: (145)
COTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids NAMEXEX: SITE
COCATION: (145)
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Ouery Match.

Best Local Similarity 96.7%; Prod. No. 5.20-27;

Hatches 58: Conservative 0; Mismatci 2: 2; Indels 0; Gaps 0;

1 FVNOHLGGSHLVEALXLVCGERGFFYTPKTRAREAEDLQVGQVELGGGPGAGSLQPEALEG 60

1 FVNOHLGGSHLVEALXLVCGERGFFYTPKTRAREAEDLQVGQVELGGGPGAGSLQPEALEG 60

42 FVNQHLGGSHLVEALXLVCGERGFFYTPKTRAREAEDLQVGQVXLGGGPGAXSLQPEALEG 101

Search completed: September 15, 2003, 12:24:35 Job time: 46-0645 secs

GenCore version 5.1.6 Copyright (c) 1993 - 2003 Compugen Ltd.

OM profeis - proteis search, using sw model

September 15, 2003, 11:56:45; Search time 14.1792 Seconds (without alignments) 583.284 Million cell updates/sec Run on:

US-09-423-100-4 463 Title: Perfect score:

1 FVNQHLCGSHLVEALYLVCG........IVEQCCISICSEYJLENYCN 86 Sequences

Scoring table:

BLOSUM62 Gapop 10.0 , Gapext 0.5

283308 seqs, 96168682 residues Sear ched:

408 + 87 hits satisfying chosen parameters: Total number of

CONTRACTOR SOUNDS CAN BE Minimum DB seq (court); 0 Maximum file send Post processing: Misirum Mater, em

Maximum Match 100% Listing first 45 summaries

Database :

PIR_76:# 1: pir1:# 2: pir2:# 4: pir3:#

SUMMARIES

Fred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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Ŧ	456	98.5	110	2	B42179	
4	454	S-86	110	~	390178	-
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ų.	417	90.1	_	•	TPDG	_
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en.	7 0.7	85.1	110	-	INMS2	insulia 2 precurso
10	145	84.7	108	?	A39883	insulin precursor
11	342	84.7	110	7	148166	insulin precursor
1.2	385	83.2	110	-	IPKT1	•
13	383	82.7	84	~	1PPG	pr
14	366.5	79.2	105	-	1980	insulin precursor
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16	534.5	72.2	108	?	S09278	insulin precursor
17	\$7078	69.2	77	_	INSH	insulin precursor
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14	277.5	59.9	109		IPRIDU	insulia precursor
20	276.5	26.7	103	~	151221	insulin precursor
21	5.65.5	57.3	106	~	IPXL2	insulin II precurs
2.5	265.5	57.3	107	_	IPCH	insulin precursor
7.7	262.5	56.7	106	-	IPXL1	insulin I precurso
24	256.5	55.4	51	_	INWHP	insulin - sperm wh
25	256.5	55.4	51	_	I NWHE.	insulin - finback
56	256.5	55.4	51	-	INEL	insulin - elephant
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RESULT 1

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C. Species and project and the control of the contr
C.Cate: 24-oct-1981 #sequence revision 23 act 1981 #lext change 08-Dec-2000
Craccession: A93222; A94253; A94216; A94251; A93144; A92075; A91186; 158114; A01579
R:Bell, G.1.; Pictet, R.L.; Rut or, W.J.; Cordell, B.; Tischer, E.; Goodman, H.M.
Nature 284, 26-32, 1980
A:Title: Sequence of the human issulin gene.
A; Reference number: A93222; MSH .80120725; PMHD:6243748
A; Accession: A93222
A:Molecule type: DNA
A; Residues: 1-110 < REL>
A:Cross-references: GB:J00265; NID:q186425; PIDN:AAA59172.1; PID:q386828
RiUllrich, A.; Dull, F.J.; Grav, A.; Brosius, J.; Sures, I.
Science 209, 612-615, 1980
AsTitle: Genetic variation in the human insulin gene.
A:Reference number: A9425s; MUID:80236313; PMID:6248962
A; Accession: A94253
A:Molecule type: DNA
A;Residues: 1-110 <ul:></ul:>
A) Cross references: GB: D01265; NID: q186429; PIDN: AAA59172.1; PID: g186828
RiBell, G.I., Swain, W.F., Pictet, R.: Cordell, B.: Goodman, B.M.; Rutter, W.J.
Nature 282, 525 527, 1979

A:Title: Nucleotide sequence of a cDNA clone encoding human preproinsulin. A:Reference number: A93216; MUID:80054779; PMID:503234 A:Accession: A93216

A.Molecule type: mRNA
A.Residues: 1-110 <BEL2>
A.Across-reterences: GR:U0265: NID:g186429; PIDN:AAA59172.1: PID:g386828
B.Sures. 1.; Gooddel: D.V.; Gray, A.; Ulirich, A.
Science 208, 57-59, 1980
A.Title: Nucleotide sequence of buman preproinsulin complementary DNA.
A.Reference number: A94251
A.Reference number: A94251
A.Molecule type: mRNA
A.Residues: 1-110 <SGR.ACOSTON: ASTERIA OF STRUCKS NID:g186429; PIDN:AAA59172.1: PID:g386828
R.Nicol, D.S.H.W.: Smith, L.F.
Nature 187, 483-485, 1960

A,Title: Amino-acid sequence of human insulin. A,Reference number: A93144 A; Accession: A93144

A:Molecule type: protein
A:Residues: 25-54:90-110 -NIC>
B:Oyer, P.E.; Cho, S.; Petterson, J.D.; Steiner, D.F.
B:Oyer, P.E.; Cho, S.; Petterson, J.D.; Steiner, D.F.
A:Title: Studies on human proinsulin. Isolation and amino acid sequence of the huma A:Reference number: A92075; MUID:71116410; PMID:510171
A:Accession: A92075
A:Accession: A92075

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Gaps

.; O

A; Residues:

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Cispercies: "ercoptiblecus authops (grees monkey, grivet)
Richer, 64.341.991 #8521056
Richersion: Bell, G.1.: Li, W.H.
Wol. 9, 193-203, 1992
A) Intle: Sequences of primate insulin genes support the hypothesis of a slower rate of A) Reference number: A42179; MUD:92219953; PMID:1560757
A) Accession: B4219
A) Molecule type: DNA
A) Residues: EMBL:K61092; NID:92219953; PMID:1560757
A) Residues: EMBL:K61092; NID:92219953; PMID:1560757
A) Residues: EMBL:K61092; NID:92219953; PMID:156099
A) NOte: Sequence extracted from NCB; backbone (NCBN:95185, NCBIP:95194)
B) Reterson, JD.; Nemtlich; S.; Oyer, P.E.; Steiner, D.F.
A) Title: Determination of the anino acid sequence of the monkey, shoep, and doa proin A) Residues: 57-87 Apple (and the anino acid sequence of t
Mol. Biol. Evol. 9, 193-203, 1992
Aritle: Sequences of primate insulin genes support the hypothesis of a slower rate of Arecession: A42179; Mulb:92219953; PMID:1560757
Arccession: A42179
Arccession: A421
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Pred. No. 2.8e-43;
0; Mismatches 0;
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86; Conservative
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Matches 85; Conservative
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Rynaithani, V.K.

A.Title: The synthesis of Cepetide of human promisulin.

A.Reference number: A91658, MUID:75040007, PMID:4803404

A.Contents: annotation: synthesis of residues 57-87

R.Geiger, R. Jaeqer, G.; Koenig, W.

Chem. Ber. 166, 2347-2352, 1973

A.Title: Synthesis of the complete sequence of human profinsulin C-peptide and its [Glu-9]
                                                                                                                                                                                                                                                                                                                                                              A:Molecule type: protein
A;Kestdies: 57-87 <KOA>
R:Lucassen, A.M.: Julier, C.; Beressi, J.P.; Roitard, C.; Froquel, P.; Lathrop, M.; Bell
Nature Genet. 4, 305-310, 1993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A.Title: Susceptibility to insulin dependent diabetes mellitus maps to a 4.1 kb segment A.Reference number: ISB114; MJID:93364428; PMID:8358440
A.Accession: ISB114
A.Status: preliminary; translated from GB/EMBiL/DDBJ
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A:Reference number: $58661; MUID:96013185; PMID:7575420
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AJCOntents: annotation: synthesis
AJNOte: disultide bended human insafin wis synthesized: the synthetic benmone was ident
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A:Cross-references: GB:L15440; NID:q307071; PrDN:AAA59179.1; PID:g307072
R:Sieber, P.: Kamber, B.; Hartmann, A.: Joehl, A.: Riniker, B.: Rittel, W.
Helv, Chim. Acta 57, 2617-2621, 1974
A:Title: Totalsynthese von Humaninsslin unfer gezietter Bildson der Disulficbindangen.
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Date: 04-Mar-1993 #sequence_revision 18-Nov-1994 #text_change 16-Jul-1999
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O
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A:Reference number: A91186; MUID:71257722; PMID:5560404
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F.25-54/Domain: insulin chain H *status experimental <BCH>
F.25-54/Oproduct: insulin *status experimental <MAT>
F.25-87/Domain: cronecting C peptide *status experimental <APE>
F.90-110/Nomain: insulin chain A *status experimental <ACPE>
F.31-96,44-109,95 100/Disulfide bonds: *status experimental <ACH>
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R.Kaufmann, J.E., Irminger, J.C., Halban, P.A.
Biochem, J. 110, 869-874, 1995
                                                         Riko, A.: Smyth, D.G.: Markussen, J.: Sundby, F.
Eur. J. Biochem. 20, 190-199, 1971
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A:Map position: 11p15.5-11p15.5
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C.Joate: 04-Mar-1993 #sequence_rev
C.Accession: A42179; S22058
R.Seino, S.: Bell, G.I.; Li, W.H.
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A;Residues: 1-59,63-110 <RES>
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Keywords: hormone; panereas
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Matches 86; Conserv
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57-87
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C; Genetacs:

Query Match

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RESULT 4

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C:Species: Canis lupus familiaris (doq)
C:Daces 24.Apr.1984 *sequence_revision 15.Nov-1984 *text_change 16.Jul 1999
C:Dacession: A92413: A01587; Sid493
R:KWok, S.C.M.; Chan, S.J.; Steiner, D.F.
J. Blol, Chem. 258, 2587-2583, 1983
A.Fitle: Cloning and nucleotide sequence analysis of the dog insulin gene. Coded am A.Reference number: A92413: MUID:83109071; PMID:6296142
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A:Molecule type: protein
A:Mesdidues: 25-54; 90-110 < SMIT>
A:Resdidues: 25-54; 90-110 < SMIT>
J. Biol. Chem. 247, 4866-4871, 1972
A:Title: Determination of the amino acid sequence of the monkey, sheep, and dog pro
A:Reference number: A92111: MUID:72258016; PMID:4626369
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A;Residues: 1-30;66.86 <HAR>
R;Residues: 1.2. Steiner, D.F.
B;rager, H.S.: Steiner, D.F.
J. Biol. Chem. 247, 7936-7940, 1972
A;Title: Primary structures of the proinsulin connecting peptides of the rat and ho A;Reference number: A92120; MUID:73061498; PMID:464093]
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C:Date: 13-Jul-1981 *sequence_revision 13-Jul-1981 *text_change 16-Jul-1999
C:Accession: A01580; A92120
R:Harris, J.I.; Sanger, F.: Mughton, M.A.
Arch. Biochem. Biophys. 65, 427-428, 1956
A;Title: Species differences in insulin.
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F:90-110/Domain: insulin chain A *status experimental <ACH>
F:31-96,43-109,95-100/Disulfide bonds: *status experimental
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           F:25-54/Domain: insulin chain B Estatus experimental <BCH> F:25-54,90-110/Product: insulin Estatus experimental <MAT>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    C:Keywords: hormone; pancreas
F:1-24/Domain: signal sequence #status predicted <SLG>
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                                  61 SLOKRGIVEQCCTSICSLYQLENYCN 86
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A:Residues: 65-85,'I',87 <PET>
C:Superfamily: insulin
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A:Residues: 1-110 <SMI>
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Matches 77; Conserv
                                                                                                                                                                                             insulin precursor - dog
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                                                                                                                                         RESULT 6
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                                                                                                    R;Wetekam, W.; Groneberg, J.; Leineweber, M.; Wengenmayer, F.; Winnacker, E.L.
Gene 19, 179-183, 1982
A;Title: The nucleotide sequence of cDNA criing for preproinsulin from the primate Macac
A;Reference number: JQ0178; MUID:83080474; MID:6184262
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A;Tille: Insulin gene expression and insulin synthesis in mammalian neuronal cells.
A;Reference number: A53438; MUID:94179230; PMID:8132571
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                 C:Species: Macaca fascicularis (crab·eating macaque)
C:Date: 07-Sep-1990 #sequence_revision 07-Sep-1990 #text_change 16-Jul-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   C;Date: 24.Apr.1984 *sequence_revision 23.Aug-1997 *text_change 18.Jun-1999 C;Accession: A53438; A01581
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                                                                                                                                                                                                                                  A Status: preliminary
A Molecule type: mRNA
A: Residues: 1-110 < DEV>
A: Cross-references: GB:U03610; NID:9467970; PIDN:AAA19033.1; PID:9467971
R; Smith, L.F.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 1130
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DB 1; Length 110;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 C.Keywords: hormone: pancreas
F.12-24/Domain: signal sequence *status predicted <SIG>F.25-54/Domain: insulin chain B *status experimental <BCH>F.25-54.90-10/Product: insulin *status experimental <HAT>F.25-54.90-110/Domain: connecting C peptide *status predicted <CPEP>F:90-110/Domain: insulin chain A *status experimental <ACH>F:31-96.43-109,95-100/Disulfide bonds: *status predicted
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 456; FR 4:
Pred. No. 1,66:47;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                91.6%; Score 424; DB 1; 90.7%; Pred. No. 5e-39;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   insulin precursor - rabbit
N;Aiternate names: preproinsulin
C:Species: Oryctolagus cuniculus (domestic rabbit)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   O: Mismar Hes
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insulin precursor - crab-eating macaque
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88'.86
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Best Local Similarity 90./*
Best Local Similarity 90./*
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A;Residues: 25-54:90-110 <SMI>
C;Superfamily: insulin
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Best Local Similarity
Matches 85: Conserv
                                                                       C; Accession: JQ0178
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                                                                                                                                                               25 FVKQHLCGSHLVEALYLVCGERGFFYTPMSRREVEDPQVAQLELGGGPGAGDLQTLALEV
                                                                              Ö
                                      Length 110;
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                                                                                Indels
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                                   Score 394; DB 1; L
Pred. No. 9.2e-36;
4; Mismatches 9;
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84.9%; Pred. No. 9.2e-36;
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                                   85.1%;
84.9%;
                             Ouery Match
Best Local Similarity 84.94
Matches 73, Conservative
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Rest Local Similarity 84.9%
The Conservative
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A;Molecule type: protein
A;Residues: 33-63 <TAG>
C;Comment: X's at positions 31-32 and 64-65 represent paired basic residues assumed (by
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A:Wolecule type: protein
A:Residues: 25.5490-110.STE>
B:Residues: 25.5490-110.F.
J. Biol. Chem. 247, 7936-7940, 1972
J. Biol. Chem. 247, 7936-7940, 1972
A:Title: Primary structures of the proinsule: "onnecting peptides of the rat and horse.
A:Reference number: A92120; MUID:73061498; PMID:4640931
A:Accession: C92120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CiSpecies: Rattus norvegicus (Norway rat)
CiDate 23-ort-1981 sequence_revision_23-oct-1981 #text_change 24-Sep-1999
CiDate 23-ort-1981 sequence_revision_23-oct-1981 #text_change 24-Sep-1999
CiAccession: 840789; B94231; C92120: 164886; A01590; B92120
R:Lomedico, P.; Rosenthal, N.; Efstratiadis, A.; Gibbert, W.; Kolodner, R.; Tizard, R.
Cell 18, 545-558, 1979
A:Tille: The structure and evolution of the two nonallelic rat preproinsulin qenes.
A:Tille: The structure and evolution of the two nonallelic rat preproinsulin qenes.
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R. Residuces 57-87 < TAGA

R. Residuces 57-87 < TAGA

R. Lomedico, P.T.; Rosenthal, N.; Kolodner, R.; Efstratiadis, A.; Giibert,

Ann. N. Y. Acad. Sci. 343, 425-432, 1980

A. Riticle: The structure of rat. preproinsulin ac. 8.

R. Reference number: 151945; MUID:80240379; PH: 249167

A. Accession: 164880
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                                                                                                     C.Keywords: hormone; pancreas
F.1-30/Domain: insulin chain B *status experimental <BCH>
F.1-30/Domain: insulin status experimental <MAT>
F.33-65/Xomain: connecting peptide *status experimental <CPEP>
F.66-86/Xomain: insulin chain A *status experimental <ACEP>
F.70-72,19-85,71-76/Disulfide bonds: *status predicted
                                                                                                                                                                                                                                                              Score 394; DB 1; Length 86;
Pred. No. 7.2e-36;
1; Mismatches 12; Indels
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Cyteywords: hormone: pancreas
F;1-24/Domain: signal sequence *status predicted <SIG>
F;25-54/Domain: insulin chain # *status experimental <BGH>
F;25-54/PO·IIO/Product: insulin *status experimental *MATP
F;7-87/Lomain: connecting peptide *status experimental <CPEP>
F;31-87/Lomain: insulin chain A *status exper: intal <ACH>
F;31-96,43-109,95-100/Disulfide bonds: *status experimental
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84.9%;
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Best Local Similarity 84.99
Matches 73; Conservative
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A; Residues: 1:110 < RES>
                                                                                   C; Superfamily: insulin
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Rifager, H.S.; Steiner, D.F.
J. Bhol. Cham. 247, 7936-7946, 1972
A.B.Itlas: Frimary Structures of the profusalin consecting peptides of the rat and he
A.Reference number: A921zus MUD57366349g; PMID:4440981
                                       A:Cross-references: GB:J00747; NID:g204956; PIDN:AAA41442.1; PID:g204957
R:Lomedico, P.; Rosenthal, N.; Efstratiadis, A.; Gilbert, W.: Kolodner, R.; Iizard,
                                                                                                                                                                                                                                                                                                                        A:Residucs: [-110 </mw.)
A:Cross-references: GB:J00747; NID:q264956; PIDN:AAA41442.1; PID:g204957
A:Cross-references: GB:J00747; NID:q264956; PIDN:AAA41442.1; PID:g204957
B:Stefner, D.F.; Clark, J.L.; Nodan, C.; Rubenstein, A.H.; Margoliash, E.; Aton, B. Recent Proq. Horm. Res. 25, 207-282, 1967
A:Title: Proinsulin and the biosynthesis of insulin.
A:Reference number: A54231; MUID:70067613; PMID:4311938
                                                                                                                  cell 18, 545-558, 1979
A:Tille: The structure and evolution of the two nonailelic rat preproinsulin genes
A:Acference number: A90789; MUID:80045035; PMID:494284
A:Accession: A90789
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C;Species: Sus scrota dom-stica (domestic pig)
C;Date: 22-Jun-1981 #sequence_revision 22-Jun-1981 #text_change 16-Jui-1999
C;Accession: A0188; A94572; S16492; A60835; B66835
R;Chance, R. E.; Ellis, R. M.; Bromer, W. W.
Science 161, 165-167, 1968
A;Title: Porcine proinsulin: characterization and amino acid sequence.
A;Reference number: A94240; MUID:68286485; PMID:5657063
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Ackression: protein
Ackresidaes: 57-87 crack
Rizomedics, P.T.; Rosenthal, N.; Kolodner, K.; Elstratiadis, A.; Gilbert,
Rizomedics, P.T.; Rosenthal, N.; Kolodner, K.; Elstratiadis, A.; Gilbert,
Ann. N. Y. Acad. Sci. 445, 425, 1980
A.; Itele: The structure of rat psoproinsulin genes.
A.; Reference number: 151945; MUID:80240379; PMID:6249167
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C;Genetics:
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C.Keywords: hormone; pancreas
F:1-24/Domain: signal sequence status predicted <SIG>
F:25-54/Domain: insulin chain B #Status experimental <BCD>
F:25-54/Domain: insulin #status experimental <ADP>
F:25-54/Domain: connecting peptide #status experimental <CPEP>
F:57-57/Domain: insulin chain A #Status experimental <CPEP>
F:31-96,43:109/Domain: insulin chain A #Status experimental <ACH>
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83.7%; Pred. No. 8.8e-35;
1ive 4; Mismatches 10
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A;Residues: 1-34,'Q',36 84 <CHA>
K:Chance, R.E.
submitted to the Atlas, July 1970
A;Reference number: A94572
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A:Molecule type: protein
A:Residues: 25-54:90-110 <STE>
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Guery Match
Best Local Similarity 83.77
Matches 72; Conservative
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A; Residues: 1-110 < RES>
A; Residues: 1-110 <COR>
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Proc. Natl. Acad. Sci. U.S.A. 84, 7423-7427, 1987
Arithe: Sequence of a New World primate insulin having low biological potency and immun A;Reference number: A39883; MUID:8804:1119; PMID:3118367
A;Accession: A39883
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[5]945; A01589
. F.M.; Ullrich, A.; Pictet, R.: Rutter, W.
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C:Species: Mesocricetus auratus (golden hamster)
C:Date: 62:504-1996 #sequence_revision 62:504-1996 #text_change 16 Jul-1999
                                                                                                         insulin precursor - douroucouli
CSpecies: Actus Lrivirgatus (douroucouli, ...tht monkey, owl monkey)
CDate: 27-Nov-1991 *sequence_revision 27-Nov-1991 *text_charge 16-Jul-;999
CAccession: A39883
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A:Molecule type: mRNA
A:Residues: 1 110 - RES>
A:Cross:references: GB:M26328: NID:g191420; PIDN:AAA37089.1; PID:q365360
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A;Title: Isolation and characterization of . cloned rat insulin gene.
A;Reference number: A90788; MUID:80045034; FMID:498283
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R.Bell, G.I.; Sanchez-Pescador, R.
Diabetes 31, 297-300, 1984
A.Title: Sequence of a CDNA encoding Syrian hamster preproinsulin.
A.Reterence number; 148166; MUID:84133036; PMID:6365663
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84.9%; Pred. No. 1.5e-35;
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C.Date: 24-oct-1981 #sequence_revision 23
C.Accession: A90788; A90789; A54231; B921.
R.Cordell, B., Bell, G.; Tischer, E.; Denc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    61 SLOKRGIVEQCCTSICSLYQLENYCN 86
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Matches 73; Conserv
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A;Molecule type: DNA
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A:Molecule type: protein
A:Residues: 57-82 cSAL>
R:Sanger, F.; Thompson, E.O.P.
Biochem, J. 53, 366-374, 1953
A:Title: The amino-acid sequence in the diyeyl chain of insulin, 2. The investigatio
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A:Residues: 25.40, "x, 32.42, "x, 44.54 «CH2>
A:Residues: 25.40, "x, 32.42, "x, 44.54 «CH2>
B:Ochem J. 60, 541-556, 1955
A:Title: The disulphide bonds of insulin.
A:Reference number: A90343
A:Title: The disulphide bonds of insulin.
A:Reference number: A9044
A:Contents: annotation; and despisal titles
B:Wenzel, T.: Eckerskorn, C.: Lottspeich, F.: Haumeister, W.
FRBS Lett. 349, 205-209, 1994
A:Title: Existence of a molecular ruler in protedsomes suggested by analysis of degratering number: S46258: MUID:94126921; PMID:805657
                                                                                                                                                                                                                              AlTitle: Bowing proinsulin: amino acid sequence of the C-peptide isolated from pancy AlReference number: A91185; MUID:71257721; PMID:5105368
A.Accession: A91185
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A:Mosiduos 25:54 csA2>
R;Cheng, R.; Kawakishi, S.
Bur, J. Blochem. 223, 759-764, 1994
A;Title: Site-specific oxidation of histidine residues in glycated insulin mediated
A;Reference number: 548184; MUID:9433378: PMID:805595)
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A;Residues: 85:105 csan>
R;Sanger, F; Tuppy, 4.
R;Sanger, F; 49: 481-490, 1951
A;Title: Tac amino-arid sequence in the phenylalanyl chain of insulin.
A;Reference number: A9044;
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F1.25-54/Domain: Insulin chain B Estatus experimental «RCH»
F1.25-54.85-105/Product: insulin #status experimental «MAT»
F1.57-82/Domain: connecting peptide #status experimental «ACPE»
F1.87-105/Domain: insulin chain A #status experimental «ACP»
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                                                          A:Molecule type: protein
A;Residues: 57-82 <STES
R:Salokangas, A.; Smyth, D.G.; Markussen, J.; Sundby, F.
Eur. J. Biochem. 20, 183-189, 1971
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A:Accession: A90342
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A/Molecule type: protein
A/Residues: 25-54 <WEN>
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A:Residues: 85-105 <CHE>
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                   A:Accession: A92074
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Cispecies: Bos primigenius taurus (cattle)
Cispecies: Bos primigenius taurus (cattle)
Cispecies: Apr. 1984 | sequence_revision 22.5pr. 1995 | block | block
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A;Molecule type: protein
A;Residues: 33.62.5N2.
R;Blundell, T; Dodson G; Bolakir, D; Morecla, D;
Adv. Protein: 259-402, 1972
A;Title: Issuin, the structure in the crystal and its rellection is chemistry and biolo
A;Reference number: A90017
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A;Note: the authors report the characterization of a connecting peptide variant lacking A;Accession: 860835
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A;Title: Isolation and characterization of proinsulin C-peptide from bovine pancreas. A;Reference number: A92074; MUID:71116409; PMID:5545080
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         -1
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A:Residues: 1-105 cDAA>
A:Cross-references: GB:M54979; NID:q163778; P:DN:AAA30722.1; PID:q163579
A:Experimental source: fetal pancreas
A:Experimental source: fetal pancreas
R:Nolan, C : Marqoliash, E.; Peterson, J E.; Steiner, D.F.
A: Biol. Chem. 246, 2780-2795, 1977
A:Title: The structure of bovine proinsulin.
A:Reference number: A92080; MUID:71166442; PH:D:4928892
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86.0%; Pred. No. . ic-34;
Live 1: Mismatches 9; Indels
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C.Keywords: hormone; pancreas
F.1-30/Coma.n: insulin chain B #status experimental <BCH>
F.1-30.64-84/Product: insulin #status experimental <MAT>
F.3-36/Loma.n: connecting poptide #status experimental <CPEP>
F.64-64/Domain: insulin chain A #status experimental <CPEP>
F.64-64/Domain: insulin chain A #status experimental <ACH>
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Horm. Metab. Res. 20, 476-480, 1988
A;Titler Profinsuin hererogeneity in pigs.
A;Reference number: A60835; MUID:89032178; PMID:3J81865
                                      A.Molecule type: protein
A.Residues: 1-84 CCH2>
R.Brown, H.: Sanger, F.; Kitai, R.
Biochem, J. 60, 556-565, 1955
A.Title: The structure of pig and sheep insulins.
A.Reference number: A90344
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A:Residues: 33-38,40-62 <SNE>
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A;Residues: 1:30;31-51 <BRO>
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Matches 74: Conserve
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A; Residues: 25-105 <NOL>
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A; Accession: A94572
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A. Molecule 1979: protein
A. Residues: 25 54,88-108 <a href="Molecule" 1996: protein
A. Residues: 25 54,88-108 <a href="Molecule" 1996: Purither 1980" A. Title: Reversed phase high-performance inquid chromatographic analyses of insulin bios A. Title: Reversed phase high-performance inquid chromatographic analyses of insulin bios A. McFersidue: A61012: MUID:89292678: PMID:2661585
A. McGession: H61612
A. Molecule type: protein
A. Molecule type: protein
A. Molecule type: protein
A. Molecule type: protein
C. Superfamily: Insulin
C. Superfamily: Insulin
C. Superfamily: Insulin
E. 1-24/Domain: siynal sequence #status experimental <BGH>
E. 25-54/Domain: insulin chain B status experimental <MAT>
E. 25-54, 88-108/Product: insulin Estatus experimental <MAT>
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A.Rosidues: 1 108 <a href="https://doi.org/10.108/10.108/10.108/10.108/10.108/10.108/10.108/10.108/10.108/10.108/10.108/10.108/10.108/10.108/10.108/10.108/10.108/10.108/10.108/10.108/10.108/10.108/10.108/10.108/10.108/10.108/10.108/10.108/10.108/10.108/10.108/10.108/10.108/10.108/10.108/10.108/10.108/10.108/10.108/10.108/10.108/10.108/10.108/10.108/10.108/10.108/10.108/10.108/10.108/10.108/10.108/10.108/10.108/10.108/10.108/10.108/10.108/10.108/10.108/10.108/10.108/10.108/10.108/10.108/10.108/10.108/10.108/10.108/10.108/10.108/10.108/10.108/10.108/10.108/10.108/10.108/10.108/10.108/10.108/10.108/10.108/10.108/10.108/10.108/10.108/10.108/10.108/10.108/10.108/10.108/10.108/10.108/10.108/10.108/10.108/10.108/10.108/10.108/10.108/10.108/10.108/10.108/10.108/10.108/10.108/10.108/10.108/10.108/10.108/10.108/10.108/10.108/10.108/10.108/10.108/10.108/10.108/10.108/10.108/10.108/10.108/10.108/10.108/10.108/10.108/10.108/10.108/10.108/10.108/10.108/10.108/10.108/10.108/10.108/10.108/10.108/10.108/10.108/10.108/10.108/10.108/10.108/10.108/10.108/10.108/10.108/10.108/10.108/10.108/10.108/10.108/10.108/10.108/10.108/10.108/10.108/10.108/10.108/10.108/10.108/10.108/10.108/10.108/10.108/10.108/10.108/10.108/10.108/10.108/10.108/10.108/10.108/10.108/10.108/10.108/10.108/10.108/10.108/10.108/10.108/10.108/10.108/10.108/10.108/10.108/10.108/10.108/10.108/10.108/10.108/10.108/10.108/10.108/10.108/10.108/10.108/10.108/10.108/10.108/10.108/10.108/10.108/10.108/10.108/10.108/10.108/10.108/10.108/10.108/10.108/10.108/10.108/10.108/10.108/10.108/10.108/10.108/10.108/10.108/10.108/10.108/10.108/10.108/10.108/10.108/10.108/10.108/10.108/10.108/10.108/10.108/10.108/10.108/10.108/10.108/10.108/10.108/10.108/10.108/10.108/10.108/10.108/10.108/10.108/10.108/10.108/10.108/10.108/10.108/10.108/10.108/10.108/10.108/10.108/10.108/10.108/10.108/10.108/10.108/10.108/10.108/10.108/10.108/10.108/10.108/10.108/10.108/10.108/10.108/10.108/10.108/10.108/1
C;Species: Mus muscalus (house mouse)
C;baccies: Mus muscalus (house mouse)
C;baccession: B26342; A48172; A01592; B61012
C;Aaccession: Chirgwin, J.M.
J. MOI. Evol. 23, 305-312, 1986
A;Titlo: Characterization of the Lwo nonallelic genes encoding mouse preprofissulin. A;Reference number: A92965; MUID:87169768; PMID:3104603
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83 AROKRGIVDOCCTSICSLYQLENYCN 108
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Best Local Similarity 81.4%
Matches 70: Conservative
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OM protein - protein search, using sw model

September 15, 2003, 11:54:00 ; Search time B.01434 Seconds (without alignments) 504.633 Million cell updates/sec Run on:

Title: Perfect score: Sequence:

US-09-423-100-4
463
1 FUNDHLGGSHLVEALYLVGG......IVEQCGTSICSLYQLENYGN B6

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

127853 seqs, 47026705 residues Searched:

12786. Total number of hits satisfying chosen parameters:

Minimum OH seq Terath: 3 Maximum OH seq Tenath: 26000005co

Postrprocessing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summeries

SwissProt_41:* Database :

Fred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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ar.	ery	100.0	100.0	98.5		91.6			85.1	85.1		84.7			82.7	81.4				72.2	67.8	6.65	59.7	57.3	57.3	v	55.4	υ,	u ·	•	53.2	\sim	53.2
	Score	463	463	456	456	474	417	413	394	394	\$64	392	192	385	383	377	366.5	366	362.5	334.5	_		276.5		265.5		256.5		9	251.5	246.5	246.5	246.5
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P18109 didelphis m	P01327 chinchilla	P07454 anser anser	09w7r2 verasper mo	PO1328 hystrix cri	P31887 trachemys s	P81423 acipenser q	P01341 lophius pis	Q9tqy7 ornithorhyn	PO4667 oncorhynchu	P13190 callorhynch	P81025 oreochromis
'NS_DIDMA	NS_CHIBR	NS_ANSAN	INS_VERMO	INS_HYSCR	INS_TRASC	NS_ACIGU	NS_LOPPI	NS_ORNAN	'NS_ONCKE	NS_CALMI	NS_ORENI
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5.1	5.1	5.1	115	51	51	52	116	51	105	£	113
51.7	50.6	50.0	49.2	49.1	49.1	48.6	47.8	47.2	47.2	46.8	46.4
239.5	234.5	231.5	228	227.5	227.5	225	221.5	218.5	218.5	216.5	215

AL. IGNMENTS

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MEDLINE-85261996; PubMed-4019786;
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Insulin family: Hormone: Glucose metabolism; Signal; 3D-structure.
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Mammalia: Eutheria: Primates: Catarrhiii; Hominidae: Pan.
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100.0%; Score 463; DB 1; Length 110; 100.0%; Pred. No. 9.2c-43; Live 0; Mismatches 0; Indels
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SIMILARITY: BELONGS TO THE INSULIN GEYRELAXIN FAMILY.
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ive 0; Mismatches 0;
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01-APR-1993 (Rel. 25, Last segmence update)
15-SEP-2004 (Rel. 42, Last annotation update)
Insulin precursor
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InterPro: FPR004825; Ins/IGF/relax.
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SMART: SM00078; IIGF; 1.
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1 FVNQH: CGSHLVEALYLVCGERGFFYTPKTRREAFDLQVGQVELGGGPGAGSLQPLALEG 60
                  25 FVNQHLGGSHLVEALYLVCGERGFFYTPKTRRFAEDLQVGQVELGGGPGAGSLQPLALEG 84
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1. Biol. Chem. 247:4866-4871(1972).

1. Biol. Chem. 247:4866-4871(1972).

1. FUNCTION: INSULIN DECREASES BLOOD GLUCOSE CONCENTRATION. IT INCREASES CELL PERMEABILITY TO MONOSACCHARIDES. AMINO ACIDS AND FATTY ACIDS. IT ACCELERATES GLYCOLYSIS, THE PENTOSE FHOSPHATE CYCLE, AND GLYCOGEN SYNTHESIS IN LIVER.

1. SUBUNIT: HETERODIMER OF A B CHAIN AND AN A CHAIN LINKED BY TWO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Peterson J.D., Nehrlich S., Oyer P.E., Steiner D.F.; *netermination of the amino acid sequence of the monkey, sheep, and dog proinsulin C-peptides by a semi-micro Edman degradation
                                                                                                                                                                                                                                                                                                                 Cercupithecus acthiops (Green monkey) (Grivel).
Eskaryota: Metazoa: Chordata; Craniala; Verrebiara; Eureleostomi;
Mammaila: Eutheria; Primates: Catarrhini; Cercepithecidae;
                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A. MEDAMED-1560757; MEDLINE-9221997; FULL LI M.; Serino S. Mell G. L. Li M.; Seguences of primate insulin genes support the hypothesis of slower rate of molecular evolution in humans and apes than in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DISULLIDE BONDS.
-!- SUBCELLULAR LOCATION: Secreted.
-!- SIMILARITY: BELONGS TO THE INSULIN/IGE/RELAXIN FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   12019 MW; 95A1F54BE7B247F9 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Insulin family: Hormone; Glucose metabolism; Siqual.
                                                                                                                                                                                         INS_CERAE STANDARD: PRT; 110 AA. P30407; P01309; TO 01-AFF-1993 (Rel. 25, Created) 01-AFF-1993 (Rel. 25, Gast Sequence update) 01-FEB-1996 (Rel. 33, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              C PEPTIDE.
INSULIN A CHAIN.
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                                                                                        85 SEQKRGIVEQCCTSICSEYQLENYCN 110
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  INTERCHAIN
                                                                    61 SLQKRGIVEQCCTSICSLYQLENYCN 86
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                InterPro: IPR004825; Ins/IGF/relax.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDLINE-72258016; PubMed-4626369;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Mol. Biol. Evol. 9:193-203(1992).
                                                                                                                                                                                                                                                                                                                                                                        Cercopitherinae: Cercopithecus.
NCbl_taxID=9534;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SMART: SM00078; IlGF: 1.
PROSITE: PS00262; INSULIN: 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EMBL; X61092; CAA43405.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Pfam; PF00649; Insulin; 1.
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87
110
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109
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HSSP, P01308: 'AIO
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                                                                                                                                                                                                                                                                                 Insulin precursor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE OF 57-87.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            procedure.";
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DISULFID
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Gaps

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Indels

Conservative

Best Local Similarity

Matches

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SIMELARITY: BELONGS TO THE INSULIN/IGF/RELAXIN FAMILY.

SIMELARITY: BELONGS TO THE INSULIN/IGF/RELAXIN FAMILY.

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                                                           1 FVNQHLCGSHLVBALYLVGGERGFFYTPKTRREAEDLQVGQVELGGGPGAGSLQPLALEG 60
                                                                             Sips
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F. HETERODIMER OF A B CHAIN AND AN A CHAIN LINKED BY TWO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      "The nucleotide sequence of cDNA coding for preproinsulin from the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FUNCTION: INSULIN DECREASES BLOOD GLUCOSE CONCENTRATION II
INCKEASES CELL PERMEABILITY TO MONOSACCHARIDES, AMINO ACTIVE AN
PATTY ACIDS: IT ACCELERATES GLYCOLYSIS, THE PENTOSE PHOSPHATE
                                                                                                                                                                                                                                                                                                                               INS.
March lascinalaris (Crab earlied bread of) (Cyncollous for 60%)
Eukaryola, Metazos, Chordata, Cram Pias Veriebria, Eurochessima
Mamaalia, Eurheria; Primoles, Calaschia, Coregliaeria; Crimoles, Calaschia, Coregliaeria
                                  ..
Score 456; iB 2; Length 110; Pred. No. 5.2e-42; 1; Indels 0; Mismatches 1; Indels
                               Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                          SEUJENCE FROM N.A.
MEDILINE 8:080414; PubMed-6184262;
Weiteker W., Groneberg J., Leineweber M., Webgenmayer F.,
Winnacker E.,..
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     11991 MW; 83C6E33A80A420F9 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRINTS: FROOZ77: INSULINE.
SMART: SMUOG7#: ILGF: 1.
PROSITE: PSUU262; INSULIN; 1.
Insulic tamlly: Hormone; Glucose metakolism: Signal.
                                                                                                                                                                                                                                                                                13-AGG-1987 (Rel. 05, Last sequence update)
01-FEB-1996 (Rel. 33, Last annotation apdate)
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                                                                                                                                          INTERCHAIN.
                                                                                                                          61 SEQUERGIVEOCCISICSLYQLENYON 86
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InterPro: IPR004825; Ins/IGF/relax
                          0;
                                                                                                                                                                                                                                                   P30406, P01309,
21 JUL-1986 (Rel. 01, Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        primate Macaca fascicularis.";
Gene 19:179-183(1982).
 98.5%;
98.8%;
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                                 Conservative
                                                                                                                                                                                                                                       STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Pfam: PF05049; Insulin;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DISHLFIDE BONDS
                Best Local Similarity
Matches 85; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 110 AA;
                                                                                                                                                                                                                                                                                                                   Insulin precursor
                                                                                                                                                                                                                                                                                                                                                                                                            NCBI_Tax1D=954;;
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   Query Match
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Score 456; DB 1; Length 110; Pred. No. 5.2e-42;

98.5%; 98.8%;

Best Local Similarity

Ouery Match

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                                                            1 FUNCHLCHSHLVEALYLVCGERGFFYTPKTPREAEDLOVGQVELGGGFGAGSLGPLALEG 60
                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                *Insulin qene expression and insulin synthesis in mammalian neuronal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FATTY ACIDS. IT ACCELERATES GLYCOLYSIS, THE PENTOSE PHOSPHATE CYCLE, AND GLYCOGEN SYNTHESIS IN LIVER.
SUBCNIT: HETERODIMER OF A B CHAIN AND AN A CHAIN LINKED BY TWO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Eukaryota, Metazoa, Chordara, Cranjata, Vertelrata, Esteleostomi,
Mammalla, Eutheria, Lagomorpha, Leporidae, Orystolagus,
Nost Lixio 9986,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE OF 56-110 FROM N.A.
SEQUENCE S.J., Carnaghi L.R., Devaskar S.U.;
Giddings S.J., Carnaghi L.R., Devaskar S.U.;
Submitted (APR-1991) to the EMBL/GenBank/NUbB. databases.
Submitted (APR-1991) to the EMBL/GenBank/NUbB. AMAINO ACIDS
INCREASES CELL PERMEMBILITY TO MOUNSACCHARDES, AMINO ACIDS
INCREASES CELL PERMEMBILITY TO MOUNSACCHARDES, AMINO ACIDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDLINE-9417923U: PutbMod+813571;
Devaskar S.U., Giddings S.U., Rajakumar P.A., Carnaghi L.R.,
Menon R.K., Zahm D.S.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          "Species variation in the amino acid sequence of insulin.":
Am. J. Med. 40:562-666(1966).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SUBCELLULAR LOCATION: Secreted.
SIMILARITY: BELONGS TO THE INSULIN/IGF/RELAXIN FAMILY.
      Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                       21-JUL-1986 (Rel. 31, Created)
61-FEB-1996 (Rel. 33, Last sequence update)
01-OCT-1996 (Rel. 34, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           INSULIN B CHAIN.
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                                                                                                                                                                                                                                                                                                                                                                                                                     110 AA
      Mismatches
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                                                                                                                                                                                                                         61 SEQRRGIVEGCTSICSLYQLENYCN 86
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Biol. Chem. 269:8445-8454,1994).
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HSSP; P01308; 1TYM.
InterPro; IPR004055; Ins/IGF/relax.
PR00049; Insulin; 1.
SMART; SM00078; I1GF; 1.
PROSITE; PS00262; INSULN; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDLINE-66160119; PubMed-5949593;
   0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Oryctolagus cuniculus (Rabbit).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE OF 25-54 AND 90-110
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EMBL: U03610; AAA19033.1; -. EMBL: M61153; AAA17540.1; -.
85; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                     STANDARD
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            insulin precursor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Smith L.F.;
                                                                                                                                                                                                                                                                                                                                                                                                                  INS KARI
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                                                                                                                                                                                                                                                                                    1 FVNQHLCGSHLVEALYLVCGERGFFYTPKTRREAEDLQVGQVELGGGPGAGSLQPLALEG 60
                                                                                                                                                                                                                                                                                                                                                        84
                                                                                                                                                                                                                                                                                                                    Gaps
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Mammalia; Eutheria: Carnivora; Fissipedia; Canidae; Canis.
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                                                                                                                                                                                     Length 110;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             !- SIMILARITY: BELONGS TO THE INSULINZIGE/RELAXIN FAMILY.
                                                                                                                                                                                                                                       Indels
                                                                                         E -> Y (IN REF. 3).
82D2975B85D77FA8 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Insulin family; Hormone; Glucose metabolism; Signal.
                                                                                                                                           91.6%; Score 424; DB 1; Le 90.7%; Pred. No. 1.4e-38; w.cmatches 5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        21-30L 1986 (Rel. 31, Created)
21-30L-1986 (Rel. 31, East Sequence (pulse)
01-FEB-1996 (Rel. 33, Last annotation update)
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           INTERCHAIN
                                   INTERCHAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                  61 SLOKRGIVEQCCTSICSLYQLENYCN 86
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34
...
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             additional C-peptide fragment.";
J. Biol. Chem. 258:2357-2363(1983).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  !- SUBCELLULAR LOCATION: Secreted.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          HSSP; P01317; 1APH.
InterPro; IPR004825; Ins/IGF/relax.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SECUENCE OF 25:54 AND 90-110.
MEDLINE-66160119; Pubmed-5949593;
Smith L.F.;
31 96 IN
43 109 IN
95 100
83 83 E
110 AA; 11838 MW;
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                                                                                                                                                                Ouery Match
Best Local Similarity 90.78
Marches 78; Conservative
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SMART: SM00078; IlGF; 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Canis tamiliaris (Dog).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DISULFIDE BONDS
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CONFLICT
                                                                                                                   SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  This SWISS-PROT entry is copyright. It is produced through a collaboration
                                                                                                                                                                     1 FVNQHI.GSHLVEALYLVGGERGFFYTPKTRREAEDLQVGQVEI.GGGPGAGSLQPLALEG 60
                                                                                                                                                                                      25 FVNQHLCGSHLVEALYLVCGERGFFYTPKARREVENDLQVRDVELAGAPGEGGLQPLALEG 84
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Tredrea M.M., Buck M.J., Guhaniyodi J., Squire T.L., Andrews M.T.;
"Regulation of PDK4 expression in a hibernating mammal.";
Submitted (JUN-2001) to the "MBL/Genbank/DDBJ databases.
-!- FUNCTION: INSULIN DECREASES BLOOD GILGOSE CONCENTRATION. IT
INCREASES CELL PERMEAFILITY TO MONOSACCHARIDES, AMINO ACIDS AND
FATTY ACCLIERTES GIVEOLYSIS, THE PENTOSE PHOSPHATE
CYCLE, AND GLYCOSEN SYNTHESIS IN LIVER.
-!- SUBUNIT: HETERODIMER OF A B CHAIN AND AN A CHAIN LINKED BY TWO
                                                                                                                                                                                                                                                                                                                                                                                                                                           Spermophilus tridecemlineatus (Thirteen-lined ground squirrel).
Eukaryota: Metazoa: Chordata; Craniata: Vertebrata; Euteleostomi;
Mammalia; Euthoria; Rodentia; Sciuroquathi; Sciuridae; Sciurinae;
                                                                                                                                        .
0
                                                                                                          Length 110;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   -!- SUBCELLULAR LOCATION: Secreted.
-!- SIMILARITY: BELONGS TO THE INSULIN/IGE/RELAXIN FAMILY.
                                                                                                                                       8; Indels
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INTERCHAIN (BY SIMILARITY)
87 C PEPTIDE.
110 INSULIN A CHAIN.
96 INTERCHAIN.
109 INTERCHAIN.
1109 INTERCHAIN.
12190 PM; A574791864A4FB98 CRC64;
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4511768D6622BEE5 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Insulin family: Hormone; Glucose metabolism; Signal.
                                                                                                        Score 417; DB 1;
Pred. No. 7.7e-38;
                                                                                                                                                                                                                                                                                                                                                               15-SEP-2003 (kcl. 42, Created)
15-SEP-2003 (kcl. 42, Last sequence update)
15-SEP-2003 (kcl. 42, Last annotation update)
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C PEPTIDE.
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                                                                                                                                        1; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     InterPro: IPR04825: Ins/IGF/relax.
Pfam: PF00049: Insulin: 1.
PRINTS: PR00277: INSULINB.
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                                                                                                        90.1%;
89.5%;
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                                                                                                                                     77; Conservative
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                                                                                                                          Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                Insulin precursor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NCB1_TaxID-43179;
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                                                                                                         1 FVNOHLCGSHLVEALYLVCGERGFFYTPKTRREAEDLQVGQVELGGGPGAGSTQPLALEG 60
                                                                                                                                  1 FVNQHLCGSHLVEALYLVCGERGFFYTPKTRREAEDLQVGQVELGGGPGAGSLQPLALEG 60
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-!- SIMILARITY: BELONGS TO THE INSULIN/IGF/RELAXIN FAMILY.
-!- CAUTION: X'S AT POSITIONS 31-32 AND 64-65 REPRESENT PAIRED HASIC RESIDIES ASSUMED BY HOMOLOGY TO BE PRESENT IN THE PRECURSOR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Tager H.S., Steiner D.F.;
"Primary structures of the proinsulin connecting peptides of the rat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Eukaryola, Motazoa, Chordata, Cranista, Periobrata, Eureleostomi,
Mammalla: Eufneria: Perissodactyla: Equifos Equis.
                                                          0
Score 413; DB 1; Length 110;
Pred. No. 2e-37;
3; Mismatches 6; Indels
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Pred. No. 1.7e-35;
1; Mismatches 12; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                          23.JUL-1986 (Rel. 01, Last sequence update)
15.JUL-1999 (Rel. 38, Last amontalion update)
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CHAIN 1 30 INSULIN B CHAIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               INSULIN A CHAIN.
                                                                                                                                                                                                                                                                                                                                                                                                  86 AA
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                                                                                                                                                                                                                                            C PEPTIDE.
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HSSP; P01317; 1APH.
InterPro; 1PR004825; Ins/IGF/relax
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                                                                                                                                                                                                                                                                                                                                                                                                                                               21-JHE-1986 (Rel. 01, Created)
21-JHE-1986 (Rel. 01, Last Seq
Query Match
Best Local Similarity 89.5%;
Matches 77; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PS00262; INSULIN; 1
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Matches 73: Conservative
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SMART; SM0078; I1GF; I:
PRUSITE: PS00262; INSULI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Equus cabalius (Borse).
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INS_HORSE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Buenzii H.F., Glatchaar B., Kunz P., Muelhaupt E., Humbel R.E.;
*Amino acid sequence of the two insulins from mouse (Maus musculus).":
*Amino acid sequence of the two insulins from mouse (Maus musculus).":
*Physiol. Chem. 353:458(1972).
*!- FUNCTION: INSULU DECREASES BLOOD GLUCOSE CONCENTRATION. IT
**INCREASES CFLL PREMEABILITY TO MONOSACCHARIDES. AMINO ACIDS AND
*FATTY ACIDS. IT ACCELERATES GLYCOLYSIS, THE PENTOSE PHOSPHAIF
*CYCLE, AND GLYCOGEN SYMPHESIS IN LIVER.
**CYCLE, AND GLYCOGEN SYMPHESIS IN LIVER.
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SMART: SM00078; IlGF: 1.
PROSITE; PS00262; iNSULIN; 1.
Insulin family; Ho-none; Glucose metabulism; Signal; Multigene family.
SIGNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sawa T., Ohqaku S., Morioka H., Yano S.; Moreular cloning and DNA sequence analysis of preproinsulin genes in the Now mouse, an animal model of human non-obese, non-insuling dependent diabetes mellius."; J. Mol. Endocrinol. 5:61-67(1990).
                                                                                                                                                                                                                                                             Mus musculus (Mouse).
Sukaryota: Metazoa: Chordata; Craniata: Vertenzata: Eutoleostomi:
Mammalia; Eutheria: Rodentia; Sriuroqnathi, Muridae; Murinae; Mus
NÇBI_TaxiD=10090:
                                                                                                                                                                                                                                                                                                                                                                                          Wentworth B.M., Schaefer L.K., VillarKearoff L., Chirawin J.M.: "Characterization of the two monalietic acaes encoding mouse
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           -i- SUBCELLULAR LOCATION: Necretod.
-i- SIMILARITY: BELVINGS TO THE INSULINZIGEZRELAXIN FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MGD; MGI:96573; Ins2.
GO; GO:0000187; Practivation of MAPK; 1DA.
GO; GO:004325; Prrequiation of phosphorylation; IDA
interPro; IPR004825; Ins/IGF/relax.
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INSULIN 2 C PEPTIDE.
INSULIN 2 A CHAIN.
                                                                                                                                                                 21-JUL-1986 (Rel. 01, Created)
13-ANG-1987 (Rel. 05, Last sequence uptate)
16-OCT-2001 (Rel. 40, Last annotation update)
                                                                                                                               110 AA
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61 SLOKRGIVEQCCTSICSLYQLENYCN 86
                                 86
                   61 PQOXXGIVEQCCTGICSLYQLENYCN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDLINE=72189455; PubMed=5063718;
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                                                                                                                               STANDARD;
                                                                                                                                                                                                                           Insulin 2 precursor.
INS2 OR INS-2.
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HSSP; P01317; 1APH.
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DISULFID
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                                                                                                   Gaps
                                                                                                                                                                                                                                                                                         Raffus norvegicus (Rat).
Eukāryotā: Metazoa: Chordata: Craniatu Virtebrata: Euteleostomi;
Māmmālia: Eutheria: Rodentia: Sciuroq: -:: Muridae; Murinae: Raffus.
                                                                                                                                                                                                                                                                                                                                                          STRAIN=Spraque=Dawley: TISSUE=Liver;
MEDLINE=80045015; PubMed-498284;
Lomedico P., Rosenthal N., Efstratiadi: A., Gilbert W., Kolodner R.,
                                                                                                                                                                                                                                                                                                                                                                                                       The structure and evolution of the tw. nonailelic rat preprofessiin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Tager H.S., Steiner D.F.; Primary structures of the proinsulin connecting peptides of the rat
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Aten B., Oyer P.E.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDINE-86510882; Pubmed-2427930;
Scares M.B., Schin E., Henderson A., Karathanasis S.K., Cate R.,
Zeitlin S., Chirqwin J., Efstratiadis A.;
*RNA-mediated gene duplication: the rat preproinsulin I gene is
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                                              Length 110;
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Lomedico P.T., Rosenthal N., Kolodner R., Elstratiadis A.,
                             85.1%; Score 394; DB 1; Length 11x
84.9%; Pred. No. 2.20-35;
84.9%; Pred. No. 2.20-35;
                      12364 MW; 3554C8803D24FDAD CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Markussen J., Sundby F.;
"Rat-proinsulin C-peptides. Amino-acid sequences.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Aten B., Oyer P.E.; *Proinsulin and the biosynthesis of insulin."; Recent Prog. Horm. Res. 25:207-282(1969).
                                                                                                                                                                                                                                  21 JULY 1986 (Reg. 01, Greated)
21 JULY 1986 (Rej. 01, fast, sequence assato)
16-60T-2961 (Rej. 40, fast amotation glade)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    'The structure of rat preproinsulin genes.";
  INTERCHAIN
                                                                                                                                 N.Y. Acad. Sci. 343:425-432(1980).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Biol Chem. 247:7936-7940(1972).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Mol. Cell. Biol. 5:2090-2103(1985)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDEINE-70067613; PubMed-4311938;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDLINE-73061498: PubMed-4640931;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE OF 25.54 AND 90-110
                                                      Best Local Similarity 84.9
Matches 73; Conservative
                                                                                                                                                                                                               STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        functional retroposon.
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                                                                                                                                                                                                                                                                      Institu Z precursor.
43 1
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between the Swiss Institute of Bioinformatics and the EMBL outstation. The European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                   This SWISS-PROT entry is copyright. It is produced through a collaboration
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Eur J. Biochem. 25:153-162(1972).
-!- FUNCTION: INTEGRASE BLOOD GLUCOSE CONCENTRATION. IT
INCREASES CELL PERMEABILITY TO MONOSACCHARIDES, AMINO ACIDS AND
FATTY ACIDS: IT ACCELERATES GLYCOLYSIS, THE PENTOSE PHOSPHATE
CYCLE, AND GLYCOGEN SYNTHESIS IN LIVER.
-!- SUBDNIT: HETENODIMER OF A B CHAIN AND AN A CHAIN LINKED BY TWO
DISULPIDE BONDS.
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Bukaryota: Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Platyrrhini; Cebidae; Aotinae; Aotus.
NCBL_maxID-9505, 9521.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 110;
                                                                                                                                                                                                                                                                                                     -:- SUBCELLULAR LOCATION: Secreted.
-:- SIMILARITY: BELONGS TO THE INSULIN/IGF/RELAXIN FAMILY.
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INSULIN 2 C PEPTIDE.
INSULIN 2 A CHAIN.
INTERCHAIN.
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01-30L-1989 (Rel. 11, Last sequence update)
16-0CT-2001 (Rel. 40, Last annotation update)
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Pfam: PF00049; insulin: 1.
SMART; SM00078; ilGF; 1.
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MEDLINE-88041119; PubMed-3118367;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EMBL: V01243: CAA24560.1; -. EMBL: J00748: NAA41443.1; -. EMBL: M75585: AAA41445.1; GMRE: M25583: AAA41440.1; GOINEL
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Matches 73; Conserv
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INTERCHAIN 61 SLOKRGIVEQCCISICSLYQLENYCN 86 Interpro: IPR004825; ins/IGF/relax. Pfam; PF00049; Insulin; 1. PRO SUBCELLULAR LOCATION: Secreted G.I., Sanchez-Pescador R.; SEQUENCE OF 25-54 AND 90-110. :: :: :: PROSITE: PS00262; INSULIN; 1 EMBL: M26328; AAA37089.1; 24 54 87 11:0 96 109 100 12268 P Ouery Match

Bost Local Similarity 84.9
Matches 73; Conservative Insulin tamily: Hormone; STANDARD; SMART; SM00078; 11GF; 1 Rattus norvegicus (Rat.). DISULFIDE BONDS insulin 1 precursor. INSI OR INS-1. 110 AA; NCBI_TaxID=10116; HSSP; F01308; INS:_RAT P01322; DISULFID DISULFID DISULFID SIGNAL PROPER CHAIN CHAIN INS1_RAT 3 င် 5 This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss institute of Bioinformatics and the EMR, outstation the European Bioinformatics institute. The European Bioinformatics institute the European Profit institutions as long as its content its most modified and this statement is not removed. Its content is in the way modified and this statement is not removed. Its profit is not seen entities in the conservation or send an email to license partners. It is not the content of send an email to license partners in the content of send an email to license partners. : FVNQHICGSHLVEALYLVCGERGFFYTPKTRREAEDLQVGGVELGGGPGAGSLQFTALEG 60 8.2 Gaps SPECIES'S Sciureus;
MEDLINE-91086593; PubMed-2263627;
MEDLINE-91086593; PubMed-2263627;
MEDLINE-91086593; PubMed-2263627;
MEDLINE-91086593; PubMed-2263627;
MEDLINE-100 and amino acid sequences of squirrel monkey (Saimiri Sciurea) insulin and glucagon...; 9766-9768(1990).

1 FUNCTION: INSULIN DECREASES BLOOD GLUCOSE CONCENTRATION. IT INCHEASES CELL PERMEABILITY TO MONOSACCHARIDES, AMINO ACIDS AN FATTY ACIDS. IT ACCELERATES GLYCOLYSIS, THE PENTOSE PHOSPHATE CYCLE, AND GLYCOGEN SYNTHESIS IN LIVER. SUBUNIT: HETERODIMER OF A B CHAIN AND AN A CHAIN LINKED BY TWO Cricetulus longicaudatus (Long-tailed harster) (Chinese hamster). ~ Length 168; Score 392: DB 1; Length Lvd Pred. No. 3.55 35; Pred. Tribbs 7; Indels 11842 MW: 186988250099731F CRC64; [2] SEQUENCE UF 25-54 AND 88-108.

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Mammalia, Euthoria, Rodentia, Sciurognathi, Muridae, Murinae, Rattus
                                                                                                                                                                                                      FUNCTION: INSULIN DECREASES BLOOD GLUCOSE CONCENTRATION. IT INCREASES CELL PERMEABILITY TO MONUSACCHARIDES, AMINO ACIDS AND FATTY ACIDS. IT ACCELERATES GLYCOLYSIS, THE PENTOSE PHOSPHATE CYCLE, AND GLYCOGEN SYNTHESIS IN LIVER.
                                                                                                                                                                                                                                                                                                                                     SUBUNIT: HETERODIMER OF A B CHAIN AND AN A CHAIN LINKED BY TWO
                                                                                                                 Neelon F.A., Delcher H.K., Steinman H., Lebovitz H.E.;
"Structure of hamster insulin: comparison with a tumor insulin.";
Fed. Proc. 32:300-300(1973).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ..
"Sequence of a cDNA encoding Syrian hamster preproinsulin."; Diabetes 33:297-300(1984).
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84.9%; Pred. No. 4.5c 35;
Mismatches 9; Indels
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21-JUL-1986 (Rel. 01, Last sequence update)
16-XXI-2001 (Rei. 46, Last annotation update)
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Insulin tamily: Hormone: Glucose metabo ism: Signal: Multigene family.
                                                                                                           The structure and evolution of the two nonallelic rat preprotesults
                                                                           Lomedico P., Rosenthal N., Efstratiadis A., Gilbert W., Kolodner R.,
                                                                                                                                                                                                                                                                                                                                                                                                                               Tager H.S., Steiner D.F., Primary Structures of the proinsulin connecting peptides of the ratand the horse. \mathbb{F}_{\ell}
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SURGNIT: HETERODIMER OF A B CHAIN AND AN A CHAIN LINKED BY TWO
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"kat-proinsulin C-peptides. Amino-acid sequences.";
Eur. J. Biochem. 25:153-162(1972).
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INSULIN I PEPTIDE.
INSULIN I A CHAIN.
INTERCHAIN.
                                                                                                                                                                                                                                       "The structure of rat preproinsulin genes.";
Ann. N.Y. Acad. Sci. 343:425-432(1980).
                                                                                                                                                                                                                                                                                                                  Steiner D.F., Clark J.L., Nolan G., Robensto
Aben B., Syver P.E.,
"Processor in and inc biosymbhesis of issued
Repost droft Born, Pos. 25 202 282(50).)
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                                             STRAIN-Sprague-Dawley: TISSUE-Liver;
MEDLINE-80045035; PubMed-498284;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Biol. Chem. 247:7936-7940(1972)
                                                                                                                                                                                                                                                                                    SEQUENCE OF 25-54 AND 90-110.
MEDLINE-70067613; PubMed:4311938;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE OF 57-87, AND REVISIONS.
MEDGINE:72177385; PubMed+4554104;
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                                                                                                                                                                                        80240379; PubMed-6249167
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SMART; SM00078; 11GF; 1.
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Ceil 18:545-558(1979).
Cell 18:533-543(1979)
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                                                                                                                                                                         SECTIONS FROM N.A.
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                                                                                   Baker E.N., Blundell T.L., Cutfield J.F., Cuttield S.M., Dodson E.J., Dodson G.G., Crowtoot Hodgkin D.M., Hubbard R.E., Isaacs N.W., Reynolds C.D., Sakabe K., Valayan N.M.:
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                                    Gaps
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"Experience with fast Fourier least squares in the refinement of the crystal structure of rhombohedral 2-zinc insulin at 1.5-A
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Marmalia, Botheria, Ordartiodaetyla, Saina, Saidae, Sus.
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MEDIJNE 68286485; PuthMed-5657063;
Chance R.E., Ellis R.M., Bromer W.W.;
"Poteine preinsulin: characterization and amino acid sequence.";
Science 161:165-167(1968).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     "Comparative sequence analysis of the INS 1GF2-H19 gene cluster
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Georges M., Andersson L.;
83.2%; Score 385; DB 1; Length 110;
83.7%; Pred. No. 2e-34;
.ive 4; Mismatches 10; Indels
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Bundell T.L., Dodson G.G., Hodgkin D., Mercola D.,
Insulin. The structure in the crystal and its reflection
chemistry and biology."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  "Complete porcine preproins (in cDNA sequence.";
Submitted (MAX 1998) to the EMBL/Genbank/DDBJ databases
                                                                                                                                                                                                                                                                                 21-JUL-1986 (Rel. 01, Created)
16-OCT-2001 (Rel. 40, Last Sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
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MEDLINE-22135958; PubMed-12140686;
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                                 Conservative
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                 Similarity
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P01315; 097SJ5;
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-1'FINCTION: INSULIN DECREASES BLOOD GLUCOSE CONCENTRATION. 11
INCREASES CELL PERMEABILITY TG MONOSACCHARIDES, AMINO ACTIOS AND
FATTY ACTIOS. 17 ACCELERATES GLYCOLNSIS, THE PENTICSE PHOSPEATE
CYCLE, AND GLYCOGN SYNTHESIS IN LIVER.

-1'SUBUNIT: HELEGGEIMER OF A POPAIN AND AN ACTIAIN LINKED BY 1991.
                                                                                                                                                                                                                                                                                           X-RAY CRYSTALLOCRAPHY (1.65 ANGSTRUMS).
Diao J.-S., Wan Z.-L., Chang W.-R., Liana D. C.;
Structure of monmeric porcine Desb1-B2 despentapeptide (826-830) insulin at 1.65-A resolution...?
Acta Crystallogr. D 53:507-512(1997).
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WWW-"http://www.expasy.org/spotlight/articles/sptit009.html".
                    Balschmidt P., Hansen F.B., Dodson E., Dodson G., Korber F.; "Structure of porcine insulin cocrystallized with clupeine 2."; Acta Crystallogr. B 47:975-986(1991).
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MEDLINE-9122450; PubMed-2025410;
MEDLINE-91222450; PubMed-2025410;
MEDGINE-0.1, Harris M.R., Reynolds C.D., Evins A.C., Dodson E.J.,
Dodson G.G., North A.C.T.,
Structure of the pig insulin dimer in the cubic crystal.
Acta Crystallogr. B 47:127:136(1991).
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EMPL: AY044828; AAU69550.1; -.
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  MEDLINE-92126280; PubMed-1772633;
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SMART; SM00078; ILGF; 1.
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16-JUN-97.
01-APR-98.
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                                                    1 FVNQHLGGSHLVEALYLVGGERGFFYTPRTRREAEDLQVGOVELGGGPGAGSLQPLALEG 60
                                                                 25 FVNQHIGGSHLVEALYINGGERGFFYTPKARRFAENPQAGAVELGG-GLGGIQALALEG 82
                             2; Gaps
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SUBUNIT: HETERODIMER OF A B CHAIN AND AN A CHAIN LINKED BY TWO
DISULFIDE BONDS.
                                                                                                                                                                                                                                                                                               Chordata, Craniara, Vertebrata, Euteleostomi,
Rodentia, Seiurognathi, Muridae, Gerbillinae,
 Score 383; UB 1; Length 108;
Pred. No. 3.3e-34;
(; Mismatches 9; Indels
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85.08;
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PRINTS, PRO077; INSULINE.
SMART: SMO078; I.GF. 1.
PROSITE: PS00262: INSULIN: 1.
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 Ouery Match
Best Local Similarity 86.0
Matches 74; Conservative
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Mammalia; Eutheria;
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                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
                                                                                                                                                                                                                                             15-JJI-1998 (Rel.
                                                                                                                                                                                                                                                          Insulin predusor
                                                                                                                                                                                                                                                                                                                                   NCB1_Tax1D-48139;
                                                                                                                                                                                                                                                                                    Psarmomys obesus
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0; Gaps 0;

Matches 70; Conservative 5; Mismatches 11; Indels

Qy	1	FVNQHLCGSHLVEALYLVGERGFFYTPKTRREAEDLQVGQVEJLGGGPGAGSLQPLALEG 60
qa	25	25 FUNGHLCGSHLVEALYLVCGERGFFYTPKFRRGVDDPQMPQLELGGSPGAGDLRALALEV 84
ογ	9	6: SLOKRGIVEQCCTSICSLYQLENYCN 86
do.	8.	85 ARQKRGIVEQCCTGICSLYQLENYCH 11)
Search co Job time	mple! β.β.:	Search completed: September 15, 2003, 12:01:30 Job time : 9.01434 secs

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RESULT 2
Q91X13
ID 091X3
AC 091X1
DT 01-DE
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                                                                  September 15, 2003, 11:54:30; Search time 33.5986 Seconds (without aliquments) 660.520 Million ceit updates/sec
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                                                                                                                                          1 FVNQHLCGSHLVEALYLVCG.... IVEQCCTSICSLYQLENYCN 86
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Description
GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.
                                                                                                                                                                                                                              Total number of hits satisfying chosen parameters;
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Maximum Match 100%
Listing first 45 summaries
                                               OM protein - protein search, using sw model
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U91X13
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Gapop 10.0 , Gapext 0.5
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sp_phage:*
sp_plant:*
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Maximum OB seq length: 200000000
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sp_bacteria:*
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Perfect score:
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442
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110 AA

091X13 PRELIMINARY: PRT; 091X13: 01-DEC-2001 (TrEMBLrel: 19, Created)

098TB2 062543

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61 SLOKRGIVEOCCTSICSLYQLENYCN 85
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 FVNQHLCGSHLVEALYLVGGERGFFYTFRTRREAEDLOVGQVELGGGPGAGSLQPLALEG 60
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                                                                                                                                                                                                                         Spermophilus tridecemlineatus (Thirteen-lined ground squirtel).
Eukaryota: Metazoa: Chordata: Craniata: Vertebrata: Euteleostomi;
Mammalia: Eutheria: Rodentia; Sciuroqnathi; Sciuridae; Sciurinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Felis silvestris catus (Cat).
Enkaryofa: Metazoa; Chordata; Graniata; ertebrata; Euteleostomi;
Mammalia; Eutheria; Carnivora; Fissipedii; Felidao; Felis.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      89.2%; Score 41%; tH 11; Tength (16; 89.5%; Pred. No. 3.36-41;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 110;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SUBSECTIONARY OCATION: SECRETED (BY STRUCKETY). SIMILARITY: BELONGS TO THE INSTITUTIONE FELAXIN FAMILY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            83.8%; Score 388; DB 6; Length 110
83.7%; Pred. No. 3.18-38;
Live 2; Mismatches 12; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               6: Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Okamoto S., Mo imatsu M.;
"cat (ESGLin.";
S.bmitted (MAY-2010) to the EMBL/Necsonk/2008.1 databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 45117685/0228EES 08764)
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01-0FC-2001 (TrEMBLrel. 19, Last sequence update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             01-MAR 2002 (PrEMBLEG), 20, Last sequence update)
01-MAR 2003 (TrEMBLEG), 23, Last adnotati u apdate)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Pred. No. 1.36-41;
3; Mismatches 6
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01 МАR-2002 (TrEMBLE) 20, Greated)
01-МАR-2002 (FEBMBLE). 20, Last semi
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pfam; PF00049; Insulin; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               InterPro: 1P8004825; Ins/IOF/relax
Pram: PFG0045; Insulin; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PROSITE: PS00262: INSULIN: 1.
SPOCENCE 110 AA: 12069 MW:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 12004 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                         PROSTER: PS 1262: INSULIN: 1.
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Matches 77; Conservative
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Matches 72: Conservative
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                                                                                                                                                                                      SEQUENCE FROM N.A.
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                                                                                                                     Spermophilus.
NCBI_TaxID+43179;
                                                                                                                                                                                                          TISSUE-Pancreas:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             O'Biberin C., Troby B., Kiein J.;
"Motestlar evolution in higher primates; gene specific and organism
                                                                                                                                                                                                                                                                                                                                                                                                                            Eukaryota, Metazod, Chordata, Craniata, Vertebrata, Euteleostomi;
Mammaila; Eutheria, Primates, Catarrhini; Kominidae, Gorilla,
NCBI_TaxID+9593,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Pongo pygmaeus (Granquitan).
Eukaryota, Metazoa, Chordata, Craniata: Vertebrata, Eufeleostomi,
Mammolia: Eutheria, Primates, Catarrhini, Norinidue, Pongo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   73.9%; Score 342; DB 6; Length 65;
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Submitted (MAK 2002) to the EMHL/SenRank/DPRJ databases
EMRL; AY092023; AAM76640.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sabmitted (MAR-20.2) to the EMBL/GenBank/Eds. databases
EMBL: AY092024; AAM76641.1; -.
Now_TER
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NON_TER 65 65 SEQUENCE 65 AA: 6920 MM; B772017FD46CABEA CRC64;
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SEQUENCE 65 AA; 6920 MW; H772017FD8BCABEA CRC64;
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01-MAR-2003 (TrEMBLIE). 23, Last sequence update)
01-MAR-2003 (TrEMBLIE). 23, Last annotation update)
                                                                                                                                                                   01-MAR-2003 (TrEMBLrei, 23, Last sequence update)
01-MAR-2003 (TrEMBLrei, 23, Last annotation update)
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100.0%; Pred, No. 4.7e-33;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              100.0%; Pred. No. 4.7e 33; tive %; Mismatches 0;
65 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 100.0%; Pred. No. 4.74
tive 0: Mismatches
                                                                                                        01-MAR-2003 (TrEMBLie), 23, Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PKT;
                                                                                                                                                                                                                                                                                                Insulin (Fragment).
Gorilla gorilla (gorilla).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               65; Conservative
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3 NOHLCGSHLVEALYLVCGERGFFYTPKTRREAEDLJVGQVELGGGPGAGSLQPLALEGSL 62
                                                                                                                                                                                                                                                                                                                                                                3 NOHLOGSHLVEALYLVC PRGFFYTPKTRREAEDLØVGOVELGGGPGAGSLØPLAL**** 58
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PLIGFLSPKSAUENE 73
                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          13; Indels 25; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Pantodon buchhoitzi (Butterflyfish).
Bukaryota: Metazoa: Chordata; Craniata; Vertebrata; Euteleostomi:
Actliopteryyii; Neopteryqii; Teleostei; Osteoglossomorpha;
Osteoglossiformas: Pantodontidae; Pantodon.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Hiodon alosoides (goldeye).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
                                                                                                                                                                                                                                                                        1;
                                                                                                                                                                                                             50.9%; Score 235.5; DB 13; Length 111; 54.1%; Pred. No. 3.7e-20;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  49,8%; Score 230.5; DB 13; Length 110; 46,4%; Pred, No. 1,4e-19;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     X MEDLINE-2120357; PubMed-1130617;
A Al-Mahrouki A.A. Irwin D.M. Graham L.C., Youson J.H.;
A Al-Mahrouki A.A. Irwin D.M., Graham L.C., Youson J.H.;
A Holdecular cloning of preproinsulin conserveral osteoglossomorphs and a cyprinid.";
Mol. Cell. Endocrinol. 174:51-58(2001).
L. SUBCELLULAR LOCATION: SECRETED (BY SIMILARITY).
-! SUBCELLULAR LOCATION: SECRETED (BY SIMILARITY).
-! SIMILARITY: BELONGS TO THE INSULIN/IGF/KELAXIN FAMILY.
R MSSP: PO1308: JHIS.
R FASS: PO1308: JHIS.
R FIGHT: PROUG45; Insulin; 1.
R SMART: SMO0078: Liger. 1.
                                                                                                                                                                                                                                                                        26: Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PROSITE, PS00262; INSULIN: 1.
SEQUENCE 110 AA: 12324 MM: BDECCU659D872E06 CRC64;
                                                                                                                                                  SEQUENCE 111 AA; 12491 MW; AC9E1902D4866D20 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             01-JUN-2031 (TERMSLEE), 17, Created)
01-JUN-2031 (TrEMSLEE), 17, Last sequence update)
01-MAR-2033 (TrEMBSLEE), 23, Last annotation update)
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01-DEC-2001 (TrEMBLrel, 19, Last sequence update)
01-MAR-2003 (TrEMBLrel, 23, Last annotation update)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          26 SQHLCGSHLVDALYMVCGEKGFFYQPKTKRUVD-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   59 ...----EGSLQ KRGIVEQCCTSICSLYQLENYON 86
                                                                                                                                                                                                                                                                     12; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              110 AA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                 63 Q-KRGIVECCTSICSLYQLENYCN 86
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PKT
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Plam: PF00049; Insuliu; 1.
PRINTS; PR00277; INSULINB.
SMART; SM00078; 11GF; 1.
PROSITE; PS00262; INSULIN; 1.
                                                                                                                                                                                                 Ouery Match
Best Local Similarity 54.1%
Matches 46; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRET IMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Ouery Match
Best Local Similarity
Matches 45; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NCB1_Tax1D-8276;
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us-09-423-100-4.rspt

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61 SL---
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       0902N4;
                                                                                                                                                                                          Q9DDE5
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0902N4
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                                                                                                                        RESULT 11
                                                                                                                                                09DDE5
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                                                                                                                                                                                                                     SOUTH TERMINATION OF THE SOUTH 
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   3 NOHLCGSHLVEALYLVCGERGFFYTPKTRRFAEDLQVCQVELGGCPGAGSLQPLAL. 58
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           3 NOHLCGSHLVEALYLVCGERGFFYTPK - TRREAEDLQVGQVELGGGPGAGSLQPLA-LEG 60
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               47.3%; Score 239; CB 13; Length 111;
49.0%; Pred. No. 4.3e-18;
Live 7; Mismatches 17; Indels 26; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Preproinsulin (Fragment).
Chinala chitula (clown kniretish).
Eukaryota: Metazoa: Chorada: Crantata: Vertebrata; Euteleostomi:
Actinopteryqii: Neopteryqii. Teleostei: steoglossomorpha:
Osteoglossiformes; Notopteridae: Chitala
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              25;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        48.1%, Shore 22.5, 08.19, Length, 110;
45.4%; Pred, No. 1 se-18;
Actinopteryqii; Neopterygii; Teleostei; Osteoglossomorpha;
Osteoglossiformes; Hiodontidae; Hiodon.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Ai-Mahrouki A.A., irwin D.M., Graham L.C., Youson J.H.,
"Molecular cloning of preprolisulth clark from several
osteoglossomorphs and a cyprinid.",
Moi. Gell. Endocrinol. 174:51-58(201).
'!- SURCELLULAR LOCATION: SECRETED (BY SIMILARITY).
ENT. ARILARITY: BELONGS TO THE INSULIN/IGF/RELAXIN FAMILY.
HNSP; P01308: 1LPH.
                                                                                                           15; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MORE THAT SPICED IN CHOOSE,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     111 AA: 12483 MW; 2470A4431376329F CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    01-JUN-2001 (TrEMBLrel, 17, Created)
01-JUN-2001 (TrEMBLrel, 17, Last Sequence update)
01-MAN-2003 (TrEMBLrel, 23, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    24 ADEYPYKOJGDLKVKRGIVEQCCHRPCNIFDLNQYCN 110
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         59 .....-EGSLQ-KRGIVEOCCTSICSLYOLENYCN 86
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           13; Mismatches
                                                                                                                                                                                                                                                                                                                     Interpro: IPR004825; Ins/IGF/relax. Pfam: PP00049; Insulio: 1. PRNTS; PR00277; INSULINB. SMARY: SMO078: IIGF: I. PROSITE: PSG0262; INSULIN: 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      InterPro: IPR004825; Ins/ISE/relax.
Ptam: PFG0049: Insulin: 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                             110 110
110 AA: 12343 MW.
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Matches 44; Conservative
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Matches 48; Conservative
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NON_TER 111 111
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                                                                                             SEQUENCE FROM N.A.
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                                              NCB1_TaxID-54904;
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4 OHLOGSHLVEALYLVCGERGFFY IPKTRRFAEDLOVGOVELGGGPGAGSLQPLALEGS++ 61
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                                                                                                                                                                                                                                                                                                                       Brachydanio rerio (Zebrafish) (Danio rerio).
Eukaryota; Metazoa: Chordata; Craniata; Vertebrata; Euteleostomi:
Actinopterygii; Neopterygii: Teleostei: Ostariophysi; Cypriniformes:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Catla catla (catla).
Eukaryota: Metazoa: Chordata; Craniata: Verteurata; Euteleostomi;
Actinoptergai; Neopterggi; Teleostel: Ostariophysi; Cypriniformes:
Cyprinidae: Catla.
NCBL_TaxID-72446:
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Bandyopadhyaya I., Wakabayasi K.;
"A new cell secreting insulin.":
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          the
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Argenton F., Zecchan E., Hortoinssi M.:
"Early appearance of pancreatic hormone expressing cells in zebrafish embryo.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Mech. Dev. 87:217-22:(1999).
-!- SUMCELLULAR LOCYTION: SECRETED (BY SIMILARITY).
-!- SIMILARITY: BEL. NGS TO THE INSULIN/IGE/RELAXIN FAMILY.
EMBL: A123756. CAC. 0169.1: -- HSSP: P01368; 1LPH.
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INSULIN B CHAIN,
INSULIN A CHAIN,
3195289272AD6D25 CRC64;
                         34 EVDEYPEKDOGDVKMKRGIVEOCCHRPCNIFDONOYCN 111
                                                                                                                                                                                                      01-MAR-2001 (TrEMBLrel. 16, Created)
01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
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01-0EC-2001 (TrEMBLIE), 19, Last sequence update)
01-MAR-2003 (TrEMBLIE), 23, Last annotation update)
-- OKRGIVEOCCISICSLYQLENYCN 86
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         73 ADFAFKDHAELTPREGIVEOCCHKPCSTFELGNYCN 108
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  --- LUKRGIVEQCCTSICSLYQLENYON 86
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      46.3%; Score 214.5; DB 1
45.8%; Pred. No. 1.1e-17;
tive 11; Mismatches 14
                                                                                                                                                              108 AA
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                                                                                                                                                              PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ZFIN: ZDB-GENE-980526-110; tos.
InterPro; IPR004825; Ins/IGr/relax.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDLINE-99425190: PubMed-10495291:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           168 AA: 11904 MW:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PROSITE; PSU0262; INSULIN; 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Pfam: PF00049; Insulin: 1.
PRINTS; PR00277; INSULINB.
SMART: SMO0078; IIGF: 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Local Similarity 45.8%
les 44; Conservative
                                                                                                                                                           PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRELLIMINARY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    108
                                                                                                                                                                                                                                                                               Insulia precursor.
                                                                                                                                                                                                                                                                                                                                                                                                Cyprinidae: Danio.
NCBL_TaxID-7955;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          4 QHIAGSHLVEALYLVGGERGFFYTPKTRREAEDLOVGQVELGGGP--GAGSLQPLALEGS 61
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      27; Gaps
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Eukaryota: Metazoa: Chordata: Graniata: Vertebrata; Euteleostomi;
Actinopterygii: Neopteryaii; Telecstei: Osteoglossomorpha;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ۳
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 45.9%; Score 212.5; DB 13; Length 108; 44.8%; Pred. No. 1.9e-17;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 45.5%: Score 210 5: DB 13: Length 87: 50.6%; Pred. No. 2.6e-17; ctive 11: Mismatches 28: Indels 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDILINE-2120357, The Manager 11306171;
A Mahrouki A.A., Irwin D.M., Graham ..., Youson J.H.;
Al-Mahrouki A.A., Irwin D.M., Graham ..., Youson J.H.;
Mahrouki A.A., Irwin D.M., Graham ..., Youson J.H.;
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Controlled to mana
Submitted (APR-2001) to the EMBL/GenRank/DDBJ databases.

- SUBCELULAR LOCATION: SECRETED (BY SIMILARITY).

- SIMILARITY: BELONGS TO THE INSULIN/IGF/RELAXIN FAMILY.

EMBL: AF373021: AAK51558.1;

HSSP: P01308: ILNP.

ILNP.

InterPro: TPR004025; Insylin: 1.

PRINTS: PR004277: INSULINB.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      14; Indels
                                                                                                                                                                                                                                                                                                                         SM00078; TlGF; 1.
E: PS00262; INSULIN; 1.
R: 108 AA: 11881 MM; D713026E22EF5D59 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PS CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (TrEMBLrel, 17, Last sequence update)
(TrEMBLrel, 23, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             2.4 ANPARKOBARVIRKATIVRUSTINIKUSTSTANDUSTUST 10.0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  12; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Best Local Similarity 44.88 Matches 43; Conservative
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01-MAR-2003
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Best Local S
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4 CHLCGSHLVEALYLVCGERGFFYTPKTFPEAEDLJVCQVELGGGPGAGSLQPLALEGS++ 61
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                                                                              Preproinsulin (Fragment).
Catostomus commersoni (White Sucker).
Catostomus commersoni (White Sucker).
Bukaryota: Metazoa: Chordata: Graniata; Vertebrata: Buteleostomi:
Actinopterygii: Neopterygii: Teleostei: Ostariophysi: Cyprinilormes;
Catostomidae: Catostomus.
NCBI_TaxID=7971:
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Centrarchidae; Ambloplites.
NCBI_TaxID=109273;
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Actinopterygii: Neopterygii: Teleostei: Euteleostei: Neoteleostei:
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Al-Mahrouki A.A., Irwin D.M., Youson J.H.;
"Molecular Cloning of prepredinsulin cDNA from the rock bass.";
Submitted (OCT-1999) to the EMBL/GenRank/Dibij databases.
-!- SUBCELLULAR LOCATION: SECRETED (BY SIMILARITY).
-!- SIMILARITY: BELONGS TO THE INSULIN/IGF/RELAXIN FAMILY.
--- BEMBL: AF199584; AAK28708.];
HSSP; P01308; ILPH.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       44.4%: Score 205.5; DH 13; Length 108; 50.0%; Prod. No. 1.30 16; (ive 12; Mismatches 24; Indels 7;
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                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A. MEDGINE 21203577: PubMed-11306171; Al-Mahrouki A.A., Irwin D.M., Graham J.C., Youson J.H.; *Molecular cloning of preproinsulin cDNAs from several
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        108 AA: 11873 MW; E426310696FBAFCB CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       91 AA; 10100 MW; E86C8B256DC69D39 CRC64;
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01-JUN-2001 (TrEMBLrel. 17, Created)
01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
61-JUN-2001 (TrEMBLrel. 17, Created)
01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
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Pfam; PF00049; Insulin; 1.
SMART; SM00078; IIGF; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Ambioplites rupestris (Rock bass).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Best Local Similarity 50.0%
Matches 43; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Preproinsulin (Fragment).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRELIMINARY;
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9; Gaps
Best Local Similarity 46.7%; Pred. No. 1.86-16;
Matches 42; Conservative 13; Mismatches 26; Indels
```

Search completed: September 15, 2003, 12:03:29 Job time: 35.5986 secs

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GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.
```

OM protein . protein search, using sw model

September 15, 2003, 11:44:15; Search time 36.5305 Seconds Run on:

(without alignments) 225.942 Million cell updates/sec

US-09-423-100-5 294 Title: Perfect score:

1 FVNQHLCGSHLVEALYLVCG.....IVEQCCTSICSLYQLENYCN 52 Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

1107864 seqs, 158726573 residies Searched: 111.7864 Total number of bits satisfying chrisen parameters:

Minimum UB seq length: 0 Maximum UB seq length: 2000000000

Post-processing: Minimum Match 08

Listing first 45 summaries Maximum Match 100%

Database :

| SIDSI/godata/geneseq/genescap-emb1/Aa1980,DAT:
| SIDSI/godata/geneseq/genescap-emb1/Aa1980,DAT:
| SIDSI/godata/geneseq/genescap-emb1/Aa1980,DAT:
| SIDSI/godata/geneseq/genescap-emb1/Aa1980,DAT:
| SIDSI/godata/geneseq/genescap-emb1/Aa1980,DAT:
| SIDSI/godata/genescap-emb1/Aa1980,DAT:
| SIDSI/godata/genescap-emb1/Aa1980,DAT: /SIDSI/gradata/geneseq/: nesegp.embl/AA1996.DAT:*/SIDSI/gradata/geneseq/c.neseqp.embl/AA1999.DAT:*/SIDSI/gradata/geneseq/qeneseqp.embl/AA2000.DAT:* /SIDS1/gcddata/geneseq/veneseqp.emb1/AA2001,5AT;*/SIDS1/gcddata/geneseq/yeneseqp.emb1/AA2002.DAT;*/SIDS1/gcddata/geneseqy/geneseqp.emb1/AA2003.DAT;* A_Geneseq_19Jun03:*

Prod. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

Description	Human insulin prec	Human pro-insulin	Proinsulin sequenc	Human pro-insulin	Human pro-insulin	Fusion protein con	hGH-mini-proinsuli	SOD-proinsulin hyb	Mating factor alph
SUMMARIES	AAY42859	AAR68901	AAR78665	AAR68900	AAR68899	AAR78662	AAY42860	AAR98897	AAR71692
CB :	20	15	16	15	15	16	20	17	16
% Cuery Match Length DB	52	26	26	63	96	96	107	116	137
8 Cuery Match	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0
Score	294	767	294	294	294	294	294	294	294
Result No.	-	2	~	4	v.	ę	7	80	σ

Mating factor alph Mating factor alph Chimeric protein, Proinsulia manlogu Example of human i	(B3 Lb1 lph lph ins	Human meture insul Human meture insul Human insulin. Ho Modified pJB59 mod Modified pJB59 mod Single chain insul	Met-Arg Met-single Single chain insul pKV142 modified in Sequence of novel (1y-A21-di-Arg-(B3) Preproinsulin 1. Ins? double-chain Ins? double-chain	ot huma odified Human id sequencoded pJB59	Modified pJB59 mod N-terminally exten Signal peptide/lea Insulin precursor YAP3 signal peptid
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12 12 13 14	115 127 128 128	22 22 23 24 25 25	8	W W W W W W W W W W W W W W W W W W W	4 4 4 4 4 4 4 4 4 4 4 4 4 4 4

ALIGNMENTS

Insulin; precursor, growth hormone, chaperone, intramolecular; folding; conformation; chimeric protein; cleavable; recombinant; production; yield. Human insulin precursor, SEQ ID 5. AAY42859 standard; protein; 52 AA 19-JAN 2000 (Lirst entry) W09950302-A1. Homo sapiens 07-0CT-1999. AAY42859; RESULT 1 AAY42859

98WO-CN00052 31-MAR-1998;

(TONG:) TONGHUA GANTECH BIOTECHNOLOGY LID 98WO-CN00052 31-MAK-1998;

Gan 2;

WPI: 1999-610839/52

New chimeric proteins containing human growth hormone fragment, used particularly for the production of human insulin $^{\circ}$

0

Gaps

..

Length 56; Indels

100.0%; Score 294; DB 15; 100.0%; Pred. No. 1.7e-26;

Mismatches

..

Guery Match
Best Local Similarity True.
The S2: Conservative

ð 2

56 AA;

Sequence

1. FUNDRED ISHLVENDARLVPGERGEFYTERTROTVHGOOTISTOSLYQLENYON 52 THE CHIEF THE CHIEF THE CHIEF THE CHIEF THE CHIEF THE CHIEF THE C

Pro-insulin is produced by treating recombinant precursor protein with a mercaptan to provide 2-10 SH residues per Cys residue, in presence of a chostropic agent and in aq. medium of pH 10-11. Lieuting the prod. with 3-50 q hydrophobic adsorber resin per 1 aq. medium of pH 4-7, isolating the adsorber resin and pro-insulin and desorbing the pro-insulin. This method produces pro-insulin and desorbing the pro-insulin. This method produces pro-insulin with correctly bonded Cys bridges. Compared with known methods it involves fewer stages (esp. no sulphibitojes) or cyanogen bromide cleavage) and overail losses during purification are reduced, i.e. the process is quirker and gives better yields. Sequences of issulin chain A, B and C are given in AAK68895-97. Sequences of pro-insulin chain A, B and C are given in AAK68895-97. (Updated on 25 MAR-2001 to correct PN 11:01)

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This sequence represents a human insulin precursor comprising insuling A and B chains. This insulin precursor is a component of the chimeric protein and B chains. Thois usulin precursor is a component of the chimeric protein and a cleavable at vivor in AAV42861. These chimeric proteins additionally contain an extension in AAV42861. These chimeric protein and a cleavable of vivor in AAV42861. These chimeric protein and a cleavable of vivor in AAV42861. These chimeric protein and a cleavable of the chimeric protein are contained in the chimeric protein are contained in the chimeric protein as as as intramolecular chaperone (IMC) for the insulin precursor, of terminal first estates which enables the hGH portion of the chimeric protein to be Lemoved after folding of the contain insulin via an hGH-proinsulin chimeric protein cofficient in the interesting of the fuse of herman insulin via an hGH-proinsulin chimeric protein and decrease not only protect insulin sequences from intracellular degradation by a microorganism host, but also promote the fusion proteins, thus allowing roiding of the fuse interactions among the fusion proteins, thus allowing roiding of the fuse of provider and decrease the intermolecular interactions among the fusion proteins, thus allowing roiding of the fuse of provider in middly setul has convential ions in protein and convential ions in the fuse of protein and the fuse of protein and acceptance of the fuse of protein and acceptanc
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mercaptan: chaotropic agent.
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                                                                Claim 12; Page 29-30; 46pp; English.
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Marches 52: Conservative
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0; daps

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Isolation of insulin that is correctly post-translationally processed - by reacting pro:insulin with a mercaptan in the presence of a chaotropic agent and purificm, after absorption to hydrophobic
                                                                                           Proinsulin; post translational modification; recombinant production;
                                                                                                                                                                    "a peptide of 4 amino acids"
                                                                                                                                                                                                                                30.55
/label* Gly-(A2-A20)-R3
/note= "human insulin A:chain"
                                                                                                                                                                                                                                                                                                                                                              3
                                                                                                                                                                                                                                                                                                                                                              Sabel
                                                                                                                                                                                       /label - Rl-(B2-B29)-Y
/noter "human insulin
                                                                                                                                            Location/Qualitiers
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                                                                                                     protein folding: conformation.
                 AAR78665 standard: profein;
                                                                                                                                                                                                                                                                                                      95EP-0101748
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                                                       (first entry)
                                                                                                                                                                                                                   /iabel x x
                                                                         Proinsuite sequence 3.
                                                                                                                                                                                                                                                                                                                                                                                 WPI: 1995-284754/38
                                                                                                                                                                                                                                                                                                                                                              Ludwig J.
                                                                                                                                                                                                                                                                                                                                          (FARH ) HOECHST AG.
                                                                                                                                                                                                                                                                                                     09-FEB-1995;
                                                                                                                                                                                                                                                                                                                        18-FEB 1994;
                                                      03-APR-1996
                                                                                                                                                                                                                                                               EP668292 A2
                                                                                                                                                                                                                                                                                    23-AUG 1995
                                                                                                                        Synthetic.
                                   AAR 184.65;
                                                                                                                                                                               Pept, ide
                                                                                                                                                                                                                           Pept ide
                                                                                                                                                                                                                                                                                                                                                              Geri M.
                                                                                                                                                                                                          Region
                                                                                                                                                    Region
RESULT 5
      AAK?8665
                                                                                                                                            Key
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treating recombinant precursor protein with mercaptan in alkali and in presence of chaotropic agent, then isolation on

Disclosure: Page 12; 15pp; German

hydrophobic resin

Produte of prolingulin with correct dissumphide bridges - by

Sabel 1.

Obermeier R,

WP1: 1994-177718/22

92DE-4240420

02-DEC-1992;

(FARH) HOECHST AG. Gerl M. Ludwig J. ö

Caps

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Indels

Sequence

Ouery March

Matches

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Length 63;

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Involves fewer stages (esp. no sulphitolysis or cyanogen bromide cleavage) and overall losses during purification are reduced, i.e. the process is quicker and gives better yields.
Sequences of insulin chain A, B and C are given in AAR68895-97.
Sequences of pro-insulin 1-4 are given in AAR68898-901.
(Updated on 25-MAR-2003 to correct PN field.)
                                                                                                                                                                                                                                                                                                 1 FVNQHLCGSHLVEALYLVCGERGFFYTPKTRGIVEOCCTSICSLYQLENYCN 52
                                                                                                                                                                                                                                                                                                                        FUNDALICESHI,VEALYI,VCGERGFFYTPKTRGIVEQCCTSICSLYQLENYCN 63
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           treating recombinant precursor protein with mercaptan in aikali and in presence of chaotropic agent, then isolation on hydrophobic resin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Pro-insulin, A-chain, B-chain, C chain, disulphide, mercaptan, chaotropic agent.
                                                                                                                                                                                                          Score 294; DB 15;
Pred. No. 1.9e 26;
                                                                                                                                                                                                                                                        0: Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sabei W;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Disclosure: Page 11: 15pp: German.
                                                                                                                                                                                                                                                                                                                                                                                                                                                       AARGSS99 Standard; poptide; 96 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Obermeier R,
                                                                                                                                                                                                          100.0%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (first entry)
                                                                                                                                                                                                   Ouery Match
Best Local Similarity 100.0
Matches 52; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (updaled)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Human pro-insulin .
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Ger! M. Ludwig J,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (FARH ) HOECHST AG.
                                                                                                                                                                   63 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                96 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          25-NOV-1993;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          25-MAR-2004
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EP600372-A1
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                                                                                                                                                                   Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                AAK68894
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                                    The present sequence is an example of a proinsulin molecule corresp. to the general formula R2-R1-(B2-B29-Y-X-Gly-A2-A20)-R3 (II) In formula (II), X = Lys, Arg or a peptide of 2-35 amino acids contg. Lys or Arg at the N- and C-termini; Y = a natural amino acid; R1 = Contg. Arg or Lys, a peptide of 2-45 amino acids contg. Arg or Lys at the N- and C-termini; R3 = a natural amino acids contg. Arg or Lys at the N- and C-termini; R3 = a natural amino acids contg. Arg or Lys at the N- and C-termini; R3 = a natural amino acids contg. Arg or Lys at the N- and C-termini; R3 = a natural amino acids contg. (A2-A20) and (B2-B29) are the insulin R9- and B-chain sequences contg. (A2-A20) and (B2-B29) are the insulin R- and B-chain sequences recombinant E.coli) is reacted with mercaptum at a ratio of 2-10 SH residues of mercaptan per Cys residue of proinsulin. The reaction control of the presence of a chaotropic auxiliary agent at the parameter of a chaotropic auxiliary agent at the print trypsin and opt. carboxypeptidase B yields correctly folded insulin. The insulin is isolated by absortion on the correctly and control on the correctly and control of the correctly control.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SURF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  presence of a chaotropic agent and in aq. medium of pH 10-11, treating the prod. with 3-50 g hydrophobic adsorber resin per 1 ag medium of pH 4-7, isolating the adsorber resin and pro-insulin and desorbing the pro-insulin. This method produces pro-insulin with correctly bonded Cys bridges. Compared with known methods it
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Pro-insulin is produced by treating recombinant precursor protein with a mercaptan to provide 2-10 SH residues per Cys residue, in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 FUNQHLOGSHLVEALYLVGGERGFFYTPKTRGIVEGCCTSICSLYQLENYCN 52
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FVNOHLGGSHLVEALYLVGGERGFFYTPKTF-31VEQCGTSTCSITYLLENYCN 56
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        treating recombinant precursor protein with mercaptan in alkall
and in presence of chaotropic agent, then isolation on
                                                                                                                                                                                                                                                                                                                                                                                                                                              98 169 (Januari I. 56)
20 269
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            indets
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Pro-insulin: A-chain; B-chain; C-chain; disulphide;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Co. M. Smart above
                                                                                                                                                                                                                                                                                                                                                                                                                                            Too by Sector of, 100,000,000, Sector No. 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Disclosure, Page 11-12; 15pp, German.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAR68900 standard; peptide: 63 AA
Example 2; Page 13; 16pp; German.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sudwig J, Obermeler R,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   mercaption; chaotropic agent.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           93EP-0118993.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     92DE-4240420
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     52: Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Haman pro-insulin 4.
                                                                                                                                                                                                                                                                                                                                                      a hydrophobic resin.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WP1: 1994-177718/22
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               hydrophobic resin
                                                                                                                                                                                                                                                                                                                                                                                                  SK AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              25 MAR-2003
02 MAR-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         25-NOV-1993;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Monto sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     02 DEC-1992;
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AAR68900;

RESULT 4

EP600372-A1 06-JUN-1994

Ger: M.

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Pro-insulin is produced by treating recombinant precursor protein with a mercaptan to provide 2-10 SH residues per Cys residue, in presence of a chaotropic agent and in aq. medium of pH 10-11, reating the product with 3-50 g hydrophobic adsorber resin per I ag medium of pH 4-77, isolating the adsorbed resin and pro-insulin and desorbing the pro-insulin. This method produces pro-insulin with correctly bonded Cys bridges. Compared with known methods it
                                                                                                                                                                                                                                                                                             involves fewer stages (esp. no sulphitolysis or cyanogen bromide cleavage) and overali losses during purification are reduced, i.e. the process is quicker and gives better yields.
                                                                                                                                                                                                                                                                                                                                                                                                              Sequences of insulin chain A, B and C are given in AAK68895-97 Sequences of pro-insulin 1-4 are given in AAK68999-901. (Updated on 25-MAR-2003 to correct PN field.)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 96;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 294; DB 15;
Pred. No. 2.9e-26;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  100.08;
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Best Local Similarity
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Gaps

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0; Mismatches

Length 96; indels

Score 294; DB 16; Pred, No. 2.9e:26;

100.0%;

Ouery Match Best Local Similarity 100.0 Warches 52, Conservative

ò £

96 AA;

Sequence

1 FVNQHLCGSHLVEALYLVCGERGFFYTPKTRGIVEQCCISICSLYQLENYCN 52

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Isolation of insulin that is correctly post translationally processed · by reacting profinsulin with a mercaptan in the presence of a chaotropic agent and purificn, after absorption to hydrophobic
       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                    Proinsulin: post-translational modification; recombinant production; protein folding; contormation,
                                            1 FVNQHLCGSHLVEALYLVCGERGFFYTPKTRGIVEQCCTSICSLYQLENYCN 52
                                                                         .;
  Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /note= "a peptide of 4 amino acids"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /label- Gly (A2-A20)-R3
/note- "human insulin A-chain"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /note~ *human insulin B chain*
                                                                                                                                                                                                                                                                                                                                                                       Fusion protein contg. proinsulin sequence 3.
  Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sabel W;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               45..74
/label- R1-(B2-B29)-Y
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ucation/gaalitiers
                                                                                                                                                                                                                     AAR78662 standard; protein; 96 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Ludwig J, Obermeier R,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Example 2: Page 8: 16pp: German.
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Insulis, precursor, growth harmons, chaperone, intramolecular, folding, conformation, chimeric protein, cleavalue, recombinant,

production; yield.

Homo sapiens

Synthetic

W09956302-A1

hGH mini-proinsulin Primeric protein

(first entry)

19 JAN 2000

AAY42860;

AAY42860 standard; profein: 107 AA

RESULT 7

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Commonder (hdf) of the sequence given in A442855, a cleavable peptide linker (AA42857), and a human insulin presursor comprising linkulin An42857), and a human insulin presursor comprising linkulin and a change of the sequence given in A442857, and a human insulin presursor comprising linkulin as an intramolecular chaperone (HWC) for the insulin precursor.

C. terminal Asq residue which enables the holl portion of the removed atter iolding hest taken place. Production of recombinant human insulin via an holl proinsulin chimeric protein can provide human insulin with correctly linked cysteine bridges with provide human insulin with correctly linked cysteine bridges with of human insulin. The IMC sequences not only protect insulin sequences from intracellular degradation by a microorganism host, but also promote the fusion protein and decrease the intermolecular interactions among the fusion proteins, thus allowing foliging of the fusion proteins, thus allowing foliging of the fusion proteins.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         at commercially useful high concentrations. The procedural steps of cyanogen bromide clevage, oxidative sulphitolysis and related purification steps on thus be eliminated, along with the use of high concentrations of mercaptan or the use of hydrophobic absorbent resins.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                This sequence represents a chimeric protein, half-mini-proinsulin.
This chimeric protein contains an N-terminal fragment of human growth
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 107;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 294; DB 20;
Pred. No. 3.2e-26;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       100.0%;
100.0%;
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New chimeric proteins containing human growth hormone fragment, used particularly for the production of human insulin.

Claim 13; Page 30; 45pp; English.

(TONG-) TONGHUA SANTECH BIOTECHNOLOGY LIB.

WPI; 1999-610839/52

2800 CNC0052 58W0 CN00052

31-MAR : 1998; 31-MAR 1998;

07-00:-1999

Matches

RESULT 8

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AAQ86425 encodes AAR71692 mating factor alpha I-Insulin precursor ArgB31. ArgB31 comprises the B and A chains of a claimed human insulin derivative. In the final claimed compose, they are covalently connected via disulphide bonds between Cys residues A7/B7 and A20/B19. The derivative, which may be present as a zinc ion complex, can be used as a fast action treatment for disbetcs. (Updated on 25-MAR-2003 to correct PN field.)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 EVNQHLOSSHLVEALZLVGGERGFFYTPKTRGTVEDGOTSTCSLZQLENYCN 52
                                                                                                                                                         Human insulin precursor ArgB31; diabetes; Zinc ion complex;
mating factor alpha 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Acylated insulin deriv, which may be present as a Zinc to complex - is used to treat diabetes and is rapid acting.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Havelund S. Jonassen 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Ouery Match 100.0%; Score 294; DB 16;
Best Local Similarity 100.0%; Pred. No. 4.1e 26;
Matches 52; Conservative 0; Mismatches 0;
                                                                                                                               Mating factor alpha 1-Insulin precursor ArgB31
                                                                                                                                                                                                                                                      Location/Qualitiers
1..85
/labet- mating factor alpha
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     AAR71692 standard; Protein; 137 AA
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//abol- B chain
117...147
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                                                                                             (first entry)
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                                                                             (chdated)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     N-PSDB; AA086425
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       16-SEP-1994;
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                                                                           25-MAR:2003
20-NOV-1995
                                                                                                                                                                                                                        Homo sapiens
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                                                                                                                                                                                                                                                                                                                                                                                                                                     23 MAR-1995
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                                       AAR71692;
                                                                                                                                                                                                                                                                         Protein
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AAR71694
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   Saps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Recombinant insulin prodn. by correctly toiding pro-insulin hybiid polypeptide - then enzymatic cleavage of folded product, does not require sulphite protection of SH nor use of cyanogen bromide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A new method for the production of recomtinant human insulin comprises folding a hybrid polypeptide comprising prolimation and conditions that permit correct disulphide bond formation and subjecting that folded protein to enzymatic cleavage. The insulin produced can then be purified. This sequence is a SOB-insulin a chain hybrid polypeptide and is encoded by chain. Any insulin A chain hybrid polypeptide and is encoded by
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  identical to the natural hormone. Hazardous and combersome procedures involving evanouen bromide and sulphitolysis to protect SH groups are avoided since the entire hybrid polypeptide folds efficiently to the native structure even with the leader attached
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              the plasmid construct pbBAST-LAT. Transformation of the proper icola host cells with pbBAST-LAT results in the efficient expression of the prointain hybrid polypeptide, useful for human insulin production. The method produces recombinant human insulin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 FVNQHLCGSHLVEALYLVCGERGFFYTPKTRGIVEOCCTSICSLYQLENYCN 52
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   Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ### Score 29: BB 17; Local Similarity 100.0%; Pred. No. 1,56-26; Ics 52; Conservative 0: Mismarches 0;
 Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Mendelovitz S.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (BIOT:) BIO-TECHNOLOGY GENERAL CORP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Example 18; Figure 7; 69pp; English
                                                                                                                                                         AAR98897 standard: Protein: 116 AA
                                                                                                                                                                                                                                                                  Soft proinsulin hybrid polypeptide
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0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    94WO-US13268.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    94WO-US13268
Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Hartman JR,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WPI: 1996-333766/33.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                and Cys upprotected.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                116 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                N PSDB: AAT34670
                                                                                                                                                                                                                                                                                                                                                         Home sapiens
                                                                                                                                                                                                                                                                                                                                                                                           W.19620724-A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    24-DEC-1244:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    29-DEC-1994;
10-JAN-1995;
                                                                                                                                                                                                                                  0: FEB-1997
                                                                                                                                                                                                                                                                                                                                                                                                                               11 JUL-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gorecki M.
                                                                                                                                                                                               AAR98897;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Soduence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Ouery Match
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Mating factor alpha l-Insulin precursor ArgBl, ArgB31 N-terminal.
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Matches

RESULT 9 AAR71692

0

Gaps

0

Indels

Length 137,

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Home sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                W09950302-A1
                                            Pept.ide
                                                             Pept.ide
                                                                               Peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RESULT 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAY42861
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Subs
                                                                                                                                                                                                                                                                                                                                     ANUMENAZO encodes AAR71694 mating factor alpha 1-insulin precursor Angli, Argalal Neterminal EDARAEAR. The insulin precursor comprises the B and A chains of a claimed human insulin derivative preceded by the Neterminal amino acids EDABAEAR. In the final ciaimed compstitutes are covalently connected via disulptime bonds between Cystresidues A7/87 and A20/819, the derivative, which may be present as a zinc ion complex, can be used as a tast action freatment for
       Human insulin precursor ArgB1, ArgB31; d abetes; Zinc ion complex; mating factor alpha 1; N-terminal EEAEAF \kappa_{\rm c}
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Human insulin precursor ArgBl, ArgB31: diabetes: Zinc ion complex;
mating factor alpha 1; N-terminal EEAEAFAER.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Mating factor alpha 1-Insulin precursor 'aBl, ArgB31 N-terminal.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 VEGCCTSICSLYQLENYCN 52
                                                                                                                                                                                                                                                                                                                                                                                                                                                                ;;
O
                                                                                                                                                                                                                                                                                                                                                                                                                                               Lengt: 145;
                                                                                                                                                                                                                                                                                          Acylated insulin deriv, which may be present as a Zine ion complex - is used to treat diabetes and is tapid acting.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                Indels
                                                                                                                                                                                                                                         .I massem I:
                                                                                                                                                                                                                                                                                                                                                                                                                                            1B 16;
4e 26;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ;
;
                                                                    /label= mating factor alpha-i
                                                                                                                                                                                                                                                                                                                                                                                                           (Updated on 25 MAR-2003 to correct PN field.)
                                                                            86..93
/label- N-terminal peptide
                                                                                                                                                                                                                                        Halstrom JB, Haveland S.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 FVNURLCGSHLVEALYLVCGERGFFYTPKT-
                                                                                                                                                                                                                                                                                                                                                                                                                                             100.0%; Score 294
100.0%; Pred. No
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Mismate
                                                                                                                                                                                                                                                                                                                      Example 5: Pages 82-83; 100pp; English.
                                              Location/Qualifiers
1..85
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAR71695 standard, Profein: 146 AA
                                                                                             94..124
/label= B-chain
                                                                                                               125.,145
/label- A-chain
                                                                                                                                                                                                                                                                                                                                                                                                                                                               ..
O
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                                                                                                                                                                                           930K 0001.44
940S-0190829
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (updated)
(first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                       Local Similarity 100.
Nos 52, Conservative
                                                                                                                                                                                                                       (NOVEL ) NOVEL NORDISK AS
                                                                                                                                                                                                                                                                WPI: 1995-131314/17
                                                                                                                                                                                                                                                                                                                                                                                                                             145 AA;
                                                                                                                                                                                                                                                                          N-PSDB: AAU86429
                                  Homo sapiens
                                                                                                                                                                                           17 - SEP 1993;
02 - FEB - 1994;
                                                                                                                                                                                                                                       Andersen AS.
                                                                                                                                         W09507931-A1
                                                                                                                                                                           16 SEP-1994;
                                                                                                                                                                                                                                                 Markussen J;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                25 MAR 2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         N:W-1995
                                                                                                                                                         23 MAR-1995
                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAR71695;
                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
                                                    Key
Protein
                                                                                              Pept ide
                                                                                                               Pept.1de
                                                                            Pept 1de
                                                                                                                                                                                                                                                                                                                                                                                                                                                               Matches
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AAR71695
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AAQ86432 encodes AAk71695 mating factor aipha 1-Insulin precursor Arg81, Arg81 Niterminal EEA NEAER. The insulin precursor comprises the B and A chains of a claimed human insulin derivative preceded by the Niterminal amino acids EEAEARER. In the final claimed companties are covalently connected via disulphide bonds between Cystresiducs A7/R3 and A20/R89. The derivative, which may be present as a zinc ion complex, can be used as a last action treatment for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Insulin; precursor; growth hormone; chaperone, intramolecular;
folding; conformation; chimeric protein; cleavable; recombinant;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        100.0%; Score 294; DB-16; Length 146; 100.0%; Pred. No. 4.4e 26; ive 0; Mismatches 0; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Acylated insulin deriv. which may be present as a Zinc ion complex of is used to treat clamates and is rapid acting.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Condssen 1:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (Updated on 25-MAR-2003 to correct PN field.)
                                              /label- mating factor alpha-1
                                                                                         /Tabei N-terminal peptide
95.125
/Tabei B-chain
126.146
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Havelund S.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Example 6; Page 85; 100pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAY42861 standard; protein; 150 AA
                                                                                                                                                                                           /label- A-chain
                                                                                                                                                                                                                                                                                                                                          94WC-DKC0347
                                                                                                                                                                                                                                                                                                                                                                                        930K 0001044
940S-0196829
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Haistroc 18,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Guery Match
Best Local Similarity 190.c.
Conservative
These 52; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Chimeric protein, SEC ID 7.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               19-JAN-2000 (first oniry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                SV ASTORON - CAON (CAON)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WPI: 1995-131314/17.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               146 AA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 production: yield
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                N-PSDB: AAQ86432.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Andersen AS,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Homo sapiens.
                                                                                                                                                                                                                                           W09507931-A1
                                                                                                                                                                                                                                                                                                                                                                                        17 SEP-1993;
02-FER 1994;
                                                                                                                                                                                                                                                                                                                                        16-SEP-1994;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Markussen J;
                                                                                                                                                                                                                                                                                         23-MAR-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Synthetic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          diabetes
                       Protein
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WPI; 1991-141828/20
                                                                                                                                                                                                                                                                                                                                                                                  57 AA;
                                                                                                                                                                                                N-PSDB; AAQ04335
                                                                                                                                                                                                                                  to tendamistate
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       29-MAY-1985;
                                                                       28-OCT-1989;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          25-MAR 2003
22:JUL-1991
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              15-NOV-1990;
                                                                                                33-N-)V-1988;
                                                                                                            19-A/G-1989;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           30-MAY-1984
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        38-FEB-1985
                                                 06-MAY-1990
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              15-MAY-1991
                          EP367163-A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EP427296-A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAR11899;
                                                                                                                                                                                                                                                                                                                                                                                  Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RESULT 14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAR11899
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            0
                                                                                                                                                                                                                 This sequence represents a chimeric protein, which contains an Kiterminal fragment of human arowth hormone (165) of the sequence given in AAVA265, a cleavable peptide linker (AAVA2657), and a broman lisuich procursor comprising instain A and B claims (AAVA2659). The BH portion of the claimstain procursor, and follows a control of the instance provided an experience of the instance provided an experience of the claimstance of the chamber has a Citerminal Ara residue which challes the host praction of the chamber that is because the perfect to be removed after folding has taken place.
                                                                                                                                                                                                                                                                                                                                                                                                     interactions among the fusion profess. Thus allowing folding of the fused insulin precursor at commercially useful high concentrations. The procedures steps of eyanogen bromide cleavage, oxidative sulphitolysis and related purification steps can thus be eliminated, along with the use of high concentrations of mercaptan or the use of hydrophobic absorbent
                                                                                                                                                                                                                                                                                                                   Production of recombinant human insulin via an hGH-profusulin chizeric protein can provide human insulin with correctly linked cystice bridges will fewer necessary procedural steps, and hence resulting in a higher yield of human insulin. The IMC sequences not only protect insulin sequences from intracelular degradation by a microorganism host, but also promote the folding of the fusei insulin precursor, lacilitate the solubility of the fusion protein and decrease the intermojecular.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /label-Lys residue linking insulin B chain to A chain
                                                                                                                                                         New chimeric proteins containing human growth hormone fragment, used particularly for the production of human insulin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Proinsulin analogue with a Lys residue 'inking the A and B chains.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 FVNOHLGGSHLVEALYLVGGERGFFYTPKTRGIVEQCCTSIGSLYQLENYCN 52
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 150;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                insulin fusion protein; pro-insulin ana.oque; tendamistate;
Lys Cys bridge; ds
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  100.0%; Score 294; DB 20; 100.0%; Pred. No. 4.5e-26;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         0; Mismatches
                                                                                (TONG-) TONGHUA GANTECH BIOTECHNOLOGY LTD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /label- Insulin B chain 37..57
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Location/Qualifiers
                                                                                                                                                                                           Claim 14; Page 30-31; 46pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAR04582 standard: protein; 57 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              100.08;
                                   98WO-CN00052
                                                          98WO-CN00052
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (updated)
(first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         52; Conservative
                                                                                                                                WPI; 1999-610839/52
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           150 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             misc-difference
                                                          41 - MAR-1998;
                                   31 MAR-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       25-MAR-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1490
         07 OCT-1999
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence
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Best Local S
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                                                                                                         Gan 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RESULT 14
AAR04582
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Key
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This separate is persenterined terminal of an Miterinial fragment contribing up. 6 direct terminal terminalistate. This lusion protein may be converted into numba insulin using known methods. The synthetic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 FVNQHLCGSHLVEALYLVCGERGFFYTPKTRGIVEQCCTSICSLYQLENYCN 52
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          6 FUNDHLCGSHLVEALYLVCGERGFFYTPKTKGIVEQCCTSICSLYOLENYCN 57
                                                                                                                                                                                                                                                                                                                                                                                              New insulin fusion proteins comprise pro-insulin analogue linked
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ..
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 57;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Indeis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Thim L;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 291; DB 11;
Pred, No. 3.80-26;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          gene was prepared by the phosphoramidite method
                                                                                                                                                                                                                                                                                     Wallmeier H;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Fiil N, Ammerer G, Hansen MT,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             See also AAQ04336.
(Updated on 25 MAR-2003 to orrect PR field.)
(Updated on 25-MAR-2003 to orrect P. field.)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Human insulin; diabetes; transpeptidation.
/label- Insulin A chain
                                                                                                                                                                                                                                                                                       Uhlmann E,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Example of human insulin precursor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAR11899 standard: Protein; 52 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                Cischasure: Page 7: 2pp; German
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             .,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                99.08;
98.18;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         84DK - 0002665.
85DK - 0000582.
                                                                                                                                                                         88DE - 3837273.
89DE - 3927449.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    90EP-0121887
                                                                                                                            89EP-0120056
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            90EP - 0121887
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (lirst colry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SA ASIURCN-OVON ( OVON)
                                                                                                                                                                                                                                                                                     Koller KP. Riess GJ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (updated)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Markussen J, Fiir
Voigt RO;
                                                                                                                                                                                                                                                                                                                               WPI: 1990-141149/19.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity
Matches 51; Conserv
                                                                                                                                                                                                                                        (FARH ) HOECHST AG.
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Human insulin; recombinant production; amorphous; monospherical form; diabetes mellitus.
                                                                                                                                                                                                                                                                                              This sequence is a specific example of an insulin derivative which can be obtained in amorphous, monospherical form by dissolving in an orpropanol/buffer mixture (pH 4.5-6.5) having n-propanol content 15% relative to water. The solution is then diluted with water to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Amorphous, mono-spherical form of insulin derivs. For treating diabetes mellitus, are produced by diluting soln. in aq. isopropanol, are stable when dried or in suspension
                                                                                This buman insulin precursor has correct y positioned disalphide bridges between the A and B chains and i more resistant to proteolytic digestion than prior art insulin precursors. Yeast strains transformed with DNA encoding this precursor can be cultured to secrete it in high yields. The precursor can be conveited into mature human itsulin by transpeptidation. See also AAR1897-98.

(Updated on 25-MAR-2003 to correct PF Lield.)
                                                                                                                                                                                                                                                                                                                        1 EVNÇHICCOSHIVEALYINCGEROFFTIFK FROTVEROTISTICSIONUENYON 5.2
                                                                                                                                                                                                                                                                                                                                          1 FVNOHLGGSHLVEALYLVGGRGFFYFPKSKGIVEQCTSIGSLYQLENYCN 52
            Human insulin precursors - expressed with correctly positioned disalphide bridges giving improved resistance to proteolysis
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Di-Arg-(B31-32)-Human insulin amorphous, monospherical deriv.
                                                                                                                                                                                                                                                                97,6%, Sente 247, 198-121, Length 521
96,3%, Pred We, here 261
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                                                                                                                                                                                                                                                                                              STARTS CO
                                                                                                                                                                                                                                                                                              2 - M. Smatterboss
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /label- insulin_A chain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                AAR6588} standard: protein: 5: AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Obermeier R,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Example 2; Page 5; 10pp; German.
                                                        Claim 3; page 18; 28pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    94DE-4313762.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (updated)
(first entry)
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es 50, Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WP11 1994 - 344579742
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (FARE ) HUECHST AG.
                                                                                                                                                                                                                                   52 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      27-APR 1993;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       25-MAR-2003
26-30N 1995
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                                                                                                                                                                                                                                       Seguence
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                                                                                                                                                                                                                                                                                                                                                                                                  RESULT 15
AAR65884
                                                                                                                                                                                                                                                                                              Matches
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Gaps
reduce a propagal content to below 15%. The resulting insulin preparation is stable and can be used for the treatment of diabetes
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                                                                                                                                                                                                                     1 FVNQHL/GSHLVEALYLVCGERGFPYTPKT RGIVEL/COTSICSLYQLENYCN
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                                                                                                                                         DB 15; Length 53;
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                                                                                                                                       Guery Match 96.4%; Score 284.5; DH 1
Best Local Similarity 98.1%; Pred. No. 2.56-25;
Matches 52; Conservative 0; Mismatches 0
                                                           (Updated on 25-MAR-2003 to correct PN field.)
                                                                                                                                                                                                                                                                                                                     Search completed: September 15, 2003, 12:00:59
Job time : 37.5305 secs
                                                                                                   53 AA;
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OM protein - protein search, using sw model

September 15, 2003, 11:57:40 : Search time 11.9283 Seconds (ithout alianments) 184.449 Million cell updates/sec Run on:

US-09-423-100-5
294
1 FVNQHLCGSHLVEALYLVCG.....IVEQCCISICSLYQLENYCN 52 Title: Perfect score. Sequence:

BLOSUM62 Scoring table:

128717 seqs, 42416858 residues Gapop 10.0 , Gapext 0.5 Searched:

Minimum OB seq length: 0 Maximum OB seq length: 2000000000

Total number of hits satisfying chosen parameters

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Issued_Patents_AA:* Database

1: /cyn2_6/ptodata/l/iaa/5A_L ...pop:*
2: /cyn2_6/ptodata/l/iaa/5B_Ct ..pep:*
3: /cyn2_6/ptodata/l/iaa/6A_Coun.pep:*
4: /cyn2_6/ptodata/l/iaa/6B_COMB.pep:*
5: /cyn2_6/ptodata/l/iaa/PCIUS_COMB.pep:*
6: /cyn2_6/ptodata/l/iaa/pCIUS_COMB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Hosel 1		1011				
N	Score	Marton	Match Length DR	S	=======================================	Dogmination
						1013 dt + 2030
-	294	100.0	5.6	-	US-08 160-476A-7	Sequence 7, Appl
7	767	100.0	56	7	US-C8-389-487-11	=
٣.	294	100.0	63	-	US-08-160 376A-6	'n,
4	294		99	-	291-	٠,
2	767	100.0	96	-	US-08-160-376A-5	'n,
9	467	100.0	96	. ~•	US-08-189 487-8	æ
7	294	0.00:	137	~	US-08-400 Z56-39	Sequence 39, App.
œ	294	100.0	137	m	US-08-975-365-39	5
J	294	100.0	145	_	US-08 400-256-45	Sequence 45, App
10	294	100.0	145	~	US-08-975 365-45	45
Ξ	767	100.0	146	-4	US-68 40)-256-48	48.
12	294	0.00:	146	*	65-68-975-365-48	Sequence 48, App
13	291	0.66	57	٦	US-08-030-731A:44	44
14	284.5	4.96	53		US-08-23 4-617-4	4
15	281.5	96.4	53	4	US-08-981-988A-42	Sequence 42, App
16	278.5	94.7	51	4	US-09-477-924 3	m
17	278.5	94.7	51	4	US-09-723-981 3	~
18	278.5	94.7	51	**	US-09-723-896-3	~,
19	277 5	94.4	53	-		~
70	277	94.2	65	۳.	US-08-900 574-3	m
2.1	276.5	94.0	52	~:	US-08-500-574-6	9
22	276.5	0.46	99	~	US-08-900-574-5	Sequence 5, Appl
5 3	276.5	0.46	67	4	US-08-981-988A-1	Sequence 1, Appl
24	276.5	94.0	67	4	US-08-981-988A-5	Sequence 5, Appl
25	276	93.9	67	~	US-08-900-574-7	7
56	275.5	93.7	53	~	US-09-261-853-2	7
27	275.5	93.7	65	-	US-08-468-674B-71	71,

0

Gaps ;; 0

Ouery Match 100.0%; Score 294; DB 1; Length 56; Best Local Similarity 100.0%; Pred. No. 4.9e-29; Matches 52; Conservative 0; Mismatches 0; Indels

Sequence 71, Appl Sequence 41, Appl Sequence 45, Appl Sequence 45, Appl Sequence 15, Appl Sequence 15, Appl Sequence 17, Appl Sequence 31, Appl Sequence 31, Appl Sequence 31, Appl Sequence 42, Appl Sequence 42, Appl Sequence 42, Appl Sequence 42, Appl Sequence 42, Appl Sequence 42, Appl Sequence 43, Appl Sequence 43, Appl Sequence 42, Appl Sequence 43, Appl Sequence 43, Appl Sequence 43, Appl Sequence 44, Appl Sequence 47, Appl Sequence 47, Appl	
93.7 65 1 US .08.78U 571 7; 93.7 89 1 US .08.468 -6748-41 93.7 91 1 US .08.78U 4571-41 93.7 91 1 US .08.78U 4571-41 93.7 104 1 US .08.40E .571-45 93.7 104 3 US .08.90E .07E .669F 3 93.7 117 3 US -08.40E .64E 3 93.7 124 1 US -08.40E .64E 3 93.7 124 1 US -08.40E .08E 3 93.7 124 1 US -08.40E .25E -3 93.7 124 1 US -08.40E .25E -3 93.7 140 3 US -08.90E .25E -3 93.7 140 3 US -08.90E .25E -3 93.7 140 3 US -08.90E .35E -3 93.7 140 3 US -08.90E .25E -3 93.7 140 3 US -08.90E .25E -3 93.7 140 3 US -08.90E .35E -3 92.7 53 3 US -08.90E .57E -4	SULI:
22222 22222 22222 22222 22222 22222 2222	SULI: -08-160-3764-7 SEQUENCE 7, APPLI RALENT NO. 547304 CENERAL INFORMAT APPLICANT: 06 APPLICANT: 06 APPLICANT: 10 CONTRESSONDENCES ATTREE: NEW COUNTRY: 07 APPLICATION APPLICATION FILING DATE: CLASSIFICATION FILING DATE: APPLICATION FILEBENCE/CO TELEBENCE/CO T
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1 FVNQHLCGSHLVEALYLVCGERGFFYTPKTRG1: OCCTSICSLYQLENYCN 52
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                                                                                                                                                                                                                        APPLICANT: Obermeler, Rainer APPLICANT: Gerl, Martin APPLICANT: Gerl, Martin APPLICANT: Ludwig. Jurgen APPLICANT: Sabel, Walter TITLE OF INVENTION: Process for Obtaining Insulin Having TITLE OF INVENTION: Orrectly Linked Cystine Bridges OWNBER OF SEQUENCES: 12
CORRESPONDENTE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Indels
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APELICANT: Gerl, Martin
APELICANT: Claudid, Jurgen
APELICANT: Laudid, Jurgen
APELICANT: Sabel, Watter
TITLE OF INVENTION: Process For Obtaining Proinsulin
TITLE OF INVENTION: Possessing Correctly idea
TITLE OF SEQUENCES: 7
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                          ADDRESSEE: Finnedan, Henderson, Faratow, Garrell &
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SUFFMARE: Patentin Release #1.0, Version #1.25 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/389,487
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match 100.0%; Score 244, DB 1; Best Local Similarity 100.0%; Pred. No. 4.9e-29; Matches 52; Conservative 0; Mismatches 0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDIUM TYPE: Floppy disk
COMPUTER: 18M PC compatible
CPERATING SYSTEM: PC:DOS/MS DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 6, Application US/08160376A
Patent No. 5473049
                                                                                                                                                        Sequence 11, Application US/08189487
Paten: No. 5663291
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NAME: Finaudi, Carol F.
REGISTRATION NUMBER: 32,220
REFRENCE/POCKET NUMBER: 0248
TELECHOMUNICATION INFORMATION:
TELEPHONE: 202-408-4000
TELEFAX: 202-408-4400
                                                                                                                                                                                                                                                                                                                                                                                                                                                1450 I Street, NW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             INFORMATION FOR SEC ID NO: 11:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ATTORNEY/AGENT INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER READABLE FORM:
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US-08-160 376A-6
                                                                                                               RESULT 2
US-08-389-487-11
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                                                                                                                                                                                                                                                                                                                                                                                                                                                     STREET
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: MORGANICA Michael
APPLICANT: Molecular Michael
APPLICANT: Marguardt, Mans-Peter
APPLICANT: Marguardt, Mans-Peter
APPLICANT: Marguardt, Mans-Peter
APPLICANT: Meiwes, Johannes
TITLE OF INVENTION: As Enzymatic Process for the
TITLE OF INVENTION: Conversion of Preproinsuins Into Insulins
NUMBER OF SEQUENCES: 5
CORRESPONDENCE ADDRESS: 5
ADDRESSEE: Finnegar, Henderson, Farabow, Garrett 6
ADDRESSEE: Dunner, Liv.P.
SIRET: 1300 I Street, N.W.
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                                                                                                                                                                                DISKETTE, 3.5 INCB, 1.44 MD STURAGE
STREET: Rt. 202-206 No. 5473049th/P.O. Box 2500 CIIY: Somerville
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Rolease #1.0, Version #1.80
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   100.0%; Score 294; DB 1;
100.0%; Pred, No. 5.6e-29;
                                                                                                                                                                                                                                                                                                               FILING DATE: December 1, 3993
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: GE P 4240420.7
FILING DATE: December 2, 1992
ATTORNEY ACRIT: NEGRONDER 2, 1992
ATTORNEY ACRIT: NEGRONDER 2, 1993
NAME: Barbara V. Mairor: Esq.
RESISTEMBRITON NUMBER: HILLS, 1289
REFERENCE/INVERTINATION:
REFERENCE/INVERTINATION: HILLS, 1289
REFERENCE/INVERTINATION: LINESTER HILLS, MAINTINATION: LINESTER HILLS, MAINTINATION: LINESTER HILLS, MAINTINATION LINESTER HILLS, 1289
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                0; Mismatches
                                                                                                                                                                                                                                                                                              APPLICATION NUMBER: US/08/160,376A
FILING DATE: December 1, 1993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           US/08/291,060B
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Patent No. 5728543
                                                                                                                                                                                                                           OPERATING SYSTEM: WINDOWS 3.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NAME: Einaudi, Carol P. REGISTRATION NUMBER: 32,220
                                                                                                                                                                                                                                                 SOFTWARE: WORDPERFECT 5.1 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (908) 231-4079
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER READABLE FORM: MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 08-AUS-1994
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TELEFAX: (908) 231-2255
INFORMATION FOR SEQ ID NO: 6
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Cuery Matc):
Best Local Similarity | 100.6
Matches | 52; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     63 Amino Acids
                                                                                    STALE,
COUNTRY: U.S.A,
21P: 08876-1268
COMPUTER READABLE FORM:
MEDIUM TYPE: DISKETTE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TYPE: Amino Acid (AA)
TOPGLOGY: not relevant
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Washington
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20005-3315
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TELEPHONE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CS-08-160-376A-6
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                                                           CITY: STATE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match 100.0%; Score 294; DB 1; Length 66; Best Local Similarity 100.0%; Pred. No. 5.9e-29; Matches 52; Conservative 0; Mismatches 0; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: Obermeier, Ranier
APPLICANT: Gerl, Martin
APPLICANT: Gerl, Martin
APPLICANT: Sabel, Walter
TILLE OF INVENTION: Process For obtaining proinsulin
TILLE OF INVENTION: Possessing Correctly Linked
TILLE OF INVENTION: Cystine Bridges
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  7 PP: 08976-1258
COMPUTER READANLE FORM:
MEDIUM TYPE: DISKETTE, 3.5 INCH. 1.44 MI: STORAGE
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Rt. 202-206 No. 54730491h/P.O. Box 2500
REFERENCE/DOCKET NUMBER: 02481.1105-02030 TELECOMMUNICATION INFORMATION: FELEPHONE: (202) 408-4366
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               REFERENCE/DOCKET NUMBER: HIS 92/F Red TELECOMMUNICATION INFORMATION:
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PRIOR APPLICATION DATA:
APPLICATION NUMBER: GE P 4240420,7
FILIDE DATE: December 2, 1992
ATTORNEY/ACENT INFORMATION:
NAME: BAFBAFA V. MAUFEY, ESQ.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICATION NUMBER: US/08/160.376A FILING DATE: December 1, 1993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 5, Application US/08160376A Patent No. 5473049
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TELEFAX: (908) 231-2255
INFOHMATION FOR SEQ ID NO: 5:
SFOURNEE CHARACTERISTICS:
                                                                                                                     TELEFAX: (202) 408 44400
INFORMATION FOR SEQ ID NO: SEGUENCE CHARACTERISTICS: ENGTH: 66 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Ouery Match
Best Local Similarity 100.0
Matches 52; Conservative
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                                                                                                                                                                                                                                                                                                                                                       single
                                                                                                                                                                                                                                                                                                                                                                                                                               MCLECULE TYPE: peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NUMBER OF SEQUENCES: 7
CORRESPONDENCE ADDRESS:
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: U.S.A.
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OPERATING SYSTEM:
                                                                                                                                                                                                                                                                                                 amino acid
                                                                                                                                                                                                                                                                                                                                                                                                    linear
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No. 57504970 No. 5750497disk of No. 5750497th America, Inc.
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1 FVNQHLGGSHLVEALYLVGGERGPFYTPKTRGIVEQCCTSICSLYGLENYCN 52
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100.0%; Pred. No. 8.8e 25;
tive 0; Mismatches 0; Indels
                                                                                                                                                                                                       APPLICANT: Gerl, Martin
APPLICANT: Gerl, Martin
APPLICANT: Ludwig, Jurgen
APPLICANT: Subel, Walter
TITLE OF INVENTION: Process for Obtaining Jusulin Having
TITLE OF INVENTION: Correctly Linked Cystine Bridges
NUMBER OF SEQUENCES: 12
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                       ADDRESSEE: Finnegan, Henderson, Farakow, Garrett, & AldvESSEE: Dunner
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SOFTWARE: Patentin Release #1.0, Version #1.25 CURRENT APPLICATION DATA:
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APPLICANT: Hals.rom, John
APPLICANT: Andersen, Ib
APPLICANT: Andersen, Asser Sluth
APPLICANT: Markussen, Jan
11TLE OF INVENTION: ACYLATED INSULIN
NUMBER OF SEQUENCES: 49
                                                                                                                                                                                                                                                                                                                                                                                                                                                            COUNTRY: United States of America
ZIP: 20005-3415
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            IBM PC compatible
SYSTEM: PC-DOS/MS-DOS
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Patent No. 5750497
                                                                                                                       Sequence 8, Application US/08389487
Patent No. 5653291
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TELECOMMUNICATION INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                              1500 1 Street, N.W.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CLASSIFICATION: 530
ATTORNEY/AGENT INFORMATION:
NAME: Einaudi, Carol P.
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Bost Loral Similarity 100.0v
Trahes 52; Conservative
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
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MOLECULE TYPE: peptide
US-08-389-487-8
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CLIY: Washington
SiATE: D.C.
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                                                                                                                                                                      INFORMATION:
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                                                                                                 US-08-389-487-8
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212-857 0123
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STAIE: New York
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      TELEPHONE:
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CITY: New Yor?
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                                                                    COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
OPFRATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTION NEWBER: US/08/400,256
FILING DATE: 03*MAR-1995
CLASSIFICATION: 514
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NAME: Lambiris, Elias J.
REGISTRATION NUMBER: 33,728
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APPLICANT: Halstrom, John
APPLICANT: Johnssen, Ib
APPLICANT: Johnssen, Ib
APPLICANT: Markussen, Jan
APPLICANT: MARKUSSEN, ASST
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                  3985.220-08
                                     United States of America
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APPLICATION NUMBER: US 08/400,256
FILING DATE: 03-MAR-1995
ATTURNEY/AGENT INFORMATION:
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COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                        ATTORNEY/AGENT INFORMATION:
NAME: Lambiris, Elias J.
REGISTRATION NUMBER: 33,728
REFRENCE/COCKET NUMBER: 3985.
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 39, Application US/08975365 Patent No. 6011307
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                                                                                                                                                                                                                                                                                                                                                                                                                                     13 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE CHARACTERISTICS:
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Matches 52; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                        amino acid
SY: linear
                             COUNTRY: United
21P: 10174-6401
                New York
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New York
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                                                                                                                                                                                                                                                                                                 1 FVNQHLCGSHLVEALYLVCGERGFFYTPKTRGIVEQCCTSICSLYQLENYCN 52
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                                                                                                                                                                                          100.0%; Score 294; DB 4; Length 137; 100.0%; Pred. No. 1.3e 28;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          100.0%; Score 294; DB 1; Length 145; 100.0%; Pred. No. 1.46.28;
                                                                                                                                                                                                                                     Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        OPERATING SYSTEM: PICTORS/MS-FOS
SOFTWARE: Patentin FC:ease #1.0, Vrision #1.25
CURRENT APPLICATION DAIA:
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                                                                                                                                                                                                                                     Mismatches
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03-MAR-1995
03-MAR-1995
1-1-1-1
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APPLICANT: Andersen, Asser Sloth
APPLICANT: Markussen, Jan
TITLE OF INVENTION: ACTIVATED INSULIN
NUMBER OF SEQUENCES: 49
CORRESPONDENCE AUDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COUNTRY: United States of America 21p: 10174-6401 COMPUTER READBLE FORM: MEDIUM TYPE: Floppy disk COMPUTER: IBM PC COMPALIBLE OPERATING SYSTEM: PC-005/MS-FOS
                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 45, Application US/08400256
Patent No. 5750497
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICATION NUMBER: US/08/400
FILING DATE: US-MAK-1955
CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: LAMBOITS, Elias J.
REGISTRATION NUMBER: 3965
FELECOMBUNICATION INFORMATION:
TELEPHONE: 212-867-9123
TELEPHONE: 212-878-9655
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TELEFAX: 212-878-9655
INFORMATION FOR SEQ ID NO: 39:
SEQUENCE CHARACTERISTICS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: Havelund, Svend
APPLICANT: Halstrom, John
                                                              LENGTH: 137 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               145 amino acids
                                                                                                                                                                                                              Best Local Similarity 100.
Matches 52: Conservative
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Matches 52; Conservative
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                                                                                                  TOPOLOGY: linear
MOLECULE TYPE: protein
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                                                                                   amino acid
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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TELECOMMUNICATION INFORMATION
                                                                                                                                                                                                                                                                                                           INFORMATION FOR SECTION OF 48: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                INFORMATION FOR SEQ ID NO: 48
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APPLICANT: Halstrom, John
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Bost Local Similarity 100.00
Matches 52, Conservative
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78-08-400-256-48
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CLASSIFICATION: 514
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US-08 975-365-48
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New York
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CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/975, 865
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APPLICANT: Halstrom, John
APPLICANT: Jonassen, Ib
APPLICANT: Andersen, Asser Sloth
APPLICANT: Markussen, Jan
TITLE OF INVENTION: ACYLATED INSULIN
                                                         APPLICANT: Havelund, Svend
APPLICANT: Halstrom, John
APPLICANT: Jonassen, Ib
APPLICANT: Andersen, Asser Sloth
APPLICANT: Markussen, Jan
IIILE OF INVENTION: ACYLATED INSULIN
NUMBER OF SEQUENCES: 49
                                                                                                                                                                                                                                                                                                       COUNTRY: United States of America 21P: 10174-6401
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APPLICATION NUMBER: US 08/400,256
FILING DATE: 03-MAR-1995
ATTOKNEY/AGENT INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                 MEDIUM TYPE: Floppy disk
COMPUTER: HM PC compatilio
OPERATINS SYSTEM: PC-COS/RS OS
Sequence 45, Application US/08975365
Patent No. 6011007
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 48. Application US/08400256 Patent No. 5750499 GENERAL APPREMATION:
APPLICANT: Havelund, Svend APPLICANT: Halstrom, John APPLICANT: Andersen, Ib APPLICANT: Andersen, Asser Sloth
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              REGISTRATION NUMBER: 33,728
REFERENCE/DOCKET NUMBER: 39,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              145 amino acids
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Best Local Similarity 106.0
Matches 52, Conservative
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                                                                                                                                                                                                                                                                                                                                             COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
                                                                                                                                                                                                   CORRESPONDENCE ADDRESS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FILING DATE:
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                                                                                                                                                                                                                             ADDRESSEE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         US-08-975-365-45
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                                                                                                                                                                                                                                                                                  STATE:
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E: No. 6011607o No. 601100741sk of No. 6011007th America, Inc. 405 Lexington Avenue, 64th Floor
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                                                                                                                                                                                                                                                                                                                                                                              Length 146;
                                                                                                                                                                                                                                                                                                                                                                                                                 0; Indels
CITY: New York
STAIR: New York
STAIR: New York
COUNTRY: United States of America
21F: 10174-6401
COMPUTER REMANIE FURN
MEDIUM TYPE: Floppy disk
COMPUTER: 1BM PC COMPATID: OPERATING SYSTEM: PC-DOSZMS: V>S
SOFTWARE: PATEMIL RCLEASE #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                            100.0%; Score 294; DB 1;
100.0%; Pred, No. i.46-28;
Live 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: Jonassen, 1b
APPLICANT: Andersen, Asser Sloth
APPLICANT: Markussen, Jan
TITLE OF INVENTION: ATYLATED INSCLIN
NUMBER OF SEQUENCES: 49
CORRESPUNDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICATION NUMBER: US 08/400,256
FILING DATE: 03-MAK-1995
ATMONEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICATION NUMBER: US/08/975,36
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Patent No. 6011007
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                                                                                                                                                                                                                                        1 FVNOHLCGSHLVEALYLVCGERGFFYTPKTRGIVEQCCTSICSLYQLENYCN 52
                                                                                                                                                                                                                                                           6 PVNOHLCGSHLVEALYLVEALYLVCGERGFFYTPKTKG1VEGCCTSTCSLYQLENYCN 57
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Derivatives
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                                                                                                                                                            Score 291, DB 1, Length 57;
Pred. No. 1.2e+28;
1; Mismatches 6; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CORRESPONDENCE ADDRESS:
ADDRESSEE: Finnegan, Henderson, Faranow, Garrett &
ADDRESSEE: Dunner
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER: IBM PC Compatible
OPERATUM SYSTEM: UC-EX-SZ/MS DES
SOFT-MARE: Fatenile Pelease #1 G. Version #1.25
CURRENT APPLICATION DATA:
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TELECOMMUNICATION INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICATION NUMBER: US/08/233,617
FILLING DATE: 25-APR-1994
CLASSIFICATION: 514
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRIOR APPLICATION DATA:
APPLICATION NUMBER: P 43 13 752.4
FILING DATE: 27.48H-1993
ATTOHNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                  Sequence 1. Application US/06/346[7]
Patent, No. 5466566
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NAME: Carol P. Einaudi
REGISTRATION NUMBER: 32,220
                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: Obermeier, Mainer
APPLICANT: Sabel, Walter
APPLICANT: Dell, Per :
APPLICANT: Geisen, F :
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98.18;
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98.18;
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                                     SEQUENCE CHARACTERISTICS:
LENGTH: 57 amino acids
                                                                                                                                                                                   Best Local Similarity 98.1
Matches 51; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                53 amino acids
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Best Local Similarity 98.1
Matches 52; Conservative
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INFORMATION FOR SEQ ID NO:
TELEFAX: 202-408-4400
INFORMATION FOR SEQ ID NO:
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                                                                                     TOPOLOGY: unknown
MOLECULE TYPE: peptide
US:08-030-731A-44
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TITLE OF INVENTION:
                                                                          amine acid
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USA
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RESULT 15
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Search completed: September 15, 2003, 12:05:32 Job time : 11.9283 secs

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Sequence 3, Appli
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Copyright (c) 1993 - 2003 Compugen Ltd
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US-09-878-380-1
US-09-878-380-1
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 Sequence 1, Appli

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 Sequence 2, Appli

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 Sequence 2, Appli

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 Sequence 12, Appli

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 Sequence 12, Appli

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 Sequence 12, Appli

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 Sequence 12, Appli

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 Sequence 10, Appli

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ALIGNMENTS

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RESULT 1

RESULT 1

RESULT 1

SEQUENCE 5. Application 35/10054873

SEQUENCE 5. Application no. US20020164712A1

GENERAL INFORMATION:

GENERAL INFORMATION: Chimeric Protein Containing an TITLE OF INVENTION: Chimeric Protein Containing an ADPRESSE: Townsend and Townsend and Crew LLP STREET: Townsend and Townsend and Crew LLP STREET: Townsend and Townsend and Crew LLP STREET: Two Embarcadero Center, Eighth Floor CITY: San Francisco STATE: California COUNTRY: USA

COUNTRY: USA

ZIPPER READABLE: FORM:

MEDIUM TYPE: Patentin Release F::0, Version #1.36

CUMPUTER: Patentin Release F::0, Version #1.36

CLASSIFICATION NUMBER: US/10/054,873

FILING DATE: 11-MR-1998

APPLICATION NUMBER: WO PCT/CN98/00052

FILING DATE: 11-MR-1998

APPLICATION NUMBER: US 09/423,100

FILING DATE: US 09/423,100
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LENGTH: 52 amino acids

TYPE: amino acid

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RESULT 4
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NUMBER OF SECUENCES: 7
CONFISSIONAL SECUENCES: 1
CONFISSIONAL SECUENCES: 1
STREET: Two Embarcadero Centor, Elahth Floor
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100.0%; Pred No. 5 'e-29;
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APPLICATION NUMBER: US 09/423.100
FILING DATE: 11-DEC-2000
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FILING DATE: 22-Jan-2002
CLASSIFICATION: <Unknown>
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SEQUENCE DESCRIPTION: SEQ 1D No. 6:
US-10-054-873-6
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MOLECULE TYPE: protein

SEQUENCE DESCRIPTION: SEQ ID NO:
US-10-054-873 5
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REGISTRATION NUMBER: 46,946
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710: 94111-3834
COMPUTER READABLE FORM:
MEGIUM TVPE: Floppy disk
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Publication No. US20020164712A1
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LENGTH: 107 amino acids
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Best Local Similarity 100.6
Matches 52, Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Conservative
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hes 52: Conserva
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GENERAL INFORMATION:
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Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 FVNQHLCGSHLVEALYLVCGERGFFYTPKTRGIVEQCCTSICSLYQLENYCN 52
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           0:
APPLICANT: Gan, Zhong Ru
TiflE OF INVENTION: Chimeric Protein Containing an
Intramolecular Chaperone-Like Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         100.0%; Score 294; DB i4; Length 150; 100.0%; Pred. No. 7.9e-29; Ive 0; Mismatches 0; Indels 0:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 278.5; DB 11; Length 51; Pred. No. 2e-27;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: Dubaquie, Yves
APPLICANT: Filvaront, Ellan
APPLICANT: Lowman, Henry B.
TITLE OF INVENTION: METHOD FOR TYEATING CARTILAGE DISORDERS
                                                                                                                                                                                                                                                                                                                                                                                SOFTWARE: Fatentin Release #1 0, Version #1.30
                                                                                                 CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, Eighth Floor
CITY: San Francisco
STATE: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           REGISTRATION NUMBER: 16,946
REFERENCE/DOCKET NUM (R: 020167-000130US
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLITATION NOMER: WO POLASMAZOUSEZ PILLING DATE: 11-MAR 1958
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICATE IN NUMBER: US 09/424, LOS PILLING DALE: 11-DEC 2000
ALTOHNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICATION NUMBER: US/10/054.87
FILING DATE: 22-Jan-2002
TASSIFICATION: «Unknows»
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CURRENT APPLICATION NUMBER: US/39/858,935H
CURRENT FILING DATE: 2002-07-02
PRIOR FILING DATE: 2006-13 15
PRIOR APPLICATION NUMBER: US 60/204,490
PRIOR FILING DATE: 2000-05-16
NUMBER OF SEQ ID NOS: 153
                                                                                                                                                                                                                                                                                                                             COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DRS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MOLECULE TYPE: profein
SEQUENCE DESCRIPTION: SEQ ID NO: 7:
US-16-054-873-7
                                                                                                                                                                                                                         COUNTRY: USA
Z 1P: 94111-3834
FOUTER REALMERE FORM:
MEDIUM TYPE: FLOREY GISK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 5, Application US/09858935B Publication No. US20030069177A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TYPE: amino a.id
STRANDEDNESS: <Unknown>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NAME: Mycroft, Frank I
                                                                                                                                                                                                                                                                                                                                                                                                  CURRENT APPLICATION DATA:
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98.18;
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Best Local Similarity 100.0
Matches 52; Conservative
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                                                                               NUMBER OF SEQUENCES:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Best Local Similarity
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ADDRESSEE: no. US2002019329xAlo No. US20020193292Aldisk of No. US2002
STREET: 405 Loxington Avenue, 64th Floor
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94.3%; Pred. No. 1.46+26;
Live 1; Mismatches 1; Indels 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER: IBM PC compatible
OPERATING SYSTEM: AC-DOS/MS:303
SOFTWARE: PatentIn Release #1.0, Version #1.30
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                                                                                                                                                                                                                                                                                                                                                                                  TILLE OF INVENTION: INSULIN DERIVATIVES NUMBER OF SEQUENCES: 26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STATE: New York
COUNTRY: United States of America
ZIP: 10174 6401
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APPLICANT: Ultsch, Mark
APPLICANT: Vajdos, Felix
TILE OF INVENTION: CRYSTALLIZATION OF IGF-1
FILE REFERENCE: P1869R1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICATION NUMBER: US/09/861,687
                                                                                                                                                                                                                                                                                                Brandt, Jakob
Kurtzhals, Poter
Hansen, Hertz Per
Kaarsholm, Niels Christian
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 19:
US-09-861-687-19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICATION NUMBER: 08/932, 082
FILING DATE: 16-DEC-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NAME: Lambiris, Elias J. REGISTRATION NUMBER: 33,728
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FILING DATE: 21-May-2001
CLASSIFICATION: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TELECOMMUNICATION INFORMATION: TELEPHONE: 212-867-0123
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER READAL & FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            // Sequence 3, Application US/10066009A
// Publication No. US20020165155A1
// GENERAL INFORMATION:
                                                                                                                                                             Sequence 19, Application US/09861687 Publication No. US20020193292A1 GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TELEFAX: 212-878-9655
                                                                                                                                                                                                                            APPLICANT: Markussen, Jan
Jonassen, Ib
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CURRENT APPLICATION DAIA:
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Best Local Similarity 94.3%
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TOPOLOGY: innear
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                                                                                                                     RESULT 7
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TITLE OF INVENTION: Method for making inserting precursors and
TITLE OF INVENTION: Method for making inserting precursor and
TITLE OF INVENTION: Method for making inserting improved ferrentation
TITLE OF INVENTION: yield in yeast
TITLE OF INVENTION: yield in yeast
TITLE OF INVENTION: yield in yeast
CURRENT APPLICATION NUMBER: D.209/844.71;
CURRENT APPLICATION NUMBER: PA 2000 00448
PRIOR APPLICATION NUMBER: PA 1999 01869
PRIOR FILING DATE: 1999-12-29
PRIOR APPLICATION NUMBER: 60/211.081
PRIOR FILING DATE: 2000-06-18
PRIOR FILING DATE: 2000-06-18
PRIOR FILING DATE: 2000-06-18
PRIOR FILING DATE: 2000-02-10
PRIOR FILING DATE: 2000-02-10
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    1; Gaps
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                                            1 FVNOHLCGSHLVEALYLVCGERGFFYTPKTRGIVEQCCTSICSLYQLENYCN 52
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 FVNOHLCGSHLVEALYLVCGERGFFYTPKTRGIVEOCCTSICSLYQLENYCN 52
                                                                 1 FVNQHLGGSHLVEAIXLVGGERGFFYTPKT-GIVEQCCTSICSIXQLENYCN 51
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 51;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       94.7%; Score 278; ; DB 14; 98.1%; Pred, No. 2e-27;
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  Mismatches
                                                                                                                                                                                                                                                             APPLICANT: DUDAQUIE, YVES
APPLICANT: LC*man, Henry
TITLE OF INVENTION: PROTEIN VARIANTS
FILE REFERENCE: P1712R1-1
CURRENT APPLICATION NUMBER: US/10/028,410
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SOFTWARE: FastSEQ for Windows Version 4.0
                                                                                                                                                                                                                                                                                                                                                                           2001 12-19
BER: US/39/477.-24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 18, Application US/09894711 Patent No. US20020137144A1
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                                                                                                                                                                           US-10-028-410-3
; Sequence 3, Application US/10028410
; Publication No. US20020160455Al
; GENERAL INFORMATION:
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ORGANISM: Artificial Sequence
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Best Local Similarity 98.11
Matches 51; Conservative
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Matches 50; Conservative
51; Conservative
                                                                                                                                                                                                                                                                                                                                                                             CURRENT FILLING DATE: 2001
PRIOR APPLICATION NUMBER:
PRICE FILLING DATE: 2000 0°
NUMBER OF SEG IP NOS: 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NUMBER OF SEU ID NOS: 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TYPE: PRT
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  Matches
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RESULT 12
US-10-054-873-4
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                                                                                                                                                                                            TYPE: PRT
ORGANISM:
                                                                                                                          SEO ID NO 4
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APPLICANT: NAKATSUBG, Kaoru
APPLICANT: NISHTZONO, Isao
TITLE OF INVENTION: Immunoassay For Measuring Human C-Peptide and Kit Therefor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ]:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match 92.9%; Score 273; DB 14; Length 50; Best Local Similarity 96.2%; Pred. No. 9.5e-27; Matches 50; Conservative 0; Mismatches 6; Indels
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Pred. No. 9.4e-26;
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APPLICANT: Filvaroff, Ellen
APPLICANT: Lowman, Henry B.
TITLE OF INVENTION: METHOD FOR TREATING CARTILAGE DISORDERS
FILE REFERENCE: P174R1
CURRENT APPLICATION NUMBER: US/09/858,935B
CURRENT APPLICATION DATE: 2002-07-02
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Indels
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CURRENT APPLICATION NUMBER: US/10/066,009A CURRENT FILING DATE: 2002-06-24
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CURRENT APPLICATION NUMBER: 05/09/874,580
CURRENT FILING DATE: 2001-06-12
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PRIOR FILING DATE: 2000-06-12
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                                                         PRIOR APPLICATION NUMBER: US 60/287,072 PRIOR FILING DATE: 2001-04-27 PRIOR APPLICATION NUMBER: US 60/267,977 PRIOR FILING DATE: 2001-02-09 NUMBER OF SEQ ID NOS: 5 SEQ ID NO 3
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: Patent No. US20020160435A1
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APPLICANT: KITAJIMA, Sachiko
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SOFTWARE: Patentin versi
SEQ ID NO 1
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ORGANISM: Homo sapiens
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Best Local Similarity
Matches 52; Conserv
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Intramolecular Chaperone-Like Sequence
                                                                                                                                                                                                                            Query Match 90.8%; Score 267; DB 11; Length 86; Best Local Similarity 60.5%; Pred. No. 9.4e-26; Matches 52; Conservative 0; Mismatches 0; Indels
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Pred. No. 9.4e 2b;
C; Mismatches 0; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 FVNQHLCGSHLVEALYLVCGERGFFYTPKT----
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                                                                                                                                                                                                                                                                                                                                                                                                                             31 ---- RGIVEQUOTSICSLYQLENYCN 52
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PRIOR APPLICATION NUMBER: US 60/204,490
PRIOR FILING DATE: 2000-05-16
NUMBER OF SEQ 1D NOS: 153
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MEDIUM TYPE: Floppy disk
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50.5%;
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Matches 52; Conservative
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ZIP: 94111-3834
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APPLICANT: Lowman, Henry
                                                                                                                                                   ; ORGANISM; Homo sapiens
US-09-858:935B-4
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60.5%; Pred. No. 1.26.25;
                                                                                                                                                                                                                                                                                                                                                                      90,8%; Score 267; CB 10; Tength 96;
60,5%; Pred. No. 1.1e 25;
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APPLICANT: Ogg, Scott
TITLE OF INVENTION: THERAPEUTIC AND DIAGNOSTIC TOOLS FOR
TITLE OF INVENTION: IMPAIRED GLUCOSE TOLERANCE CONDITIONS
FILE REFERENCE: 00786/351004
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EARLIER FILING DATE: 1998-05-15
NUMBER OF SEQ 1D NOS: 328
SOFTWARE: FastSEQ for Windows Version 4.0
SEC 1D NO 125
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                                                                                                                                                                                                                                                                            LOCATION: 1.96
SEQUENCE DESCRIPTION: SEQ. 10 NO: 4:
U.9. 947-563-4
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EARLIER APPLICATION NUMBER: 08/857,076
EARLIER APPLICATION NUMBER: 08/857,076
EARLIER APPLICATION NUMBER: 08/888,534
EARLIER FILLING DATE: 1997-07-07
        TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 408-4000
ELEFERAY: (202) 408-4400
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                ORGANISM: Escherichia coli
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 125, Application US/09205658
Patent No. US20010029617A1
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                                                                                                           LENGIH: 96 amino acids
                                                                                                                             TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                        Protein
                                                                                                                                                                 TOPOLOGY: linear MOLECULE TYPE: protein ORIGINAL SOURCE:
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Best Local Similarity 60.00
The Szi Conservative
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Matches 52, Conservative
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US-09-815-229-3
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICAN: BURNACOUR Reinhold
TITLE OF INVENTION: Improved process for obtaining
TITLE OF INVENTION: Improved process having correctly bonded cystine bridges
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     34
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ADDRESSEE: Finnegan, Henderson, Farrabow, Garrett &
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 86;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Indels
COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: PatentIn Release #1.0, Version #1.30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Version #1.30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICATION NUMBER: 09/134,836
FILING DATE: <UNKNOWN>
ATTORNEY/AGENT INFORMATION:
NAME: Leslie McDonell
REGISTRATION NUMBER: 34,872
REFERENCE/DOCKET NUMBER: 02481.1600-00000
                                                                                                                                                                                                                                                           NAME: Mycroft, Frank J
REGISTRATION NUMBER: 46,946
REFERENCE/DOCKET NUMBER: 020167-300130GS
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           . 14;
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                                                                                                                                      PRICK APPLICATION DATA:
APPLICATION NUMBER: WO PCT/CN98/C0052
FILING DATE: 31-MAR-1998
APPLICATION NUMBER: US 09/423,100
FILING DATE: 11-DEC-2000
ATTORNEY/AGENT INFORMATION:
                                                    CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/054,873
FILING DATE: 22-Jan-2002
CLASSIFICATION: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER: 1BM PC COMPALIED OURSAIN SYSTEMARE: PATENTIN Release #1.C CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICATION NUMBER: US/09/947,563
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 U; Mismatch
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 FVNOHLCGSHLVEALYLVCGERGFFYTPKT-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 267;
Pred. No. :
                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE DESCRIPTION: SEQ ID NO: 4: US-10-054-873-4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                31 - --RGIVEQCCTSICSLYQLENYCN 52
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        61 SLUKRGIVEQCCTSICSLYQLENYCN 86
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: Rubroder, Franz-Josef
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SIREET: 1300 I Street, N.W.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FILING DATE: 07-Sep-2001
CLASSIFICATION: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 4, Application US/09947563 Patent No. US20020156234A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                      STRANDEDNESS: <URKNOWES
                                                                                                                                                                                                                                                                                                                                                                GENETH: 86 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity 60.5%;
Matches 52; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                         TOPOLOGY: Linear MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Dunner
                                                                                                                                                                                                                                                                                                                                                                                   TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CITY: Washington
STATE: D.C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        US-09-947-563-4
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Patent No. US20020058614A1
GENERAL INFORMATION:
APPLICANT: FILVATOFF, Ellon H.
APPLICANT: FLAVATOFF, Ellon H.
APPLICANT: FLAVATOFF, Ellon H.
TITLE OF INVENTION: USE OF INSULIN FOR THE TREATMENT OF CARTILAGENOUS DISORDERS CHERENT FILLING DATE: 2001-03-29
CURRENT APPLICATION NUMBER: US 50/192,103
PRIOR FILLING DATE: 2000-03-24
NUMBER OF SEQ ID M.S: 17
SEQ ID NO 3
LENGTH: 110
TYPE: PRT
ORGANISH: HOMO SapienS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      US-09-815-229-3
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t: Indets 34;

Query March 90.8a; Shore 267: ERES; locath 110; Best Local Similarity 60.5a; trou No. 1.25.25; Matches 52; Conservative B; Misser G.S. Conservative

31 --- RGIVEQCCTSICSLYOLENYON 52 iiiiiiiiiiiiiiiiiiiiii 85 85 SLQKRGIVEQCCTSICSLYOLENYON 1:0

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Search completed: September 15, 2003, 12:23:36 Job time : 22.8065 secs

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version	- 2003
GenCore	(c) 1993 - 2003
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OM protein - protein search, using sw model
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protein
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September 15, 2003, 11:56:45; Search time 8:57348 Seconds (without alignments) 583.284 Million cell updates/see Run on:

US-09-423-100-5 294 ! FVNOHL/GSHLVFALYLVCG......IVFOCTTSICSLYOLENYON 52

Title: Perfect score: Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

283308 segs, 96168682 residies Searched:

Total number of bots sutisfying classon parameters:

Minimum DB seq rength: 0 Maximum DB seq rength: 2000500000

Post-proressing: Minimum Match 0% Maximum Match 106% Listing first 45 summaries

pir_76:*
1: pir1:*
2: pir2:*
3: pir3:* Database :

Prod. No. is the number of results predicted by chance to have a store greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

		æ				
Result No.	Score	Query Match	Length	CB	ID	Description
		93.0	5	: -	JHMNI	de micros en militario.
~	274.5	9 3 0	51	_	INWHE	
~	273.5	93.0	5.1	-	: NEL	٠
₹	27 4	92.8	96	~	PC7082	-
ی	271.5	92.3	51	-	INHY	
æ	268.5	91.3	51	-	: NMSSE	
	267.5	91.0	51	~	A5915;	pr
st.	267	8.06	110	_	IPHU	
J.	267	8.05	110	~	B42179	_
2	267	8.08	110	~	A42179	insulin precursor
=	26.7	90.8	110	~	JQ0178	
1.2	263.5	9.68	5.1	-	INWHIS	
~	263.5	89.6	51	-	INGT	
77	263.5	9.68	51	_	INCMA	insulin - Arabian
	763	89.5	84	~	IPPG	p
16	26.4	89.5	110	-	INKE	insulin precursor
13	262.5	e. 58	51	-	INCT	insulin cat
π.	747	89.1	110	_	1 PDG	insulin precursor
13	261.5	88.6	51	_	INMKSO	insulin - common s
50	260	88.4	110	7	148166	insulin precursor
.: ~	258.5	87.9	105	_	IPBO	insulin precursor
2.2	256.5	87.2	51	~	JQ0362	insulin - North Am
53	252.5	85.9	77	-	INSH	insulin precursor
24	252	85.7	98	-	IPHO	insulin precursor
25	251.5	85.5	51	~	INCB	insulin - Chinchil
56	251	85.4	108	~	A39883	insulin precursor
2.7	250	85.0	108	-	INMS1	insulin 1 precurso
58	249	84.7	110	-	IPKT1	insulin 1 precurso
57	248.5	84.5	51	_	INGS	insulin - goose

		insulin II - North	insulin I2 - No	insulin - creste	insulin - turkey	insulin - ostric	insulin - black	insulin - slide	insulin precurso	insulin - Amphi	insulin - duckbill	insulin precursor		insulin - American	
IPRT2	I NMS2	S44469	S44470	INPO	INTK	INOS	A61129	A50414	151223	561361	863590	IPCH	IPDK	INAO	INGXA
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110	110	52	25	5.1	51	5 1	51	51	103	5.2	51	107	81	51	52
84.4	84.4	83.7	83.7	83.2	83.2	83.2	83.2	83.2	81.1	61.0	80.1	79.8	79.4	78.7	78.6
8	248	246	246	244.5	244.5	244.5	244.5	244.5	238.5	238	235.5	2:4.5	234.5	231.5	231
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ALIGNMENTS

HESTIT 1 INWHP INSHIP INSHI	Ouery Match 94.08; Score 273.5; DH 1; Longth 51; Best Local Similarity 96.28; Pred. No. 1.5e 24; Matches 50; Conservative 0; Mismatches 1; Indols 1; Gaps 1; Matches 50; HVOHLGGSHLAFALYLVGGENGFYTPKTRGIVEGCCTSLGSLAQLENYCN 52 HILLIFITHIHITHIHIHIHIHIHIHIHIHIHIHIHIHIHIHIH	FRESHLT 2 INWHF INSULID 7 INWHF INSULID 7 INSU
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insulin procursor - jack boan (fragments)
NiAlternate names: hypodytycemic agent; plant insulin
CiSpecies: Canavalia ensiformis (jack bean)
CiSpace: 07-Dec-1999 *sequence_revision 07-Dec-1999 *text_change 10-Dec-1999
CiAccession: B59151: A59151
ROUIVEIRA A.E.A.; Machado, 0.1., ; Gomes, V.M.; Kavier-Neto, J.; Pereira, A.C.P.;
Procein Pept. Lett. 6, 15-21, 199
A:Title: Jack bean seed coat cont ins a protein with complete sequence homology to I
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Hoppe-Seyler's 2, Physiol, Chem. 353, 444-456, 1972
Affitie: Isolation and partial structural analysis of insulin from mouse (Mus muscu
AfReference number: A01591; MUID:72189454; PMID:5628210
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              C:Species: Acomys cantrinus (Egyptian spiny mouse)
C:Date: 15-Jul 1981 #sequence_revision 13-Jul-1981 #text_change 31-Mar-2000
C:Accession: A01591
R:Buenzli, H.F.: Humbel, R.F.
                                                                                                          C.Species: Criccinae qen. sp. (hamster)
C.Date: 31.Mar.1992 #sequence_revision 31.Mar-1992 #text_change 16.Jul 1999
                                                                                                                                                                                                                         Rinecton, F.A.; Delcher, H.K.; Steinman, H.; Lebovitz, H.E. Fed. Proc. 32, 300, 1973
Ariticle: Structure of hamster insulin: comparison with a tumor insulin A; Accession: A91456
A; Accession: A91456
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 EVNOHICGSHLVEALYLVCLBRGFFYTPKTRGIVEUCTSICSLYCLENYCN 52
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Cikeywords: hormone; pancreas
E:1-80/Domain; insulin chain B *status experimenta; <BCH>E:1-50,31 bi/Product; insulin *status experimental <MAT>E:3-52/Domain; insulin chain A *status experimental <ACH>E:3:52/Domain; insulin chain A *status experimental <ACH>E:3:52/Domain; insulin chain A *status experimental <ACH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A; Wolecule type: protein
A; Wesidues: 1-30.31-51 < BUE>
C; Superfamily: insulin
C; Keywords: hormone; pancreas
F:1-30/Domain: insulin #status predicted < BCH>
F:1-30/Domain: insulin #status predicted < AGH>
F:31-51/Domain: insulin chain A *status predicted < AGH>
F:7-37,19-50,36-41/Disultide bonds: *status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Outry Maich 92.4%; Score 271.5; DR Limer Local Smilarity 94.2%; Pred No. 25e 24; Matches 49; Mismatches 0; Mismatches 0.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 268.5; DB 1;
Prod. No. 5.5e-24;
i; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         insulin - Egyptian spiny mouse (tentative sequence)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                   A:Molecule type: projeto
A:Residuos: 1-30,31-5, <NED-
C:Superfamily: insulin
C:Keywords: hormone; pancreas
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A:Reference number: A59151
A:Accession: B59151
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Local Similarity
nes 48; Conserv
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A;Accession: A01591
                                                                                                                                                                                             C:Accession: A91456
                                                                     insulin - hamster
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
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Cispectors: Elephantidae gen. Sp. (elephant)
Cispectors: Elephantidae gen. Sp. (elephant)
Cispectors: 24-Apr-1954 *Sequence_revision 4: Sequence of insulin.
Cispectors: Abista
Risanth, L.F.
And 40, 60, 665-666, 1966
Artitle: Species variation in the amino acid sequence of insulin.
Aireference number: A9029; MUID:66160119; PMID:594993
Accession: A01584
Aireference number: A9029; MUID:66160119; PMID:5949993
Aireference number: A9029; MUID:66160119; PMID:5949993
Aireference number: A0029; MUID:66160119; PMID:5949993
Aireference number: A9029; MUID:66160119; PMID:5949993
Aireference number: A90299; MUID:66160119; PMID:5949993
Aireference number: A90299; MUID:66160119; PMID:5949993
Aireference number: A90299; MUID:66160119; PMID:66160119; PM
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                                                                                                                                                                                    Length 51;
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                                                       <ACH>
F.1-30, 31-51/Product: insulin #status experimental <MAT>
F.31-51/Domain: insulin chain A #status experimental <ACI
F.7-37,19-50,36-41/Disulfide bonds: #status predicted
                                                                                                                                                                           DB 1;
e 24;
es 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 273; DB 2; L
Pred. No. 2.9e-24;
); Mismatches 0;
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94.2%; Pred. No. 1.5e-24;
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                                                                                                                                                                                                                                                              0; Mismatches
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                                                                                                                                                                           93.0%; Score 273.5; 96.2%; Pred. No. 1.
                                                                                                                                                                                                                    Pred.
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96.2%;
                                                                                                                                                                                                                    96.2%;
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Best Local Similarity 96.20
Matches 50, Conservative
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Matches 50: Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          insulin · elephant
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               eqt-set
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A; Accession: A59151

RESULT 5

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Length 51;

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Resideber, P., Kamber, B.; Kartener, A.; Joehl, A.; Riniker, B.; Rittel, W. (1907) A.; Coll. Chim. Acta 57, 2617-2621, 1974
A.; Title: Totalsynthese you Hamaninsulin unter aczielter Bildung der Disulfidbindung. A: Friederene unmer: A: A: Marker is annotation; Synthesis Mullo: 7507/277; PMID: 4443293
A. Marter disulting booded human insuitu was synthesized; the synthetic hormone was in A: Note: article in German with English abstract. Repercence unmer: A: Physiol. Chem. 354, 659-672, 1973
A. Marthani, V. K.
B. Marthani, V. K.
A: Reference number: A91658 Mullo: 75040007; PMID: 4803564
A. Title: The synthesis of C-peptide of human proinsulin.
A: Reference number: A91658 Mullo: 75040007; PMID: 4803564
A. Contents: annotation: synthesis of residues 57-67
Chem. Ber: 106, 2347-2352, 1973
A. Title: Synthesis of the complete sequence of human proinsulin C-peptide and its [.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       insulin precursor - green monkey
Cispecies: Cercopithecus aethiops (green monkey, grivet)
Cispecies: Cercopithecus aethiops (green monkey, grivet)
CiAccession: B42179; A65212; S16494; S22056
CiAccession: B42179; A65212; S16494; S22056
Rissino, S.; Bell, G.I.: Li, W.H.
Mol. Biol. Evol. 9, 191-203, 1992
Airlie: Sequences of primate insulin genes support the hypothesis of a slower rate
A;Ritle: Sequences of primate insulin genes support the hypothesis of a slower rate
                                                                                                                                       A:Molecule type: protein
A;Residues: 57-87 «KOA»
K:Lucassen, A.M.: Julier, C.; Beressi, J.P.; Boitard, C.; Froguel, F.; Lathrop, M.;
Nature Genet. 4, 305-310, 1993
                                                                                                                                                                                                                                                                               A:Title: Susceptibility to insulin dependent diabetes mellitus maps to a 4.1 kb segn
A:Reference number: 158114: MUID:94364428: PMID:8458440
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Biochem, J. 310, 869-874, 1995
A:Title: Sequence requirements for proinsulin processing at the B-chain/C-peptide j
A:Reference number: $58661; MUID:96013185; PMID:7575420
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A; Cross-references: GB:L15440; NID:q307071; PIUN:AAA59179.1; PID:g307072
                           A:Title: Amino acid sequence of the C-peptide of human proinsulin.
A:Reference number: A91186; MUID:71257722; PMID:5560404
A:Accession: A91186
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 110;
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1-24/Domain; signal sequence Astatus predicted (SIG)
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60.5%; Pred. No. 1.6e-23;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A.Contents: annotation; synthesis of residues 57 87 R;Kaufmann, J.E.; Irminger, J.C.; Haiban, P.A. Biochem, J. 310, 869-874, 1995
                                                                                                                                                                                                                                                                                                                                                                                               A;Status: preliminary: translated from GB/EMBL/DDBJ
A;Molecule type: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          0; Mismatches
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A;Map position: 11p15.5-12p15.5
A;Introns: 63/1
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A:Reference number: A92075; MUID:71116410; PMID:5101771
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       N'Alternate names: proprinibation
C.Species: Homo sapiens (man)
C.Species: Homo sapiens
C.Species: Homo sapiens
C.Bate: 2-3-oct-1981 #sequence_revision 23-oct-1981 #text_change 08-Dec-2000
C.Bate: G.S.Species: A94253; A93216; A94251; A93144; A92075; A91186; ISB114; A01579;
R.Bell, G.S.Species: R.L.; Rutter, W.J.; Lordell, B.; Tischer, E.; Goodman, H.M.
Nature 284, 26-32, 1980
A.Title: Sequence of the human insulin gene.
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A:Reference number: A91216; MUID:80054779; PMID:501234
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A.Cross-references: GB.100265: NID:q186429: PIDN:AAA59172.1; PID:q386828 R:JUlrich, A.; Dull, T.J.; Gray, A.; Brosius, J.; Sures, I. Science 209, 612-615, 1980 A:Title: Genetic variation in the human insulin gene. A:Title: Genetic variation in the human insulin gene. A:Reference number: A94253; MulD:80236313; PMID:6248962
A;Molecule type: protein
A;Residues: 31-51 cMACA>
A;Residues: 31-51 cMACA>
C;Comment: The two chains are probably produced from the same precursor.
C;Superfamily: insulin
F;1-30,31-51/Product: insulin *status experimental cMAT>
F;1-30,71-50/Domain: chain B *status experimental cha>
F;31-51/Domain: chain A *status experimental cha>
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R;Bell, G.L; Swain, W.F.; Pictet, R.; Cordell, B.; Goodman, H.M.; Rutter
Nature 282, 525-527, 1979
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R:Sures: I.: Goeddel: D.V.: Gray, A.: Ultrich, A.
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R:NIcol, D.S.H.W.: Smith, L.F.
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A:Reference number: A94251; MUID:80147417; PMID:6927840
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92.3%; Pred. No. 7.2e-24;
tive 1; Mismatches 2;
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J. Biol. Chem. 246, 1375-1386, 1971
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Eur. J. Biochem. 20, 190-199, 1971
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A:Reference number: A93144
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A:Residues: 25-54:90-110 <NIC>
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Nature 187, 483-485, 1960
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A:Residues: I:110 <8EL2>
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Best Local Similarity
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A;Residues: 1-110 <BEL>
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A;Residues: 1-110 <ULL>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A;Accession: A9425;
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Cincoession: JULIAN JULIAN BENEARANDER, M.; Wengenmayer, F.; Winnarker, E.L. Gene 19, 179-183, 1982
A:Title: The nucleotide sequence of CDNA coding for preproinsulin from the primate M. A:Teference number: JQ0178, MUID:8308(474; PMID:5184262
A:Reference number: JQ0178, MUID:8308(474; PMID:5184262)
A:Recassion: JQ0178
A:Residues: J-110 GWET>
A:Residues: J-110 GWET>
A:Cross-references: GB:JQ0336; NID:9342121; PIDN:AA36849.1; PID:9342122
C:Superfamily: Insulin GET-A:Cross-references: GB:JQ0336; NID:9342121; PIDN:AA36849.1; PID:9342122
C:Superfamily: Insulin #status predicted <MAI>F:25-54, DQnmain: Signal Residues predicted <MAI>F:25-54, DQnmain: insulin chain B *status predicted <CPT>
F:59-10/Domain: insulin chain A *status predicted <CRT>
F:90-110/Domain: insulin chain A *status predicted <CRT>
F:31-96,43-109,95-100/Disuifide bonds: *status predicted <CRT>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Rishihara, Y.; Sailo, T.; Ito, Y.; Fujino, M.
Nature 181, 1468-1469, 1958
A:Title: Structure of sperm- and sei-whale insulins and their breakdown by whale pep.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             C:Species: Balaenoptera borealis (ser whale)
C:Date: 13 Jul-1981 #sequence_revision 13-Jul-198: #text_change 16-Jul-1999
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C.Date: 13-Jul-1981 #sequence_revision 13-Jul-1981 #text_change 16-Jul 1999
         C:Date: 07-Sep-1990 *sequence_revision 07-Sep-1990 *text_change 16-Jul-:5999
C:Accession: JQ0178
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               90.8%; Score 267; 36.2; Length 110;
6.5%; Pred. No. 1.6e-23;
tive 0; Mismatches n; Indels
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A;Reference number: A90029; MUID:66160119; PMID:5949593
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 FVNQHLCGSHLVEALYLVGGERGFFYTPKT ..........
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A:Molecule type: protein.
A:Residues: i-30,31-51,<1SH>
C:Superfamily: insulin
C:Keyeords: hormone; panereas
F:1-30/Domain: insulin chain B #status experimental <POH>
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nes 52, Conservative
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Am. J. Med. 40, 662-666, 1966
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A; Residues: 1-30;31-51 <SMI>
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                                                                        A:COSS TEFETENCES: EMBL:X61092; NID:q22808; PIDN:CAA43405.1; PID:q22809
A:COSS TEFETENCES: EMBL:X61092; NID:q22808; PIDN:CAA43405.1; PID:q22809
A:Note: sequence extracted from NCBI backbone (NCBIN:95185, NCBIP:95194)
A:Note: sequence extracted from NCBI backbone (NCBIN:95185, NCBIP:95194)
A:Note: sequence extracted from NCBI backbone (NCBIN:95185, NCBIP:95194)
A:Note: Sequence extracted from NCBI backbone (NCBIN:95186)
A:Reference number: A92111; MUID:72258016; PMID:4626369
A:Reference number: A92111; MUID:72258016; PMID:4626369
A:Residues: 57-87 <PET>
C:Genetics:
A:Rolecule type: protein
A:Residues: 57-87 <PET>
C:Genetics:
A:Introns: 63/1
C:Superfamily: insulin
C:Reywords: hormone; pancreas
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C;Date: (4-Mar-1993 #sequence_revision 18-Nov-1994 #text_change 16-Jul 1999
C;Dates: (3-Mar-1993 #sequence_revision 18-Nov-1994 #text_change 16-Jul 1999
C;Accession: A42179; S22058
R;Selno, S.: Bell, G.I.: Li, W.H.
MOL Biol: Evol. 9, 193-203, 1992
A:Title: Sequences of primate insulin genes surport the hypothesis of a slower rate of A:Reference number: A42179; MUID:92219951; PR ::1540757
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A:Note: sequence extracted from NCHI backLone (NCHIP:95067)
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Pred. Nc. 1 5e-23;
0: Mismatches 0: Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     F.25-54/Domain: Insurin chain B status producted (BoH).
F.25-54/Domain: Insurin chain B status producted (BoH).
F.57-87/Hounding connecting peet the Both areas experienced copes.
F.90-110/Romain: Insulin chain A Batatus producted ACH.
F.31-96,43-109,95-100/Disulfide wonds. Estatus producted
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C;Species: Macaca fascicularis (crab-eating macaque)
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Matches 52; Conserv
                                                    A; Residues: 1-110 <SEI>
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A:Molecule type: DNA
A:Residues: 1-110 <SET>
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A; Accession: B42179
A; Molecule type: DNA
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Best Local Si
Matches 52;
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Search completed: September 15, 2003, 12:04:20
Job time : 9.57348 secs
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A. Receive number: A92782
A. Receive number: A92782
A. Receive number: A92782
A. Receive type: protein
A. Residues: 1.30;31:51
A. Residues: 1.30;31:
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C;Superfamily: insulin
C;Keywords: hormone; pancreas
P:1-30/Dmomain: insulin chain B *status experi...n'al <BCH>
P:1-10, 31-51/Poduct: insulin *status experiment: | <MAT>
P:31-51/Domain: insulin chain A *status experimental <ACH>
F:7-37,19-50,36-41/Disulfide bonds: *status predicted
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                                                                                                                                                                                                                                                                                                                                               89,6%; Score 263,5; DB 1 90,4%; Pred. No. 2,1e-23;
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CiSpecies: Sus serola aumestica (domestic pro-
CiDate: 22.50m 1981 *sequence_revision 22.50m
CiDate: 22.50m 1981 *sequence_revision 22.50m
CiDate: 22.50m 1981 *sequence_revision 22.50m
RiChance, R.E.: Ellis, R.M.; Bromer, W.W.
Science 361, 385 167, 1964
AFITHER: Poreine proinsulin: characterization
A.Reference number: 594240; MUID:68286446; pw.
A.Reference number: 594240; MUID:68286466; pw.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             insulin Arabotu camel (restative sequence)
C/Species: Camelas diverdatius (Araboan erse)
C/Date: 31-Mar 1992 Esequence_revision (1-Mar
C/Accession: A4278.
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Biochem, J. 60, 556-565, 1955
A;Tille: The structure of piq and sheep insu-
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R;Snel, L.; Damqaard, U.
Horm. Metab. Res. 20, 476-480, 1988
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A;Residues: 1-44,707,35-84 «CHA-
R;Chance, R E.
Submittled to the Atlas, July 1970
A;Reference number: A44572
A;Accession: A34572
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Best Local Similarity 90.45
Matches 47; Conservative
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A;Residues: 1-30;31-51 <BRO>
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A;Residues: 1 84 <CH2>
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THITHHIT HITLLHESS REPETER REASON ON THE FUNDHICGS SUCCESSION OF SEPETER ARREASON ON THE STATE OF STATEMENT O
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Fig. 30, 64 84/Product: insuffin #status experimental PMATS
Fig. 6.3/pointain: connecting peptide #status experimental CPEPs
Fig. 84/pointain: fissufficers A. #status experimental - ACHS
Fig. 70, 19-64, 69, 74/fissuffide bonds: #status experimental
A;Title: Proinsulin heterogeneity in pigs.
A;Reference number: A60835; MUID:89032178; PMID:3181865
A;Accession: A60835
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GenCore version 5.1.6 Copyright (c) 1993 - 2003 Compugen Ltd.

OM protein - protein search, using sw model

September 15, 2003, 11:54:00; Search time 4.84588 Seconds (Without alignments) 564:633 Million cell updates/sec Run on:

Title: Perfect score: Sequence:

US-09-423-100-5
294
1 FVNQHLGGSHLVEALYLVCG......LVFGCCTSICSLYQLENYCN 52

Scoring table:

BLOSUM62 Gapop 10.0 , Gapext 0.5

12786 (seqs) 470.26205 (espekas) Searched:

127864 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

SwissProt_41:* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

		æ				
Result		Query				
2	Score	Match	Length	8 0	ro	Description
1	273.5	93.0	51	-	INS_BALPE	POLSTS balaencolor
~	273.5	93.0	51	~	INS ELEMA	
	268.5	91.3	51	-	INS_ACOCA	
4	797	8.06	110	-	INS_CERAE	
5	267	90.8	110	_	INS_HUMAN	
9	26.7	8.06	110	-	I NS_MACEA	_
7	267	90°.	110	_	INS_PANTR	P30410 pan (roglod
œ	263.5	89.6	51	-	INS_BALHO	
57	263.5	89.6	<u>1</u> 5	-	INS_CAMDR	-
10	264.5	89.6	51	~	INS_CAPH1	_
11	263	89.5	108		INS_FIG	
12	263	3.58	110	~	INS_RABIT	, 4
13	263	89.5	110	. 1	INS_SPETR	,~
14	262.5	89.3	51	-	INS_FELCA	S
15	797	89.3	110	_	INS_CANEA	
16	260	88.4	110	٠.	INS_CRILO	P01313 Cricetalus
17	258.5	87.9	105	-	INS_BOVIN	P01317 bos taurus
18	257	87.4	110	-	INS_PSAOB	
19	256.5	87.2	51	-	INS_DIDMA	~
20	254.5	86.6	105	-	INS_SHEEP	P01318 OV:S dries
21	252	85.7	86	_	INS_HORSE	
22	251.5	85.5	51	-	INS_CHIBR	_
23	251	85.4	108	-	INS_AOTTR	P10604 actus trivi
24	250	85.0	108	-	INS1_MOUSE	Pol325 mus musculu
57		84.7	110	~	INSI_RAT	PO1322 rattus norv
76	248.5	84.5	51	-	INS_ANSAN	P07454 anser anser
27	248	84.4	110	~	INS2_MCUSE	P01326 mus musculu
78	248	84.4	110	~	INS2_RAT	
29			52	_	INS_ACIGU	P81423 acipenser q
30	244.5		51	-	INS_HYSCR	80
31		83.2	51	~	INS_TRASC	P31887 trachemys s
32	238.5	81.1	103	-	INS_SELRF	P51463 selasphorus
33	235.5	80.1	51	-	INS_ORNAN	O9tgy7 ornithorhyn

PC1332 gallus gall	P12703 alligator m	P09476 lepisosteus	P12708 zaocys dhum	P01334 crotalus at	P12706 xenopus lae	P12707 xenopus lae	P14806 petromyzon	P09477 platichthys	P29335 amia calva	P23187 oncorhynchu
INS_CHICK	INS_ALLMI	INS_LEPSP	INS_ZAODH	INS_CROAT	INSL_XENLA	INS2_XENLA	INS_PETMA	INS_PLAFE	INS_AMICA	INS_ONCGO
e 1 -		٦.	-	_	_	٦,	,∼ 1	-	-	,-4
107	2.5	52	Ç.	51	106	106	57	<u>.</u>	52	50
8.65	7.8.7	78.6	77.7	77.4	77.0	77.0	75.5	73.5	72.8	71.8
234.5	231.5	231	2.28.5	227.5	226.5	226.5	222	216	214	211
34	36	37	38	3.0	40	4]	42	43	44	ır.

ALIGNMENTS

RESULT 1	KESSECT 1			
Ê	1 NS_HALPH	STANLARD	×	5. AA.
AC				
: t	21-331,-1986	(Rel. 01, freated)	ced)	
: t:	01-00T-1986	(Ref. (41) Jast 5	sequence update)	pdate) update)
DE	Insulin.			
z 9	INS.	total on though	() [:: 4:: 4:: 6	
so	Physeter cat	odon (Sperm whe	aie) (Physe	barachophera physaids (rimbark whate) (rommon forqual), and Physeter catodon (Sperm whate) (Physeter macrocephalus).
ပ္ပ	Eukaryota: M	etazoa; Chorda	la: Craniat	a; Vertebrata; Eufeleostomi;
ပ္ပ င	Mammalia; Eu	theria, Cetart	iodactyla; (Cetacea: Mysticeti:
38	MCBI TaxID-9	baldenopteridae; Baldenoptera. NCBI Taxib≂9770. 9755∙	ora.	
N.	[1]			
Жb	PARTIAL SEQUENCE	ENCE.		
<u>ي</u> د يو	SPECIES B. physalus.	ysalus;		
χ. Σ.	"Tho amino a	anı K., Sakakı	S., Narita	
K.	J. Biochem.	The amino acto sequence in the whate insuling J. Blockem, 56:285-293(1964).	t tin-widte	insulin:
α Z	[2]			
g. ;	SEQUENCE.			
¥.5	SPECIES-P. ca	Lodon;	:	
ς ε Σ 3	"Shindra Y.,	Salto I., ito	Y., Fajino	
. t	whale censis	: sperm - and st	. 1. wild in	sectionals of special and seri-whale insulins and their preakdown by whale consists.
2	Nature 181:1	468 1469719581		
×	[3]	forest tones and		
۲. م	SEQUENCE.			
S S	SPECIES-P.catodon;	todos;		
KA	Harris J.I.,	Sanger F., Nai	aghton M.A.	
ĸŢ	"Species dif	terences in ins	sulin.";	
RL S	Arch. Bioche	m. Biophys. 65	4.7-438(19	Arch. Biochem. Biophys. 65:427-438(1956).
S 6	-:- FUNCTION	: INSULIN DECRE	EANES BLOOD	GLUCOSF CONCENTRATION. IT
) ()	FATTY AC	S CELL PERMEABLE	SATES GLYCOL	INTERSES CELL PERMEABILE .T TO MONOSALCHARIDES, AMINO ACTOS AND FATTY ACTOS - IT ACCELERATES (LYCOLYSIS - THE DENTISE PROSPHATE
88	CYCLE. A	ND GLYCOGEN SY!	NI SISHIN	LIVER
၁၁	-!- SUBUNIT:	HETERODIMER OF	P A B CHAIN	SUBUNIT: HETERODIMER OF A B CHAIN AND AN A CHAIN DINKED BY TWO
၁	DISULFIDE BONDS.	E BONDS.		
ပ (၁	-i- SUBCELLU	LAR LOCATION: 8	secreted.	SUBCELLULAR LOCATION: Secreted.
: : :	PIP SIMILARI	TY: RELONGS TO	THE INSULI	N/IGE/RELAXIN FAMILY.
30.0	PIK: A91142:	1 VICTOR		
D.R.	HSSP; P01317; 1APH.	1APH.		
Dĸ	InterPro; IP.	InterPro; IPR054825; Ins/IGF/relax	F/relax.	
DR	SMART: SM000	SMART: SM00078; 11GF: 1.		
R :	PROSITE; PS0	0262; INSULIN;		
₹ E	Insulin rami	Insulin family: Hormone; Glu		:011SE.
11	NON CONS	30 30	NSULIN B CRAIN	3 CHAIN.
Ŧ	CHAIN		INSULIN A CHAIN	A CHAIN.
FT	DISULFID		INTERCHAIN.	ïN.
FJ	DISULFID		INTERCHAIN	. <u>z.</u>
FT		4 1		
SO	SEQUENCE 5	51 AA; 5766 MW;		9007B514691A7CDD CRC64;

Gaps

- 1

Indels

DB 1; Length 51;

51 AA

INCREASES CELL PERMEABILITY TO MONOSACCHARIDES, AMINO ACTI: AND FATTY ACIDS. IT ACCELERATES GLYCOLYSIS, THE PENTOSE PHOSPHATE CYCLE, AND GLYCOGEN SYNTHESIS IN LIVER.
SUBUNIT: HETERODIMER OF A B CHAIN AND AN A CHAIN LINKED BY TWO J. Med. 40:662-666(1966). FUNCTION: INSULIN DECREASES BLOOD GLUCUSE CONCENTRATION. :F Smith L.F.; "Species variation in the amino acid sequence of insulin."; SUBCELLULAR LOCATION: Secreted. DISULFIDE BONDS.

MISCELLANEOUS: THE SPECIES OF ELEPHANT IS NOT GIVEN, HOT IT IS MOST PROBABLY THE INDIAN ELEPHANT (ELEPHAS MAXIMUS). SIMILARITY: BELONGS TO THE INSULIN/IGF/RELAXIN FAMILY. INSULIN B CHE'N. Insulin family: Hormone: Glucose metabolish, CHAIN 30 INSULIN B CHAIN NON_CONS 30 31 IPR004825; Ins/IGF/relax. SM00078; 11GF; 1. ; PS00262; INSULIN; 1. HSSP: P01308: InterPro: SMART: SM PROSITE;

9007B5000B457P6D CRC64; INSULIN A CHAIN. INTERCHAIN. INTER HAIN. 5752 MW: 51 37 50 7 19 36 51 **AA**: DISULFID DISULFID DISULFID SECUENCE CHAIN

Score 273 5; DB 1; Length 51; Score 2/3 7.
Pred, No. 4.90-27;
Pred, Trucks 1: Indels 1: Mismarches 93.08; 94.28; Conservative Best Local Similarity .64 Query Match Matches

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Sde

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1 FVNQHLCGSHLVEALYLVCGERGFFYTPKTRGIVEQCCTSICSLYQLENYCN 52

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INS_ACCA P01324; 21 JUL 1986 (Rel. 01, Created) (Re). (Re). 21 - JUL 1986 01 - NOV - 1947 Insulin. INS_ACOTA RESULT

Eukaryota: Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia: Eutheria; Rodentia; Sciurognathi; Muridae: Murinae; Acomys. Acomys cahirinus (Egyptian spiny mouse).

01, Last sequence update) 35, Last annotation update)

S. AA

7. ..

Buenzli H.F., Humbel R.E.; "Isolation and partial structural analysis of insulin from mouse (Mus Gaps musculus) and spiny mouse (Acomys canificus).";
10-pope-Seyler's Z. Physiol. Chem. 35:444-450 (1927).
11- FUNCTION: INSULIN DECREASES BLOOD GLUGOSE CONCENTRATION. IT
INCREASES CELL PERMEABILITY TO MONOSACCHARIDES, AMING ACIDS AND
FAITY ACIDS. IT ACCELERATES GLYCOLYSIS, THE PENTOSE PHOSPHATE
CYCLE, AND GLYCOGEN SYNTHESIS IN LIVER.
11- SCHOULT: HETERODIMER OF A B CHAIN AND AND A CHAIN LINKED BY TWO 1 FVNQHLCGSHLVEALYLVCGERGFFYTPKFRGIVEQCCTSICSLYQLENYCN 52 1 FVBQHLCGSHLVEALYLVGGERGFFYTPRS GTVVQACTSTCSLYQGENYCN 51 Score 268.5: DB 1: Length 51: -1- SIMILARITY: BELONGS TO THE INSCLINZINGEZERLAXIN FAMILY.PIR., Ac1591: INMSSP. INTERCHAIN (BY SIMILARITY) INTERCHAIN (BY SIMILARITY). 992BD8B629C47D3D 17RC64; 20-26; Insulin family: Hormone: Glumose metaper.sm. CHAIN 1 vol. 1NSULIN B CHAIN INSULIN A CHAIN. 3; Mismatches BY SIMILARITY Pred. No. Enterprise (PRC0482%) insytracyretax SMART SM00024% (108%) ii. SUBCELLULAR LOCATION: Secreted COMPOSITION.
MEDLINE=72189454; PubMed=5028210; PROSTITE PSHOZ6ZE INSHITNE 92.38; 5768 MW. Local Similarity 92.3 bes 48: Conservative DISULFIDE BONDS MSSP: Pel 508; 17YM 15 36 AA; NCBI_TaxID=10068; NON_CONS CHAIN DISULEID DISULEID SEQUENCE DISULFID Query Match CHAIN Matches SO THE FEET SO SO SO SO SET THE SET THE SO SO SO SO SO SO SO SET THE FEET THE SO SET THE SO SET THE SET THE SET THE SO SET THE SET TH QC. õ

P30407; P01309; 01-APR-1993 (Rel. 25, Created) 01-APR-1993 (Rel. 25, Last sequence update) 01-PEH-1996 (Rel. 33, Last annotation update) 110 AA PRT: STANDARD: INS_CERAE

Cercopithecus aethiops (Green monkey) (Grivet). Eukaryota, Metazoa: Chordata: Craniata: Vertebrata; Euteleostomi; Mammalia; Eutheria: Primates; Catarihini; Cercopithecidae; Cercopithecinae, Corcopithecus, SEQUENCE FROM N.A. Insulin precursor. NCBI_TaxID=9534;

MEDLINE-92219953; PubMed-1560757; Schio S., Rell G.L., ii M., Sequences of primate insulin genes support the hypothesis of "Sequences of primate organism genes support the hypothesis of Slower rate of molecular evolution in humans and apes than in Mol. Biol. Evol. 9:153 203(1992) monkeys."

:0

Peterson J.D., Nebrlich S., Oyer P.E., Steiner D.F.; Determination of the amino acid sequence of the monkey, sheep, and dog proinsulin C-peptides by a semi-micro Edman degradation procedure."; SEQUENCE OF 57-87, MEDLINE-72258016; Pubmed-4626369;

Biol. Chem. 247:4866-4871(1972).
- FUNCTION: INSULIN DECREASES BLOOD GIUCOSE CONCENTRATION. IT INCREASES CELL PERMENBLITY TO MONOSACCHARIDES, AMINO ACIDS AND FATTY ACIDS. IT ACCELERATES GLYCOLYSIS, THE PENTOSE PHOSPHATE CYCLE, AND GLYCOGEN SYNTHESIS IN LIVER.

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 FVNQHLCGSHLVEALYLVCGERGFFYTPKT-----------------
SUBUNIT: HETERODIMER OF A B CHAIN AND AN A CHAIN LINKED BY TWO DISULIPIDE BONDS.
SUBCELLULAR LOCATION: SECRETEG.
SIMILARITY: BELONGS TO THE INSULIN/1GF/RELAXIN FAMILY.
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Eukaryota: Metazoa: Chordata: Cruniata: Vc. Brata; Eufeleosfomi:
Mammalia: Eufheria: Primates: Catarrhini; Frinidae; Horo.
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Bell G.I., Swain W.F., Pictet R.L., Cordell B., Goodman H.M.,
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Bell G.L., Pictet R.L., Rutter W.J., Cordell B., Tischer E.
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21-JUL-1986 (Rel. 01, Last sequence update)
15-SEP-2003 (Rel. 42, Last annotation update)
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Ullrich A., Dull T.J., Gray A., Brosius J.,
"Genetic variation in the human insulin q
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InterPro: IPR004825; Ins/iGF/relax.
Ptam: PF:00045; Ins.lin; l
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Matches 52; Conservative
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Altschul S.E., Zenberg B., Gross E.B., Lorge J.G.,
A Klausner R.D., Collins F.S., Wagner L., Sheumen C.M., Schuler G.D.,
A Altschul S.E., Zenberg B., Buetow K.E., Schaffer C.E., Batz N.K.,
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MEDLINE-71116410; PubMed-5101771;
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MEDLINE-75077277; PubMed-4443293;
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                                  Nature 282:525-527(1979).
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MEDITHES 23 16 1201. PUDMed 469PS 9.
Gender R., Jacober S., Kenna W., Thenthes, s. terms profusely be peptides with the properties s. terms profusely between the peptides (n° peptides). Schome for the synthesis and proparation the sequence 28 % of summan professions of peptide ";
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MEDLINE-841/0233; Pubmed-6424111;
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SYNTHESIS OF 57-87.
MEDLINE=75040007; PubMed=4803504;
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VARIANT HIS 89
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Yano H., Kitano N., Morimoto M., Polonsky K.S., Imura H., Seino Y.;

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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation \cdot
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Eukaryota: Metazoa; Chordata; Craniala; Vertebiata; Eutelcostomi;
Mammalia: Eutheria; Primates; Catarrhin; Percapithecidae;
Cercopithecimes Macacu.
NCRI TaxID=9541;
"A novel point mutation in the human insulin gene giving rise to
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-i- SIMILARITY: BELONGS TO THE INSULIN/IGF/RELAXIN FAMILY.
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21-JUL-1986 (Rel. 01, Created)
13-MUC-1987 (Rel. 05, Last sequence update)
01-FFB-1996 (Rel. 33, Last amotation update)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          0; Mismatches
                  hyperproinsulinemia (proinsulin Kyoto).";
J. Clin. Invest. 89:1502-1907(1992).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 FUNCHLOGSHLVEALYLVOGERGFFYTPKT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 267;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            95 SLOKRGIVEQCCISICSLYOLENYON 310
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         31 ----RGIVEQUOTSICSLYQLENYON 52
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRT;
                                                                                                                                                                                                                   Biochemistry 29:10545:10555(1990).
                                                                               STRUCTURE BY NMR.
MEDI.INE-91104966; PubMed-2271664;
                                                                                                                                                                                                                                                                                                                                                                                                                                                            91265527; PubMed-1646635;
                                                                                                                                                                                                                                                                                MEDLINE-91242467: PubMed-2036426;
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MEDLINE-83080474; Pubmed-6184262;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           90.8%;
60.5%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Best Local Similarity 60.58
Matches 52: Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STANDARD;
                                                                                                                                                                                                                                                                                                          Hua Q. - X., Weiss M.A.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DISULFIDE BONDS
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INS_BALBO
P01314;
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DISULFID
SEQUENCE
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DISULFID
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CHAIN
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INS_BALBO
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the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                      This SWISS-PROT entry is copyright. It is produced through a collaboration
                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RIGHT EVOL. 9:193 203(1992).
FINCTION: INSULIN DECREASES BLOCK GLATOSE CONCENTRATION. IT FUNCTIONS: INSULIN DECREASES BLOCK GLATOSE CHARIDES, AMINO ACIOS AND FAITY ACIDS. IT ACCELERATES GLYGOLYS: THE PENTOSE PHOSPHATE CYCLE, AND GLYCOGEN SYMTHESIS IN LIVE.
SUBBUNIT: HETERODIMER OF A B CHAIN AND AN A CHAIN LINKED BY TWO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Eukaryota: Metazoa; Chordata; Craniata; V.rtebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Pan.
NCBI_TaxID+9598;
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                                                                                                                                                                                                                                                                                                                       90.8%: Score 267: DB 1; Length 110; 60.5%: Pred. No. 6.3e-26;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SIMILARITY: BELONGS TO THE INSULIN/ICF/RELAXIN FAMILY.
                                                                                                                                                                                                                                                                                                                                                   0; Indels
                                                                                                                                                                                                                                                                                             11991 MW; 83C6E33A80A4Z0F9 CRC64;
                                                                                                                                                                                        Insulin family; Hormone; Glucose metabolism; Signal.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                01-APR-1993 (Rel. 25, Created)
01-APR-1993 (Rel. 25, Last sequence update)
15-SEP-2003 (Rel. 42, Last annotation update)
                                                                                                                                                                                                                                         INSOLIN A CHAIN.
                                                                                                                                                                                                                 INSULIN B CHAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           11.0 VA
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                                                                                                                                                                                                                                                                     INTERCHAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                             SLOKRGIVEOCCISICSLYQLENYCN 11C
                                                                                                                                                                                                                               PEPTINE.
                                                                                                                                                                                                                                                                                                                                                                                                                                --- RGIVEQCCTSICSLYQLENYCN 52
                                                                                          PIK: JO0178; JQ0178.

HSSP: P01308; 1A10.

InterPro: IPR004825; Ins/IGF/relax.
Ptam: PF00049; Insulin: 1.

PKINTS; PR00277; INSULINB.
SMART; SM00078; IIGF: 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRT;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDLINE-92219953; PubMed-1560757;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Pan troglodytes (Chimpanzee).
                                                                                                                                                                          PS00262; INSULIN; 1.
                                                                                 EMBL; J00336; AAA36849.1; -.
                                                                                                                                                                                                                                                                                                                                                   Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STANDARD;
                                                                                                                                                                                                     24
54
87
110
96
109
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Best Local Similarity
Local 52; Conserve
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DISULFIDE BONDS
                                                                                                                                                                                                                                                                                             110 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Insulin precursor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEUDENCE FROM N.A.
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P30410;
                                                                                                                                                             SMART; SM
PROSITE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     monkeys."
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                                                                                                                                                                                                                                                                                             SEQUENCE
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PROPEP
CHAIN
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34; Gaps
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-!- SUMONAIT: HETERODIMEN OF A B CHAIN AND AN A CHAIN LINKED BY TWO DISCLEDE BONDS.
                                                                                    Pfam: PF00049; Insulin; 1.
PRINTS: PR00277; INSULINB.
SMART: SM0078; INSULINB.
PROSITE: PS00268: INSULIN: 1.
Insulin family; Hormone; Glucose metabolism; Signal: 3D-structure.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Ishihara Y., Saito T., Ito Y., Fujino M.; "Structure of sperm- and sel-whale insulins and their breakdown by whale pepsin."

Nature 181:1468-1469(1958).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Eukaryota, Metazoa, Chordata, Cramiata, Verrebrata, Euteleostomi, Mammalia, Eutheria, Cetartiodactyla, Cetacea, Mysticeti; Balaenopteridee, Balaenoptera, WCBI_Taxib=9768;
                                                                                                                                                                                                                                                                                                          Length 110;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            -!- SUBCELLUIAR L/CATION: Secreted.
-!- SIMILARITY: BELONGS TO THE INSULIN/IGE/RELAXIN FAMILY
                                                                                                                                                                                                                                                                                                                                       0; Indels
                                                                                                                                                                                                                                                                             12025 MW; 41EB8DF798+77FF5 CRC64;
                                                                                                                                                                                                                                                                                                                         76;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      21-00-1986 (Rel. (H, Created)
21-J0L-1986 (Rel. 01, Last sequence update)
01-00T-1996 (Rel. 34, Last annotation update)
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INSULIN A CHAIN.
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Pred. No. 6.40
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                                                                                                                                                                                                                                                                                                                                         0; Mismatches
or send an email to license@isb-sib.ch)
                                                                                                                                                                                                                                 INTERCHAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          INTERCHAIN
                                                                                                                                                                                                                                                INTERCHAIN
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85 SEQKRGIVEGCEISICSLYCLENYCN 110
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        INTERCHAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                  31 ----RGIVEOPPTSICSLYCLENYON 52
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PIR; AG1582; 1NWHIS.
HSSP; P01317; 1APH.
INTERPO; IPPR004825; INS/IGF/relax.
SMART; SM00078; 11GF: 1.
PROSITE: PS00262; INSULIN: 1.
                                             PIR; A42179; A42179.
PDB; 1EFE; 29-MAR-00.
InterPro; IPR004825; Ins/IGF/relax
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Balaenoptera borealis (Sei whale).
                                                                                                                                                                                                                                                                                                            40.8%;
60.5%;
                              EMBL: X61089; CAA43403.1; -.
                                                                                                                                                                                                                                                                                                                                           Conservative
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                                                                                                                                                                                                 87
110
                                                                                                                                                                                                                                                                             110 AA;
                                                                                                                                                                                                                                                                                                                          Best Local Similarity
                                                                                                                                                                                     25
57
90
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                                                                                                                Gaps
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3. Fac. Med. Bayhdad 14:16:28(1972).
1. Fac. Med. Bayhdad 14:16:28(1972).
1. Fac. Med. Bayhdad 14:16:28(1972).
1. FUNCTION: INSULIN DECREASES BLOOD GLUGOSE CONCENTRATION. II.
1. INCREASES CELL, PERMEAHLLITY TO MONOSACCHARIDES, AMINO ACIDS AND FATTY ACTOS. IT ACCELERATES GLYCOLYSIS, THE PENTOSE PHOSPHATE CYCLE. AND GLYCOGEN SYNTHESIS IN LIVER.
1. SUBUNIT: HELECODIMER OF A B CHAIN AND AN A CHAIN LINKED BY TWO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi;
Mammalia, Eutheria, Cetartiodactyla, Ruminantia, Pecora, Bovoidea,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Camelus dramadirius (Dremedary) (Arabias errety,
Eukarysta: Metavasy Phariatas (ricinta) Werretaata, Esteseesta:
Mammalia, Estiveta, Cetarrandaryja: ylogoda, ramejas
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                                                                                                                                                                                           | FVNOHIGGSHIJEALYINGGERGEFYTPKA-GIVEGGGASTGSLYGLENYCN 51
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Danko W.O.:
*The isolation and characterization of issulin of came) (Camelus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 FVNUHLCGSHLVEALYLVCGERGEFYTPKTRGIVEQCCTSICSLYULENYCN 52
                                                                                                                                                              1 FVNQHLCGSHLVEALYLVCGERGFFYTPKTRGIVEQCCTSICSLYCLENYCN 52
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Pred, No. 8.2e-26;
                                                      DB 1: Length 51;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    -:- SUBGELLUTAR LOCATION: Secreted.
-: SIMILARITY: BELONGS TO THE INSULIN/IGF/RELAXIN FAMILY
                                                                                                          Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          901E8#BA085A7DDD CRC64;
9007B50E400A7DDD CRC64;
                                                   Score 263.5; DB 1
Pred. No. 8.2e-26;
                                                                                                                                                                                                                                                                                                                                                                                                                                          Last sequence applate)
Last annotation update)
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21.JUL.1986 (Rel. 01, Last sequence update)
01 FFR-1996 (Rel. 33, Last annotation update)
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                                                                                                          0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                            PRT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Interpro: 1PE004825; Ins/1GP/relax.
SMART: SM00078: 11GF; 1.
                                                                                                                                                                                                                                                                                                                                                                                                       21-JUL 1986 (Rei. 01, Created)
21 JUL-1986 (Rel. 01, Last seq
01 FEB-1996 (Rel. 34, Last anno
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PROSITE: PS00262; INSULIN: 1.
                                                89.6%;
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90.48:
5723 MW;
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                                                                             Best Local Similarity 92.3
Matches 48; Conservative
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37
50
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PIR: A92782: INCMA
HSSP: P01317; ZINS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Best Local Similarity
51 AA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          51 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NCBL LaxID=9848;
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19.
8.
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PC1320:
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CHAIN
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DISULFID
SEQUENCE
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SEQUENCE
                                                      Query Match
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1- SUHUNIT: HETEKODIMER OF A B CHAIN AND AN A CHAIN LINKED BY TWO
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Sus.
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Chance R.E., Ellis R.M., Bromer W.W.;
"Porcine proinsulin: characterization and amino acid sequence.";
Science 161:165-167(1968).
                                                                                                                                                                                                                                                                                                                                                                                                                                                          "Comparative sequence analysis of the INS 1GF2-H19 gene cluster
                                                                                                                                                                                                                                                                                                                                                                                                                                   1;
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                                                                                                                                                                                                                                                                                                                                                                                                        DB 1; Length 51;
                                                   MEDLINE-66160119; PubMed-5949593;
Smith L.F.;
Species variation in the amino acid sequence of insulin.";
Am. J. Med. 40:662-666(1966).
                                                                                                                                                                                      -:- SUBCELLULAR LOCATION: Secreted.
-:- SIMILARITY: BELGAGS TO THE INSHLIN/IGE/RELAXIN FAMILY
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Han X.G., Tuch B.E.;
"Complete portine proproinsul | cDNA sequence.";
"Complete profine proproinsul | cDNA sequence.";
Submitted (MAY-1998) to the EMBL/GenBank/DEbJ databases.
                                                                                                                                                                                                                                                                                                                                                                               1.007B50CDB4E7DFD CRC64;
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Mammalia, Eutheria, Cetartiodactyla, Suina, Suidae,
                                                                                                                                                                                                                                                                                                                                                                                                                     No. 8.2e-26;
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Last annotation update)
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LIERCHAIN.
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STRAIN-Large white;
MEDLINE-22135958; PubMed 12140686;
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21-JUL-1986 (Rel. U), Created)
26-CCT-2001 (Rel. 46, Last seq.,
28 FEB-2003 (Rel. 41, Last ann
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Mamm. Genome 13:388-398(2002).
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Matches 47; Conservative
Bovidae: Caprinae: Capra.
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               NCBI_TaxID=9925;
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DISULF:D
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                                                                                                                                                            X-KAY CRYSTALLOGRAPHY (1.5 ANGSTROMS).
ISABCRS N.W., Adarwal R.C.:
Experience with fast Fourier least squares in the refinement of the
crystal structure of rhombohedral 2-zinc insulin at 1.5-A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     X-KAY CRYSTALLOSKAPHY (1 5 ANISSPORS).
MEDLINE BROYSKLEL FURMON 2805485;
BAKET E.N., Blunderl T.J., Culfools C.E., Cuttell S.M., Dedson E
                                                                                                                                                                                                                                                                                                                      Dodson G.C., Crowfoot Holdkin G.M., Butterd R.E., Isaars N.W., Reynolds C.D., Sakabe K., Sakabe N., Vijayan N.M.; "The structure of 22n pig insulin crystals at 1.5 A resolution."; Philos. Trans. R. Soc. Lond., B. Biol. Sci. 19:369-456(1988).
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*Structure of the pig insulin dimer in the cubic crystal.";

Acta Crystallogr. B 47:127-136(199!).
                                                           X-SAY CRYSTALLOGRAPHY (1.9 ANGSTROMS).
Blundell T.L., Dodson G.G., Hodgkin D., Mercola D.;
*Insulin. The structure in the crystal and its reflection in chemistry and biology.*;
Adv. Protein Chem. 26:279-402(1972).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SUBCELIULAR LOCATION: Secreted.
SIMILARITY: BELONGS: 70 THE INSULIN/IOF/RELAXIN FAMILY.
INTERFASE: NAME-FPOLEIN SPOLIIGHT;
NOTE-ISSUE 9 OF APTIL 2001;
                              Submitted (JUL-1970) to the PIR data bank.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RAY CRYSTALLOGRAPHY (1.65 ANGSTROMS)
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EMHL; AY044828; AAL69550.1; -.
                                                                                                                                                                                                                                             Acta Crystallogr. A 34:782-791(1978)
                                                                                                                                                                                                                                                                                                                                                                                                                           MEDLINS-92126280; PubMed-1772633;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDLINE-91222450; PubMed-2025410;
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4INS; 31-JUL-94.
REVISION TO 59.
Chance R.E.;
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31-JAN-94. 15-0CT-91. 15-0CT-91. 15-0CT-91. 29-JAN-96.

112A;

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25 FVNQHEGGSHLVEALYLVGGERGFFYTPKARREAENPQAGAVELGGGLGGLQALALEGPP 84
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Insulin family; Hormone; Glucose metabolism; Signal; 3D structure.
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Mammalia, Eutheria, Jagomorpha, Leporidae, Oryctolagus,
NCBI_TaxID+9986;
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MEDLINE-94179230; PubMed-8112571;
Devaskar S.U., Giddings S.J., Rajakumar P.A., Carnaqhi L.R.,
Menon R.K., Zahm D.S.:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               "Species variation in the amino acid sequence of insulin."; Am. J. Med. 40:662-666(1966).
                                                                                                                                                                                                                                                                                                                                  89,5%; Score 263; DB I; Length 108; 60,7%; Pred. No. 1.96-25;
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(Rel. 34, Last annotation update)
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PDB: 1MPJ: 29-JAN-96.
PDB: 3MTH: 29-JAN-96.
PDB: 1DEI: 16-JUN-97.
PDB: 1SDB: 01-APR-98.
PDB: 1EXI: 16-FEB-97.
PDB: 1ZKI: 28-JAN-98.
PDB: 1ZKI: 28-JAN-98.
PDB: 1ZKI: 28-JAN-98.
INTEFPTO: IPR004825; Ins/ISF/relax.
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MEDLINE=66160119; Pubmed=5949593;
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01-FEB-1996 (Rel. 33, Last sequ
01-OCT-1996 (Rel. 34, Last anno
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                                                                                                            Ptam: PF00049; Insulin;
SMART: SM00078; IIGF: 1.
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"Requiation of PDR4 expression in a hibernating mammal.";
Submitted (JUN-2001) to the EMBL/GenBank/DDBJ databases.
-! FUNCITON: INSULIN DERREASES BLOOD GLUCOSE CONCENTRATION. !T
INCREASES CELL PERMEABILITY TO MONOSACCHARIDES, AMINO ACIDS AND
FATTY ACIDS. IT ACCELERATES GLYCCLYSIS, THE PENTOSE PHOSPHAIE
CYCLE, AND GLYCOSEN SYNTHESIS IN LIVER.
-!- SUBUNIT: HETERODIMER OF A B CHAIN AND AN A CHAIN LINKED BY TWO
INCREASES CELL PERMEABILITY TO MONOSACCHARIDES, AMINO ACIDS AND FATTY ACIDS. IT ACCELERATES GLYCOLYSIS, THE PENTOSE PHOSPHAIE CYCLE, AND GLYCOCAD SYNTHESIS IN LIVER.
SUBUNIT: HETEKODIMER OF A B CHAIN AND AN A CHAIN LINKED BY TWO
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Eukaryota: Metazoa: Chordala: Graniata: Vertebrata: Euteleostomi:
Mammalia: Eutheria: Rodentia: Sciuroquathi. Sciuridae: Sciurinae;
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                                                                                                                                                  SUBCELLULAR LOCATION: Secreted.
SIMILARITY: BELONGS TO THE INSULINJ: //RELAXIN FAMILY.
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8202975885077FA8 CRC64;
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15 SEP 2003 (Rel. 42, Last sequence update)
15 SEP 2003 (Rel. 42, Last annotation update)
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INSULIN A CHA.
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SMART; SM00078; IIGF; 1.
PROSITE; PS00262; INSULIN; 1.
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EMBL: M61153; AAA.7540.1;
PIR; A53448; INPR
RSSP; P01308; I1YM.
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nes 51; Conservative
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformaties and the EMBL outstation the European Bioinformatics institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entitles requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 FVNQHLCGSHLVEALYLVCGFRGFFYTPKF------30
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"Characterization of cat. insulin.";
Arch Biochem. Biophys. 2-20 (1984)
1. FUNCTION: INSULIN DECREASES BLOOD GLUCCSE CONCENTRATION. IT
INCREASES CELL PERREABILITY TO MONESACCHARIDES, AMINO ACIDS AND
FATTY ACIDS. IT A CELERATES GLYCOLYSIS, THE PENTOSE PHOSPHATE
CYCLE, AND GLYCOLON SYNTHESIS IN LIVER.
CYCLE, AND GLYCOLON SYNTHESIS IN LIVER.
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Bukaryota Metazoa: Chordata: Craniata: Vertebrata: Enteleostomi:
Manmalia: Eutheria: Carnivora: Fissipedia: Felidae: Felis.
NCBL_TaxID-9685;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                89.5%; Score 263; DB 1; Length 110; 59.3%; Prod. No. 1.96-25;
Live 1; Mismatches 0; Indels
-:- SUBCELLUE DE LOCATION: Secreted.
-:- SIMILARITY: BELONGS TO THE INSULIN/IGF/RELAXIN FAMILY.
PIR; A01589; INCT.
HSSP: 101317: 1APH.
InterPro; IPRO04825; Ins/IGF/relax.
PRINTS; PR00277; INSULINB.
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INTERCHAIN (HY SIMILARITY).
BY SIMILARITY.
4511768D6622HEE5 CRC64;
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PROMODER PROJECT INSULING.

PROSTIE: PROJECT INSULING.

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CONTING CHAIN.
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06, Last sequence update)
46, Last annotation update)
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                                                                                                                                                                                                                                                                                                                       PMBL: AY038604; AAK72558.1; -. HSSP; P01308; 1LNP.
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110 AA;
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hes 51; Conserv
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01-JAN-1988 (Rel.
16-OCT-2001 (Rel.
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P06306;
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between the Swiss Institute of Bioinformatics and the EMBL outstation. The European Bioinformatics Institute. There are no restrictions on its mose by non-profit institutions as lone as its content is in no way modified and this statement is not remove! Usage by and for commercial entities requires a license agreement (See http://www.isb.sh.ch/announce/or send an email to license*lisb.ch).
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                                                                                                                                                                                                                                                                                                                                                                              1; Gaps
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-1. FUNCTION: INSULIN DECREASES HIGHD SILICUSE CONCENTRATION. II
INCREASES CELE PERMEMBILITY TO MON'SACCHARIDES, AMIN'S ACIDS AND
FATTY ACIDS. IT ACCELERATES GLYCKYSIS, THE PENYOSE PHOSPHATE
CYCLE, AND GLYCKGEN SYNTHESIS IN LIVER.
-1. SUBUNIT: HETERODIMER OF A B CHAIN AND AN A CHAIN LINKED BY TWO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
MEDINES 8109071. Stoiner D.F.;
KWOK S.C.M., Chan S.J., Stoiner D.F.;
"Cloning and nucleotide sequence analysis of the dog insulin gene.
"Cloning and sequence of canine preproinsulin predicts an
additional C-pentide Tragment.".
J. Biol. Chem. 258:2357-2483(1983).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Eukaryota: Metazoai Čhordata: Graniala: viitebrata; Eureleostumi;
Mammalia: Eutberia: Carnivora; Fissipedi: Panidae; Panis.
NOBI_TaxiD=9615;
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                                                                                                                                                                                                                                                                                                                 Score 262.5; DB 1; Length 51; Pred. No. 1.1e-25;
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"Species variation in the amino acid sequence of insulin.";
Am. J. Med. 40:662-666(1966).
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SIGNAL.
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                                                                                                                                         INSULIN A CHAIN.
INTERCHAIN.
INTERCHAIN.
                                                       Insulin tamily; Hormone; Glucose metabolism. CHAIN.
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21-301-1986 (Rel. 0), tast sequence appl
01-FEB-1996 (Rel. 3), Last annotation up
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Pfam; PF00049; Insulin; 1.
SMART: SM00078; IIGF; 1.
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PROSITE; PS00262; INSULIN; 1.
                              PROSITE: PS00262; INSULIN; 1.
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Matches 47: Conservative
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SMART; SM00078; IIGF; 1
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54 INSULIN B CHAIN.
87 C PEPTIDE.
1130 INSULIN A CHAIN.
96 INTERCHAIN.
109 INTERCHAIN.
100
v: 12190 MM. A574791864A4Fb98 CRC64;
                                                                                         Score 262: DB 1;
Pred. No. 2.6e-25;
0; Mismatches 1;
                                                                                          89.1%; Score 262;
59.3%; Pred. No. 2
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Matches 51; Conservative
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Search completed: September 15, 2003, 12:01:46 Job time: 4.84588 secs

GenCore version 5.1.6 Copyright (c) 1993 - 2003 Compugen Ltd.

OM protein - protein search, using sw model

September 15, 2003, 11:54:30 ; Search time 20.3154 Seconds (without aliquments) 660.520 Million cell updates/sec Run on:

.....IVEQCCTSICSLYQLENYCN 52 US-09-423-100-5 294 1 FVNQHLCGSHLVEALYLVCG. Title: Perfect score: Sequence:

Scoring table:

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Database :

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sp_unclassified:*
sp_rvirus:*
sp_bacterlap:* SPTREMBL_23:•

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2: Sp_bacteria:•
8: Sp_fund:•
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5: Sp_luman:• sp_mhc:*
sp_organelle:*
sp_phage:*
sp_plant:*
sp_rodent:* sp_mammai.* 100112 Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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11	187.5	63.8	87	13	Q98TA9	
12	186.5	63.4	108	13	Q98TB1	098tbl catostomus
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DT 01-DEC-2001 (TEMBLE-19, Created)

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0 8 X	Ouery Match Best Lovai Sim Matches 52:	h Similarity 60. 52: Conservative	u u	5	ore 267; DB 6; ed. No. 1e-28; Mismatches	Length 110: 0: Indeis 34	: Gaps 1;
ς qα	1 FV 11 25 FV	NOHLOGSHLVP 	SALYE	25/2	FVNOHLGGSHLVEALVLYGGERGFFYTFKF	130 vod. oo taaooac	30 ODIALEG 94

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          34; Gaps
                                                                                                                                                   Tredrea M.M., Buck M.J., Gahaniyogi J., Squire P.L., Andrews M.T., Tredrea M.M., Buck M.J., Gahaniyogi J., Squire P.L., Andrews M.T., Reditation of PDK4 expression in a hibernating mammal.;
Submitted (JUN-201) to the EMBL/Genbank/DBSJ databases.
--- SIMICARITY: BELOWS TO THE INSULIN/GE/RELAXIN FAMILY,
EMBL AVOSB64, AAK725-88.1.
HSSP: POLGE INF.
INF.
                                       Spermophilus tridecemlineatus (Thirteen-liked ground squirrel)
Eukaryota: Metazoa: Chordata: Craniata: Vellebrata: Euteleostomi:
Mammalia: Eutheria: Rodentia: Sciurognathi, Sciuridae: Sciurinae
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Eutaleostumi.
Mammalia: Butheria: Carnivora: Pissipedia: Pelidae: Felis.
                                                                                                                                                                                                                                                                                                                                                      89.5%; Score 26%; DB 11; Length 110; 59.3%; Pred. No. 4.6e-28;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 110;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 FVNOHLCGSHLVEALYLVCGERGFFYTPKT----------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          2: Indels
                                                                                                                                                                                                                                                                                                                            12004 MW: 4511768066228EES CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PROSITE: PS00262: INSULIN: 1.
SEQUENCE 110 AA: 12069 MW: 95FB6E170C7BECA4 CRC64;
01-0FC-2001 (TrEMBLrel, 19, Last sequence update) 01-MAR-2003 (TrEMBLrel, 23, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              01-MAR-2002 (TrEMBLrel, 25, Created)
01-MAR-2002 (TrEMBLrel, 20, Last Sequence update)
01-MAR-2003 (TrEMBLrel, 23, Last annotation update)
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55.8%; Pred. No. 1.6e-26;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NA CI!
                                                                                                                                                                                                                                                                                                                                                                                   1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                              1 FVNOHLCGSHLVEALYLVCGERGFFY1PKT--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     85 ALOKRGIVEQCCTSICSLYQLENYCN 110
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      31 ---- RGIVEQCCTSICSLYQLENYON 52
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         InterPro: IPR004825; Ins/IGF/relax
Plam, PR00494; Insulin; 1,
PRINTS; PR00277; INSULINB.
SMART; SM00078; IIGF; 1,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Felis silvestris catus (Cat).
                                                                                                                                                                                                                                                                                                               PSG0262: INSULIN; 1.
                                                                                                                                                                                                                                                                                PRINTS: PROUZZZ: INSCLING
SMART: SMOUGZB: 11:3F; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Okamoto S., Morimatsu M.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Best Local Similarity 55.89
Matches 48; Conservative
                                                                                                                                                                                                                                                                                                                                                                     Best Local Similarity 59.3
Watches 51, Cobservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRELIMINARY;
                                                                                                                                                                                                                                                                   Ptam: PF00049: Insuling
                                                                                                                                                                                                                                                                                                                            110 AA;
                                                                                                                            SEUCENCE FROM N.A.
                                                                                                NCB1_Tax10-43179;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NCB1_Tax1D+9685;
                                                                                                                                           TISSUE-Paucreas;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TISSUE-Pancreas;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        insulin."
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                                                                                   Spermophilus
                                                                                                                                                                                                                                                                                                                           SEQUENCE
                                                                                                                                                                                                                                                                                                               PROSITE:
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                              Instilin
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OBWINE
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frwin D.M., Sivarajah P.;
Proinsulin cOMAS from the leopard froq, Rana pipiens: evolution of
Proinsulin processing.":
Comp. biochem. Physiol. 1258:405 410(2000).
                                                                                                                                                                                                                                                                                                                                                              Rana Elpions (Northern Jeopard froq).
Enkaryota Metazoaz Chordatas Craniatas Vertebratas Euteieostomis
Amphillas Barachias Aberra, Neobatrachias Rancideas Ranidaer Rana
NYH.Laxib 8404.
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Eukaryota: Metazoa: Chordata: Graniato: Vertebrata: Euceleostomi:
Actinopterygii; Neopterygii; Teleostel: Östeoglossomorpha:
Osteoglossiformes; Pantodoniidae: Pantonon.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 31;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   74.78; Score 219.5; 38-13; Length 106; 49.48; Pred No. 36.22;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 -:- SUBGELLUIAR LÓGATION: SPYRETEO (BY SIMITARITY).
-:- SIMILARITY: BELONGS TO THE INSULINZIGEZELLAXIN FAMILY
EMBL: AF227187: AAF87285.1; -:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     106 AA; 12183 MW; 3A870EEC70217F92 CRC64;
                                                                                                                                                                                                                                                   61 OCT-2000 (TERMLIE), 15, Created)
01-OCT-2000 (TERMLIE), 15, Jast sequence update)
01-MAR-2003 (TERMLIE), 23, Last annotation update)
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01-30N-2001 (TIEMBLIEL, 17, Last sequence update)
01-MAR-2003 (TIEMBLIEL, 23, LAST annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ٠.
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                                                                                                                                                                                                     106 AA
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7: Mismatches
                                 85 PLOKRGIVEOCCASVCSLYQLEHYCN 110
--- RGIVEQUOTSICSLYQLENYCN 52
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            444744 : (114 44111)
84 KPGIVEOCCHNFCSLYDLENYCN 106
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          -GIVEQCCTSICSLYOLENYCN 52
                                                                                                                                                                                                     P8.7;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 InterPro: TPK004825: Ins/IGF/reiax
Term: PP00494: Insulin: 1.
PRINTS: PR00277: INSULINS:
SMART: SM00078: IIGF: 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDILINE-20362507; Pubmod 10418274;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Best Local Similarity 49.4
Matches 41; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRELIMINARY:
                                                                                                                                                                                                     PRELIMINARY;
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                                                                                                                                                                                                                                                                                                                                               Preproissulia.
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   <u>-</u>
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                                                                                                                                          RESULT 4
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Created)
Last sequence update)
Last annotation update)
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Chitala chitala (clown kniiefish).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Literard: 1PR004825; lbs/tdb/telax
Pram: PP00494; lbsu.in: 1.
PRINTS: PR06277: TNSULINB:
SMART: SM00078; l1GE: 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 31 RGIVEQCCTSICSLYGLENYCN 52
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Ptam; PF00049: Insulin; 1,
SARAT: SAM0076: IIGF; 1,
NON-TER ill 111
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           66.5%;
45.1%;
               19,
19,
23,
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Best Local Similarity 45.1v
Best Local Similarity 45.1v
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Best Local Similarity 44.29
Matches 38; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRELIMINARY;
            01-DEC-2001 (TrEMBLrel, 01-DEC-2001 (TrEMBLrel, 01-MAR-2003 (TrEMBLrel,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NCBI_1axID=112163;
                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                  NCBI_TaxID-72446;
                                                                                                          Preproinsulin.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE
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               SORRERERENCE OCCOORDED TO THE SORRER OCCOORDED TO THE 
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                                                                                                                                                                                                                                                                                                          35; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Brachydanio rerio (Zebrafish) (Danio rerio,
Eukaryota: Metazoa: Chordata: Craniaia: Ver orata: Euteleostomi:
Actinopteryati: Neopteryati: Teleoster: Ostariophysi: Eyplimiformes:
Cyprinidae: Danio.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEGUENCE FROM N.A.
MEDLINE-94425190; PubMed-10495291;
Arquiton F., Zecchin E., Bortolussi M.;
Edijy appearance of pancreatic hormone expressing cells in the
Zetiafish embryo.";
                                                                                                                                                                                         DB 13; Length 110;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DB 13; Length 108;
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-: SUBLIARLY: BELONGS TO THE INSULIN/IGE/RELAXIN FAMILY.
EMHI, AJ237750: CAC20109.1; -.
HSSP: ROAGE 180526-110: h.s.
InterPro: JPROG4225, 108/IGE/relax.
PHO04425, INS/IGE/relax.
                                                                                                                                                                   Score 201.5; DB 13; Lengum
Pred, No. 8.9e.20;
S. Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  66.5%; Score 195.5; DB-13; Length
45.1%; Pred; No. 5.8e-19;
Live 5; Mismatches 7; Indels
Interpro; IPR004825; Ins/IGF/relax.
Pfam; PF06049; Insulin; 1
SMART; SM00078; ILGE, ILGE, ILGE, SMORTS; SMOOTS; ILGE, ILGE, SEGUENCE, PS00262; INSULIN; 1.
SEQUENCE, 110 AA; 12324 MW; BDECCD659 972E06 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           24 53 INSULIN B CHAIN.
86 108 INSULIN A CHAIN.
108 AA; 11964 MW: 3195289572AD6025 CRC54;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          01-MAR-2001 (TrEMBLrel. 16, Created)
01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    108 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           106 AN
                                                                                                                                                                                                                                           8; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     POTENTIAL.
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86 KVKK33VEQCCHHPCNIED ONYON :::
                                                                                                                                                                                                                                                                                                                                                                                                                           31 ---RGIVEQCCTSICSLYQLENYCN 52
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                                                                                                                                                                                      68.58;
43.58;
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                                                                                                                                                                                   Query Match
Best Local Similarity 43.5
Matches 37; Conservative
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Matches 37, Conservative
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0902N4
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Catla catla (catla).
Eukaryota: Metazoa: Chordata: Graniata: Vertebrata: Euteleostomi;
Actinopterygii; Neopterygii; Teleostei: Ostariophysi: Cypriniformes:
Cyprinidae: Catla.
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Actinopteryaii; Neopterygii: Teleostel; Osteoglossomorpha:
Osteoglossiformes; Notopteridae; Chitala.
                                                                                                                                                                                                                                                            Bhattacharya S., Roy S.S., Dasqupta S., Ravikumar L., Mukherjee Bandyopadhyaya I., Wakabayasi K.; "A new celi secreting insulin": "A new celi secreting insulin": Submitted (APR-2001) to the EMBL/GeoBank/DDR; databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    33;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 195.5; DB 13; Length 108; Pred, No. 5.8e-19; 5; Mismatches 7; Indels 33;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  66.3%; Score 195; DB 13; Length 111; 44.2%; Pred. No. 7e-19; Live 3; Mismarches 9; Indels 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDI, INE-21203577; Put.Med-1120517; MEDI, INE-21203577; Put.Med-1120517; Medine L.C., Youson J.H.; Amahrouki A.A., Irwin D.M., Graham L.C., Youson J.H.; Molecular cloning of preproinsulin connection several osteoglossomorphs and a cyptibid."; Mol. Cell. Endecrinol. 174:51-58(2001).

- SUBCELLULAR LOCATION: SECRETED (BY SIMILARITY).

- SUBCELLULAR ELONGS TO THE INSULIN/IGF/RELAXIN FARILY: EMBL. AF199586; AAK28710.1.

HSSP: P01308; 11.PH.
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FMEL, APATYCE: MELONINS TO THE INSULINTIGEZEETAXIN FAMILY FMEL, APATYCE: ANESCORE OF THE TREATMENT FAMILY HSSE; ROLLOGE THE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PS00262: INSULIN; 1.
108 AA: 11881 MM: D713026E22EF5D59 CRG64;
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01-JUN-2001 (TrEMBLIF), 17, Last sequence update)
01-MAR-2003 (TrEMBLIF), 23, Last annotation update)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  2. SURDINSHLIVE (* 1447.) (* 1447.) (* 1447.) SORDINGHUSER SOUGHEVDEYPYKEQGED.
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                                                                                                                                                                                                                                                                                                                                                                          65.18; Score 191.5; DH 13; Length 111; 41.28; Pred; No. 2.1e 18; tive 10; Mismatches 5; indels 35;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             35;
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Mol. Cell. Endocrinel. 174:51-58(2001).
-!- SUBCELLOLAR LOCATION: SECRETED (BY SIMILARITY).
-!- STHILARITY: BELONGS TO THE INSULIN/IGF/RELAXIN FAMILY.
EMBL; AF195589. AAK28713.1; -.
HSSP; P01315; 1MPJ.
InterPro: JPR004255: Insylin; 1.
PRINTS; PR0049; Insulin; 1.
PRINTS; PR0049; Insulin; 1.
SMART; SM00078; IlGF: 1.
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01-JUN-2301 (TrEMBLrel, 17, Last sequence update)
01-MAR-2003 (TrEMBLrel, 23, Last annotation update)
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42.9%; Pred. No. 5.8e-18;
Live 5: Mismatches 8;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 31 ---RGIVEDOCESICSLYQLENYON 52
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDLINE=21203577; PubMed=11306171;
                                                                                                                                                                                                                                                               PROSITE; PS00262: INSULIN; 1
                                                                                                                                                                                                                                                                                                                                                                                                              est Local Similarity 41,29
atches 35; Conservative
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Matches 36; Conservative
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RESULT 12

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Actinopterydii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
Catostomidae; Catostomus.
NCBL_TaxIb=7971;
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01-MAR-2004 (TrEMBLrel. 23, Last annota : update)
01-MAR-2004 (TrEMBLrel. 23, Last annota : update)
Amblophises rupestris (Gook bass)
Eukaryota: Metazoa: Chordata: Craniala: ...retrata: Eutelrostemi;
Actinopteryaii: Neopteryqii: Neopteryqii: Telecstel; ...reivostel: Neolcieostel;
Centrarchidae: Ambloplites.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              63.4%: Score 186.5; DB 13; Lenath 108; 41.9%: Pred. No. 9.80-18; tive 4; Mismatches 9; Indels 33;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Al Mahrouki A.A., Irwin D.M., Youson J.H.;
"Misocular cloing of preproinsulin crow trom the rock bass.";
Submitted (oCT-1999) to the EMBL/Genhank/LOHK; databases.
**Submitted (oCT-1999) to the EMBL/Genhank/LOHK; databases.
**Submitted (oCT-1999) to the EMBL/Genhank/LOHK; databases.
**Submitted (oCT-1998) to the EMBL/Genhank/LOHK; databases.
**Submitted (oCT-1998) to the INSULIN/ F/METAXIN FAMILY.
**HSSP: P01308; 1LPH.
                                                                                                                                                                                                                                                                                                                                                                                                                                                         108 AA: 11873 MW; E426310696FBAFC8 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              10100 MW; E86C8B256DC69D39 CRC64;
                                                                           (TrEMBLrel. 17, Created)
(TrEMBLrel. 17, Last sequence update)
(TrEMBLrel. 23, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  VY 15
        108
                                                                                                                                                                                                      Preproinsulin (Fragment).
Catostomus commersoni (White sucker).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          4 ORLIGGSHLVEALYLVCGERGFFYTPK
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   InterPro: IPR004825; Ins/IGF/relax
Pfam: PF00049; Insulin; 1.
SMART: SMG0078; IIGF: 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      InterPro: IPR004825: Ins/IGF/relax
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PROSITE: PS00262; INSULIN: 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRUSITE; PS00262; INSULIN; 1.
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    PRELIMINARY;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Best Local Similarity
Matches 36; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              91 AA:
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                                                                                        01 - JUN - 2001
                                                                                                                       01-JUN-2001
01-MAR-2003
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NON_TER
SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A. O'blids N.A. O'blids N. C. Tichy H., Klein ...
"Molecular evolution in higher primates: gene specific and organism specific characteristics."
Submitted (MAK-2002) to the EMBL/GenBunk/HubBJ databases.
EMBL: AY092023; AAM76640.1: ...
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A. O'DUDGIN C., Tichy H., Klein J.: O'budgin C., Tichy H., Klein J.: Wolecular evolution in higher primates: gene specific and organism specific characteristics.". Submitted (MAR-2002) to the EMBL/GenBank/UDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Gorilla,
NCBI_TaxID=9593,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Pongo pygmaeus (Orangutan).
Eukaryota: Metazoa: Chordata: Craniata: Verfebrata: Eufeleostomi:
Mammalia: Eutheria: Primates: Catarrhini: Hominidae: Pongo.
                                                                39:
63.1%; Score 165.5; DH 13; Length 91; 40.9%; Pred. No. 1.1e-17;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 146; DB 6; Length 55;
Pred, No. 2e-12;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 146: DB 6; Length 65;
                                                                Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            0; 1ndels
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01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
Insulin (Fragment).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ol-MAR ZOS (TrEMBGrel, 25, Last sequence qefite)
Ol-MAR-ZeOs (TrEMBGrel, 2s, East ambdation update)
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                                                                                                                 4 OHLCGSHLVEALYLVCGERGFFYTPK------
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                                                             5; Mismatches
                                                                                                                                                                                                                                  TRGIVEQCCTSICSLYQLENYCN 52
                                                                                                                                                                                                                                                                                         5
                                                                                                                                                                                                                                                                    64 MEMMYKRGIVEQCCHHPCNIFDLGRYCN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Created)
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NON TER 1
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Gorilla gorilla (gorilla).
                                                             Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                      PRELLIM: NARY;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ol-MAK-ZODS (FERMSLE).
01-MAK-ZODS (TERMSLE).
Query Match
Best Local Similarity
Matches 36: Conserv
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Best Local Similarity
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OBHZ81
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Search completed: September 15, 2003, 12:03:30 Job time: 21:3154 secs

us-09-423-100-6.rag

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GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.
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- protein search, using sw model OM protein September 16, 2003, 12:31:20 ; Search time 31.642 Seconds Run on:

(without alignments) 536.746 Million cell updates/sec

US-09-423-100-6

Title:

587

1 MFPTIPLSRLFDNAMLRAHR.....IVEQCCTSICSLYQLENYCN 107 Sequence:

Scoring table:

BLOSUM62 Gapop 10.0 , Gapext 0.5

1107863 seqs, 158726573 residues Searched:

1107863 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database:

/SIDS1/gcgdata/geneseq/geneseqp-emb1/AA1999.DAT:* /SIDS1/gcgdata/geneseq/geneseqp-emb1/AA2000.DAT:* /SIDS1/gcgdata/geneseq/geneseqp-emb1/AA2001.DAT:* /SIDS1/gcgdata/geneseq/geneseqp-emb1/AA2001.DAT:* /SIDS1/qcqdata/geneseq/geneseqp-embl/AA1989.DAT:* /SIDS1/qcqdata/geneseq/reneseqp-embl/AA1990.DAT:* /SIDS1/qcqdata/geneseq/geneseqp-embl/AA1991.DAT:* /SIDS1/qcqdata/ygeneseq/geneseqp-embl/AA1992.DAT:* /SIDS1/gcgdata/geneseg/genesegp-embl/AA2003.DAT:* /SIDS1/gcgdata/geneseq/geneseqp-embl/AA1980.DAT:* /SIDS1/gcqdata/geneseq/geneseqp-emb1/AA1982.DAT:*/SIDS1/gcqdata/geneseq/geneseqp-emb1/AA1983.DAT:*/SIDS1/gcgdata/geneseq/geneseqp-emb1/AA1984.DAT:* /SIDS1/gcgdata/geneseq/geneseqp-embl/AA1985.DAT:*/SIDS1/gcgdata/geneseq/geneseqp-embl/AA1986.DAT:*/SIDS1/gcgdata/geneseq/geneseqp-embl/AA1987.DAT:*/SIDS1/gcgdata/geneseq/geneseqp-embl/AA1987. /SIDS1/gcqdata/geneseq/geneseqp-emb1/AA1993.DAT: /SIDS1/gcgdata/geneseq/geneseqp-emb1/AA1994.DAT: /SIDS1/gcgdata/geneseq/geneseqp-emb1/AA1995.DAT: /SIDSI/gcgdata/geneseq/geneseqp-emb1/AA1996. /SIDSI/gcgdata/geneseq/geneseqp-emb1/AA1997. /SIDS1/gcgdata/geneseq/genes A Geneseq 19Jun03:* 35

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Overy Score Match Length DB ID Description	100.0 107 20	555.5 94.6 150 20 AAY42861 Chimeric protein	53.7 116 17 AAR98897	51.8 63 15 AAR68900	51.8 117 17 AAR98896	51.5 137 16 AAR71692	50.9 56 15	50.9 56 16 AAR78665	
Score 1	1								
Result No.		7	m	4	S	9	7	œ	

Fusion protein con	factor.	Mating ractor alpn		Proinsulin analogu	Glycosylphosphatid	Example of human i	Preproinsulin 1.	pKV142 modified in	Modified pJB59 mod	Modified pJB59 mod	N-terminally exten	Amino acids encode	EEAEPK-MI3 insulin	DNA construct pAK7	pAK855 protein seq	Synthetic leader p	Insulin precursor	EEAEPK-MIS insulin	Amino acids encode	evistae	factor	factor	Di-Arg-(831-32)-Hu	Insl double-chain	Protein sequence o	A Bacillus pectate	Amino acids encode	 EEAEPK-MIl insulin 	Human proinsulin a	Amino acids encode	Human preproinsuli	Signal-leader-p-in	Yeast signal/leade	Sedneuce encoded p	Signal peptide/lea
AAR78662	MAR/1034	AAR/Ibys	AAY42859	AAR04582	AAR79056	AAR11899	AAW47365	AAR87086	AAR96047	AAR96048	AAR88188	AAP94645	AAW19240	AAW69160	AAW78751	ABB82578	ABP55059	AAW19242	AAP94643	AAW04890	AAR71693	AAR71690	AAR65883	AAW18007	AAW78752	AAB30705	AAP94644	AAW19241	AAP20002	AAP94648	AAY53589	AAP94649	AAR71684	AAP71019	AAR88179
16	9 (9 6	?	1	16	12	19	7	7	-	7) 	18	19	19	24	24	18	10	17	16	16	-	~	-	22	10	18	3	ã	2	16	16	œ	17
96	* *	4 C	25	57	160	52	65	138	58	59	65	109	123	123	124	124	124	125	138	138	140	140	53	53	117	408	94	120	9	105	153	102	104	55	8
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IÇ I				4	4	4	4	*	4	*	*	4	4	4	4	4	4	4	4	4	4	4	4	4	4	4	4	4	4	4	4	4	4	4	4
299	7	22.5	734	293	288.5	287	287	287	284.5		284.5				284.5		284.5	284.5	284	284	284	284	283.5	283.5	283.5	283.5	282	282	Θ	281.5	8	281	281	æ	280.5
01	17	77	13	14	15	16	17	18	19	20	21	22	23	24	25	56	27	28	29	30	31	32	33	34	35	36	37	38	39	40	41	42	43	44	45

ALIGNMENTS

AAY42860 standard; protein; 107 AA. AAY42860; RESULT 1

19-JAN-2000 (first entry)

hGH-mini-proinsulin chimeric protein.

Insulin; precursor; growth hormone; chaperone; intramolecular; folding; conformation; chimeric protein; cleavable; recombinant; production; yield.

Synthetic. Homo sapiens.

07-0CT-1999. BX B

98WO-CN00052. 31-MAR-1998;

98WO-CN00052. 31-MAR-1998; (TONG-) TONGHUA GANTECH BIOTECHNOLOGY LID.

WPI; 1999-610839/52.

New chimeric proteins containing human growth hormone fragment, used

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This sequence represents a chimeric protein, which contains an N-terminal fragment of human growth hormone (hCH) of the sequence given in AAY42865, a cleavable petide linker (AAY42857), and a human insulin precursor comprisaing it to fold correctly. The hCH nortion of the chimeric protein acts as an intramolecular chaperone (IMC) for the chimeric protein acts as an intramolecular chaperone (IMC) for the chimeric protein to be removed after folding has taken place. Production of recombinant human insulin vith correctly linked cystoine bridges with fewer necessary procedural steps, and hence resulting in a higher protein can provide human insulin with correctly linked cystoine bridges with fewer necessary procedural steps, and hence resulting in a higher promote the folding of the fused insulin precursor, facilitate the solubility of the fusion protein and decrease the intermolecular interactions among the fusion proteins, thus allowing folding of the fusion proteins, thus allowing folding of the concentrations. The procedural steps of cyanogen bromide cleavage, oxidative sulphifolysis and related purification steps can thus be eliminated, along with the use of hydrophobic absorbent
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          61 TPSNREETQQKSNLELLRISLLLIQSMLEPVQLGTGPRFVNQHLGGSHLVEALYLVGGER 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 MFPTIPLSRLFDNAMLRAHRLHQLAFDTYQEFEEAYIPKEQKYSFLUNP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Insulin; proinsulin; hybrid polypeptide; protein folding;
enzymatic cleavage; cyanogen bromide; sulphitolysis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             particularly for the production of human insulin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GFFYTPKTRGIVEQCCTSICSLYQLENYCN 107
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Mendelovitz S;
                                  Claim 14; Page 30-31; 46pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (BIOT-) BIO-TECHNOLOGY GENERAL CORP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SOD-proinsulin hybrid polypeptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAR98897 standard; Protein; 116
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           94.68;
71.38;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           952A-0000142.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Hartman JR,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity
Matches 107; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 150 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    29-DEC-1994;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            W09620724-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      29-DEC-1994;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           10-JAN-1995;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                03-FEB-1997
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     20
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                                                            This sequence represents a chimeric protein, hGH-mini-proinsulin.

This chimeric protein contains an N-terminal fragment of human growth hormone (hGH) of the sequence given in AAV4285, a cleavable peptide linker (AAV42857), and a human insulin precursor comprising insulin A and B chains (AAY42857). The hGH portion of the chimeric protein acts as an intramolecular chaperone (IMC) for the insulin precursor, can intramolecular chaperone (IMC) for the insulin precursor, can be chained in the fold correctly. The cleavable peptide linker has a C-terminal Arg residue which enables the hGH portion of the chimeric protein to be removed after folding has taken place. Production of the combinant human insulin via an hGH-proinsulin chimeric protein can provide human insulin with correctly linked cysteine bridges with fewer necessary procedural steps, and hence resulting in a higher yield of human insulin with correctly linked cysteine bridges with fewer necessary procedural steps, and hence resulting in a higher yield of human insulin adelaction by a microoraganism host, but also promote the folding of the fused insulin precursor, facilitate the solubility of the fusion protein and decrease the intermolecular interactions among
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ö
                                                                                                                                                                                                                                                                                                                                                          the fusion proteins, thus allowing folding of the fused insulin precursor at commercially useful high concentrations. The procedural steps of cyanogen bromide cleavage, oxidative sulphitolysis and related
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 MFPTIPLSRLFDNAMLRAHRLHOLAFDIYQEFEEAYIPKEQKYSFLQNPLGTGPKFVNQH 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 MFPTIPLSRLFDNAMLRAHRLHQLAFDIYQEFEEAYIPKEQKYSFLONPLGTGPRFVNQH 60
                                                                                                                                                                                                                                                                                                                                                                                                               purification steps can thus be eliminated, along with the use of high concentrations of mercaptan or the use of hydrophobic absorbent resins
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           New chimeric proteins containing human growth hormone fragment, used
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             conformation; chimeric protein; cleavable; recombinant;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ..
O
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Insulin; precursor; growth hormone; chaperone; intranolecular;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     100.0%; Score 587; DB 20; Length 107; 100.0%; Pred. No. 4e-42; ive 0; Mismatches 0; Indels 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                particularly for the production of human insulin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (TONG-) TONGHUA GANTECH BIOTECHNOLOGY LTD.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAY42861 standard; protein; 150 AA
                                  Claim 13; Page 30; 46pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              98WO-CN00052
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Chimeric protein, SEQ ID 7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          al Similarity 100.
107; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WPI; 1999-610839/52.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    107 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              production; yield.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              31-MAR-1998;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Synthetic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sednence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAY42861;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               folding;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RESULT 2
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64 -----

Gaps

Indels

Length 150;

DB 20;

us-09-423-100-6.rag

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Pro-insulin is produced by treating recombinant precursor protects with a mercaptan to provide 2-10 SH residues per Gys residue. In presence of a chaotropic agent and in ag. medium of pH 10-11. It reating the prod, with 3-50 g hydrophobic adsorber resin per i and desorbing the prod, with 3-50 g hydrophobic adsorber resin per i and desorbing the pro-insulin. This method produces pro-insulin and desorbing the pro-insulin. This method produces pro-insulin with correctly bonded Cys bridges. Compared with known methods in involves fewer stages (egp. no sulphitolysis or cyanogen bromide the process is quicker and gives better yields.

C sequences of insulin chain A, b and C are given in AAR68895-97.

Sequences of pro-insulin 14 are given in AAR68898-901.

(Updated on 25-MAR-2003 to correct PN field.)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        51 GTGPREVNQHLGGSHLVEALYLVCGERGFFYTPKTKGTVEOCCTSICSLXGLENYCN 107
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A new method for the production of recombinant human insulin comprises folding a hybrid polypeptide comprising proinsulin under conditions that permit correct disulphide bond formation and subjecting that folded protein to enzymatic cleavage. The insulin produced can then be purified. This sequence is a SOD-insulin B chain-Lys-Arg-insulin A chain hybrid polypeptide and is encoded by the plasmid construct pBAST-R. Transformation of the proper E.coli
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Recombinant insulin prodn. by correctly folding pro-insulin hybrid polypeptide - then enzymatic cleavage of folded product, does not require sulphite protection of SH nor use of cyanogen bromide
                                                                                                                                                                                                                                                                                                                                                                                                                                                            51.8%; Srore 304; DB 15; Length 63, 94.7%; Pred. No. 1.3e-18;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Insulin: proinsulin, hybrid polypeptide; protein folding;
enzymat ? cleavage; cyanogen bromide; sulphitolysis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          C: Mismatches
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                                         Disclosure: Page 11-12; 15pp; German.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Example 1A; Figure 6; 69pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (BIOT-) BIO-TECHNOLOGY GENERAL CORP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAR98896 standard; Protein; 117 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SOD-proinsulin hybrid polypeptide.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                94WO-US13268.
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ses 54; Conservative
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  hydrophobic resin
                                                                                                                                                                                                                                                                                                                                                                                                                   63 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   N-PSDB; AAT34669
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                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   4.5 YSFL; 2NPLGT --- GPRPVNQHLCGSHLVEALYLVCGERGFFYT PKTRGTVEQCCTSLCSL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                 Recombinant insulin prodm. by correctly tolding pro-insulin hybrid polypeptide - then enzymatic cleavage of folded product, does not require sulphite protection of SH nor use of cyanogen bromide
                                                                                                                                                                                                                         comprises folding a hybrid polypeptide comprising proinsulin under conditions that permit correct dissulphide bond formation and subjecting that folded protein to enzymetic cleavage. The insulin produced can then be purified. This sequence is a SOD-insulin broduced can then be purified. This sequence is a SOD-insulin broduced can then be purified. This sequence is a SOD-insulin by the plasmid construct pDBAST-LAT. Transformation of the proper E.coli host cells with pDBAST-LAT results in the efficient expression of the proinsulin hybrid polypeptide. Wasful for human insulin producion, the method produces recombinant human insulin identical to the natural hormone. Hazardous and cumbersome
                                                                                                                                                                                                                                                                                                                                                                                                                                                     procedures involving cyanogen bromide and sulphitolysis to protect. SH groups are avoided since the entire hybrid polypeptide folds efficiently to the native structure even with the leader attached
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Prodn. of pro-insulin with correct dissulphide bridges · by treating recombinant precursor protein with mercaptan in alkali and in presence of chaotropic agent, then isolation on
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ~
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DB 17; Length 116;
                                                                                                                                                                                                      A new method for the production of recombinant human insulin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    5: Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Pro-insulin: A-chain: B chain; C-chain; disulphide;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 315.5; DB I'
Pred. No. 2.5e-19;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2: Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sabel W
                                                                                                                                                          Example 1B; Figure 7; 69pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAR68900 standard: peptide; 63 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gerl M, Ludwig J, Obermeier R,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      53.7%;
85.3%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (updated)
(first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Local Similarity 85.3 tes 58; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               and Cys unprotected.
1996-333766/33
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         116 AA;
                     N-PSDB; AAT34670
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     25-NOV-1993;
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02-MAR-1995
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Matches

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AAR68900 RESULT

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Indels

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Human pro-insulin 3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WPI; 1994-177718/22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gerl M, Ludwig J,
                                                                                                                                                                                                                                                                                                                                                                                                                                                           (FARH ) HOECHST AG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                hydrophobic resin
                                       137 AA
                                                                                                                                                                                                                                                                                                                                                             Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                     25-NOV-1993;
                                                                                                                                                                                                                                                                                                                                                                                                                                         02-DEC-1992;
                                                                                                                                                                                                                                                                                 25-MAR-2003
                                                                                                                                                                                                                                                                                                                                                                               EP600372-A1
                                                                                                                                                                                                                                                                                             02-MAR-1995
                                                                                                                                                                                                                                                                                                                                                                                                  08-JUN-1594
                                                                                                                                                                                                                                                               AAR68901;
                                       Sequence
                                                         Query Match
                                                                              Matches
                                                                                                                                                                                                                          RESULT 7
                                                                                                                                                                                                                                    AAR68901
   8×3333
                                                                                                                                                                                            q
                                                                                                                                                                                                                                                      g
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                                                                                                                                                        g
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                                                                                                                                   AAQ86425 encodes AAR71692 mating factor alpha 1-Insulin precursor ArgB13. ArgB13 comperises the B and A chains of a claimed human insulin derivative. In the final claimed compsn. they are covalently connected via disulphide bonds between Cys residues A7/B7 and
                                                                                                                  Gaps
host cells with pBAST-R results in the efficient expression of the proinsulin public projection of the proinsulin projection or the method produces recombinant human insulin identical to the natural hormone. Hazardous and cumbersone procedures involving evanogen bromide and sulphitolysis to protect SH groups are avoided since the entire hybrid polypeptide folds efficiently to the native structure even with the leader attached and Cys improtected.
                                                                                                                  4
                                                                                              51.8%; Score 304; DB 17; Length 117; 82.6%; Pred. No. 2.3c-18; tive 3; Mismatches 5; Indels
                                                                                                                                                                                                                                                                                                                              precursor ArgB31; diabetes; Zinc ion complex; alpha 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         present as a Zinc ion and is rapid acting.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Jonassen I;
                                                                                                                                                                                                                                                                                                              Mating factor alpha 1-Insulin precursor ArgB31.
                                                                                                                                                                                                                                                                                                                                                                                                  /label- mating factor alpha-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Havelund S,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Acylated insulin deriv. which may be complex - is used to treat diabetes
                                                                                                                                                                                                                                                                                                                                                                               Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Example 5; Page 78; 100pp; English.
                                                                                                                                                                                                                                            AAR71592 standard: Protein: 137 AA
                                                                                                                                                                                                                                                                                                                                                                                                                     /label- B-chain
                                                                                                                                                                                                                                                                                                                                                                                                                            117..137
/label- A.chain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               94WO-DK00347
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 93DK - 0001044
94US - 0190829
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Halstrom JB,
                                                                                                                                                                                                                                                                                             (tirst entry)
                                                                                                         Best Local Similarity 82.6
Matches 57; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                          ..116
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (NOVO ) NOVO-NORDISK AS
                                                                                                                                                                                     109 LYQLENYCN 117
                                                                                                                                                                          99 LYQLENYCN 107
                                                                                                                                                                                                                                                                                 (updated)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WPI; 1995-131314/17.
                                                                             117 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      N-PSDB; AAQ86425
                                                                                                                                                                                                                                                                                                                             Human insulin
                                                                                                                                                                                                                                                                                                                                          mating factor
                                                                                                                                                                                                                                                                                                                                                            Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                          W09507931-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              16-SEP-1994;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Andersen AS,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  17-SEP-1993;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           02-FEB-1994;
                                                                                                                                                                                                                                                                                 25-MAR-2003
                                                                                                                                                                                                                                                                                            20-NOV-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             23-MAR-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Markussen J
                                                                                                                                                                                                                                                               AAR71692;
                                                                               Seguence
                                                                                                Query Match
                                                                                                                                                                                                                                                                                                                                                                                        Protein
                                                                                                                                                                                                                                                                                                                                                                                                           Peptide
                                                                                                                                                                                                                                                                                                                                                                                                                              Pept. ide
                                                                                                                                                                                                                          RESULT 6
                                                                                                                                                                                                                                   AAR71692
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   8×8668888×8
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48
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                                                                                                                                                                                                                                                                                                                                                                                                                                                  87
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    pro-insulin is produced by treating recombinant precursor protein with a mercaptan to provide 2-10 SH residues per Cys residue, in presence of a chaotropic agent and in aq. medium of pH 10-11, treating the prod. with 3-50 g hydrophobic adsorber resin per i aq. medium of pH 4-7, isolating he adsorbed resin and pro-insulin and desorbing the pro-insulin. His method produces pro-insulin with correctly bonded cys bridges. Compared with known methods it involves fewer stages (esp. no sulphitolysis or cyanogen bromide cleavage) and overall losses during purification are reduced, i.e. the process is quicker and gives better yields. Sequences of insulin chain A, B and C are given in AAR68895-97. Sequences of pro-insulin 1-4 are given in AAR68898-901.
                                                                                                                                                                                                                                                                                                                                                                                                                                                     ...----PRFVNQHLCGSHLVEALYLVCGERGFFY; PKTRG
                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Prodm, of pro-insulin with correct disamphide bridges - hy
treating recombinant precursor protein with mercaptam in alkaim
and in presence of chaotropic agent, then isolation on
                                                                                                                                                                                                                                                       39;
                                                                                                                                                                                       DB 16; Length 137;
                                                                                                                                                                                                                                                                                                                    2 FPTIPLSRLFDNAMLRAHRLHQLAFDTYQEFEEAYIPKEQ--KYSFLQ--
A20/B19. The derivative, which may be present as a zinc ion complex, can be used as a fast action treatment for diabetes (Updated on 25-MAR-2003 to correct PN field.)
                                                                                                                                                                                       51.5%; Score 302.5; UB 16; Length
50.0%; Pred. No. 3.6e-18;
.ive 4; Mismatches 27; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Pro-insulin: A-chain; B-chain; C-chain; disulphide;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 3
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Disclosure, Page 12; 15pp; German.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   88 IVEOCCTSICSLYQLENYCN 107
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 118 IVEOCCTSICSLYQLENYCN 137
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAR68901 standard; peptide:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           mercaptan: chaotropic agent
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      92DE-4240420
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (updated)
(first entry)
                                                                                                                                                                                                                         Local Similarity 50.0° nes 70; Conservative
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55 REVNQHICGSHLVEALYLVCGERGFFYTPKTRGIVEQCCTSICSLYQLENYCN 107
bridges. Reaction with trypsin and opt. carboxypeptidase B yields correctly folded insulin. The insulin is isolated by absortion on
                       a hydrophobic resin.
                                              56 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                      25-NOV-1993;
                                                                                                                                                                                                                                                                                                                                                                                                                                            02-DEC-1992;
                                                                                                                                                                                                                                                                                                                                                 Home sapiens
                                                                                                                                                                                                                                                   25-MAR-2003
                                                                                                                                                                                                                                                                                                                                                                       EP600372-A1
                                                                                                                                                                                                                                                                                                                                                                                              08-JUN-1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
                                               Sequence
                                                                                                                                                                                                                           AAR68899
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gerl M,
                                                                                                                                                                             RESULT 9
                                                                                                                                                                                       AAR68899
 202×8
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O
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                                                          Caps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             presence
                                                                                                                                                                                                                                                             Proinsulis; post-translational modification; recombinant production: protein folding; conformation.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Isolation of insulin that is correctly post-translationally processed - by reacting pro:insulin with a mercaptan in the presence of a chaotropic agent and purificn. after absorption to hydrophobic
                                                                                 55 REVNQHLCGSHLVEALYLVCGERGFFYTPKTRGIVEQCCTSICSLYQLENYCN 107
                                                                                             4 REVNOHLGGSHLVEALYINGGENGEFFTPKTRGIVEQCCTSICSLYGLENYCN 56
                                                          ö
                                 Length 56;
                                                         Indels
                                                                                                                                                                                                                                                                                                                                                           /note= "a peptide of 4 amino acids"
                                                         0:
                                 Score 299; DB 15;
Pred. No. 3.2e-18;
                                                                                                                                                                                                                                                                                                                                                                                 /label= K1-(B2-B29)·Y
/note= "human insulin B-chain"
                                                                                                                                                                                                                                                                                                                                                                                                                                                       /note- "human insulin A-chain"
                           50.9%; Sco.,
100.0%; Pred. No. ...
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sabe: W;
                                                                                                                                                                                                                                                                                                                                                                                                                                 36..56
/label- Gly-(A2-A20)-R3
                                                                                                                                                                                                                                                                                                                         Location/Qualitiers
                                                                                                                                                                 AAR78665 standard; protein; 56 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Example 2; Page 13; 16pp; German.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Obermeier R,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             95EP-0101748
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   94DE-4405179
                                                                                                                                                                                                                                                                                                                                                /label- R2
                                                                                                                                                                                                                 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                    /label x x
                                                         53; Conservative
                                                                                                                                                                                                                                        Proinsulin sequence 3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gerl M, Ludwig J,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WPI; 1995-284754/38
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (FARH ) HOECHST AG
                                               Similarity
             56 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    18-FEB-1994;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             09-FEB-1995;
                                                                                                                                                                                                                03-APR-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EP668292-A2
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                                                                                                                                                                                                                                                                                                   Synthetic
              Sequence
                                                                                                                                                                                        AAR78555
                                  Query Match
Best Local
                                                                                                                                                                                                                                                                                                                                                                       Pept ide
                                                                                                                                                                                                                                                                                                                                                                                                                                 Peptide
                                                                                                                                                                                                                                                                                                                                      Region
                                                                                                                                                                                                                                                                                                                                                                                                          Region
                                                           Matches
                                                                                                                                                       AAR7856°
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Fro insulin is produced to treating recombinant precursor protein with a mercaptan to pro. .e 2-10 SH residues per Cys residue, in presence of a chaotropic agent and in aq. medium of pH 10-11, creating the prod. with 3-50 g hydrophobic adsorber resin per I aq. medium of pH 4-7, isolating the adsorbed resin and pro-insulin and desorbing the pro-insulin. This method produces pro-insulin with correctly bonded Cys bridges. Compared with Known methods it involves fewer stages (esp. no sulphitolysis or cyanogen bromide the process is quicker and gives better yields.

C the process is quicker and gives better yields.

C sequences of insulin chain A, B and C are given in AAR68895-97.

Sequences of pro-insulin I-4 are given in AAR68898-901.
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                                                        Sales
                                                                                                         55 REVNQHLCGSHLVEALYLANGERGFFYTPKTRGIVEQCCTSICSLYQLENYCN 107
                                                                                                                                     4 REVNOHLOGSHLVEALYLVGGERGEFYTPKTRGIVEGCCTSICSLYGLENYCN 5-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              in alkalı
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 96;
Length 56,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Prodm. of pro-insulin with creek dissulphide bridges
treating recombinant precular protein with mercaptan is
and in presence of chack pic agent, then isolation on
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Pro-insulin; A chain; B chain; G-chain; disulphide;
mercaptan; chaotropic agent.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       50.9%; Score 299; DB 15;
100.0%; Pred. No. 5.1e-18;
tive 0; Mismatches 0;
  Score 299; DB 16;
Pred. No. 3.2e-18;
           100.0%; Pred. mc.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sabel
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Disclosure: Page 11; 15pp; German.
                                                                                                                                                                                                                                                                                                  AAR68899 standard: peptide: 96 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  œ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Operment
  50.98;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   93EP-0118993.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                (first entry)
  Query Match 50.9°
Best Local Similarity 100.
Matches 53; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                    (updated)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Human pro-insulin 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Ludwig J,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WPI; 1994-177718/22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Best Local Similarity
Matches 53; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (FARH ) HOECHST AG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           hydrophobic resin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    96 AA;
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Gaps

Indels

44

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The present sequence is that of a fusion protein, produced in E.coli which contains an example of a proinsulin molecule corresp.

To the general formula R2-R1-(B2-B29)-Y-X-G1y (A2-A20)-R3 (II). In formula (II), X = Lys, Arg or a peptide of 2-35 amino acids contg.

Lys or Arg at the N- and C-termini; Y = a natural amino acid; R1 = C Phe or a bond; R2 = H, Arg, Lys, a peptide of 2-35 amino acid; R1 = C Phe or a bond; R2 = H, Arg, Lys, a peptide of 2-45 amino acid; R1 = C Phe or a bond; R2 = H, Arg, Lys, a peptide of 2-45 amino acid; R1 = C Arg or Lys at the N- and C-termini; R3 = a natural amino acid; (A2-A20) and (B2-B29) are the insulin A- and B-chain sequences contg. Arg or Lys at the N- and C-termini, R3 = a natural amino acid; (A2-A20) and (B2-B29) are the insulin A- and B-chain sequences of acid, (A2-A20) and (B2-B29) are the insulin A- and B-chain sequences of a chaotropic auxiliary agent at residues of mercaptan per Cys residue of proinsulin. The reaction C takes place in the presence of a chaotropic auxiliary agent at phiddes. Reaction with trypsin and opt. carboxypeptidase B yields correctly folded insulin. The insulin is isolated by absortion on
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Isolation of insulin that is correctly post-translationally processed - by reacting pro:insulin with a mercaptan in the presence of a chaotropic agent and purificn. after absorption to hydrophobic
                                                                                                                                                                  post-translational modification; recombinant production;
                                                                                                                                                                                                                                                                                                    "a peptide of 4 amino acids"
                                                                                                                                                                                                                                                                                                                                                                                                                                     /note- "human insulin A-chain"
                                                                                                                                                                                                                                                                                                                                                /note- "human insulin B-chain
                                                                                                                                   Fusion protein contg. proinsulin sequence 3.
                                                                                                                                                                                                                                                                                                                                                                                                     76..96
/label= Gly-(A2-A20)-R3
                                                                                                                                                                                                                                                                                                                                    R1-(B2-B29)-Y
                                                                                                                                                                                                                                                    Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Example 2; Page 8; 16pp; German
                               AAR78662 standard; protein; 96
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Obermeier
                                                                                                                                                                                  protein folding; conformation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        95EP-0101748
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                                                                                                                                                                                                                                                                    41..44
/label- R2
                                                                                                   (first entry)
                                                                                                                                                                                                                                                                                                                                                                                     /label- x
                                                                                                                                                                                                                                                                                                                            label-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WPI; 1995-284754/38
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Ludwig J,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (FARH ) HOECHST AG.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      09-FEB-1995;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        8-FEB-1994;
                                                                                                   03-APR-1996
                                                                                                                                                                    Proinsulin;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EP668292-A2
                                                                                                                                                                                                                    Synthetic
                                                               AAR78662;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gerl M,
                                                                                                                                                                                                                                                                                                                                                                                                   Peptide
                                                                                                                                                                                                                                                                                                                     Pept.ide
                                                                                                                                                                                                                                                                    Region
                                                                                                                                                                                                                                                                                                                                                                       Region
RESULT 10
AAR78662
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Sabel W;

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Caps
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                                                                                                                                                                                                                                             ArgB31; diabetes; Zinc ion complex;
                                                                                                                                                                                                                     precursor ArgBl, ArgB31 N-terminal.
                                                 SERGFFYTPKTRGIVEQCCTSICSLYQLENYCN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         .,
                                    55 REVNOHLCGSHLVEALYLV GERGFFYTPKTRGIVEQCCTSICSLYQLENYCN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 145;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       insulin deriv. When may be present as a 2inc ion \dot{\tau} is used to treat diabetes and is rapid acting.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               avelund S, Jonassen I;
ilarity 100.0%; Pred. No. 5.1e-18;
Conservative (; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              50.9; Score 299; DB 16; 100.0% Pred. No. 7.3e-18; tive ); Mismatches 0;
                                                                                                                                                                                                                                                                                                                       1.85
/label- mating factor alpha-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (Updated on 25-MAR-2003 to correct PN field.)
                                                                                                                                                                                                                                                                                                                                                           /label- N-terminal peptide
                                                                                                                                                                                                                                                        nal EEAEAEAR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Example 5; Pages 82-83; 100pp; English.
                                                                                                                                                                                                                                                                                                         Cocation/Unalifiers
                                                                                                                              AAR71694 standard; Protein; 115 AA
                                                                                                                                                                                                                                                                                                                                                                                   /label- B-chain
125..145
/label- A-chain
                                                                                                                                                                                                                     Mating factor alpha 1-Insul:
                                                  94WO-DK00347
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                93DK-00C1044
94US-0190829
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Acylated insulin deriv. wh
                                                                                                                                                                                                                                              Human insulin precursor Arc
                                                                                                                                                                                                                                                          mating factor alpha 1; N-te
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Halstrom JB,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (NOVO ) NOVO-NORDISK AS
                                                                                                                                                                                 (updated)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WPI; 1995-131314/17.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity
Matches 53: Conserv
Best Local Similarity
Matches 53; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      145 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  N-PSDB; AAQ86429
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Andersen AS,
Markussen J;
                                                                                                                                                                                                                                                                                    Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        16-SEP-1994;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                17-SEP-1993;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             02-FEB-1994:
                                                                                                                                                                                                                                                                                                                                                                                                                                      WO9507931-A1
                                                                                                                                                                               25-MAR-2003
20-NOV-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                23-MAR-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence
                                                                                                                                                       AAR71694;
                                                                                                                                                                                                                                                                                                            Key
Protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       complex
                                                                                                                                                                                                                                                                                                                                                Peptide
                                                                                                                                                                                                                                                                                                                                                                          Peptide
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AAY42859 standard; protein; 52 AA
                                                                                                                                                                                                                                                                                                                                                                    WPI; 1999-610839/52.
                                                                                                                                                          production; yield.
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                                                                                                                                                                                                          W09950302-A1
                                                                                                                                                                                                                                                                                         31-MAR-1998;
                                                                                                                                                                                                                                                               31-MAR-1998;
                                                                                                                                                                                   Homo sapiens
                                                                           19-JAN-2000
                                                                                                                                                                                                                                      07-0CI-1999.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence
                                                    AAY42859;
                                                                                                                                           folding;
                                                                                                                                                                                                                                                                                                                                           Gan 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RESULT 14
RESULT 13
             AAY42859
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAQ86432 encodes AAR71695 mating factor alpha 1-Insulin precursor Arghl, Argala N-terminal EEAEARAER. The insulin precursor comprises the B and A chains of a claimed human insulin derivative preceded by the N-terminal amino acids EEAEAEAER. In the final claimed compsn. they are covalently connected via disulphide bonds between Cys residues A7/P3 and A20/B19. The derivative, which may be present as a zinc ion complex, can be used as a fast action treatment for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            94 RFVNOHLGGSHLVEALYLVCGERGFFYTPKTRGIVEQCCTSICSLYQLENYCN 146
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               55 RFVNQHLCGSHLVEALYLVCGERGFFYTPKTRGIVEQCCTSICSLYQLENYCN 107
Human insulin precursor ArgB1, ArgB31: diabetes: Zinc ion complex;
mating factor alpha 1; N-terminal EEAEAEAER.
                                                                                                                                                                     Mating factor alpha 1-Insulin precursor ArgBl, ArgB31 N-terminal.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 146;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Acylated insulin deriv. which may be present as a Zinc ion complex - is used to treat diabetes and is rapid acting.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Jonassen I;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         7.4e-18;
hes 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DB 16;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (Updated on 25-MAR-2003 to correct PN field.)
                                                                                                                                                                                                                                                                                         /label- mating factor alpha-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          50.9%; Score 299; DB
100.0%; Pred. No. 7.4.
ive 0; Mismatches
                                                                                                                                                                                                                                                                                                      86..94
/label- N-terminal peptide
95..125
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Havelund S.
                                                                                                                                                                                                                                                               Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Example 6; Page 85; 100pp; English.
                                                                               Ş
                                                                              AAR71695 standard; Protein; 146
                                                                                                                                                                                                                                                                                                                                          /label- B-chain
                                                                                                                                                                                                                                                                                                                                                      126..146
/label- A-chain
                                                                                                                                                                                                                                                                                                                                                                                                                                               94WO-DK00347
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        93DK-0001044
94US-0190829
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Halstrom JB,
                                                                                                                                (updated)
(first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Similarity 100.
53; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (NOVO ) NOVO-NORDISK AS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WPI; 1995-131314/17.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   146 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             N-PSDB; AAQ86432
                                                                                                                                                                                                            mating factor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Andersen AS,
                                                                                                                                                                                                                                                                                                                                                                                                                                               16-SEP-1994;
                                                                                                                                                                                                                                       Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                             W09507931-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        17-SEP-1993;
02-FEB-1994;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Markussen J;
                                                                                                                                25-MAR-2003
                                                                                                                                             20-NOV-1995
                                                                                                                                                                                                                                                                                                                                                                                                                       23-MAR-1995.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence
                                                                                                     AAR71695;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
             93
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              diabetes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Local
                                                                                                                                                                                                                                                                            Protein
                                                                                                                                                                                                                                                                                                                               Peptide
                                                                                                                                                                                                                                                                                                      Peptide
                                                                                                                                                                                                                                                                                                                                                        Peptide
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Matches
                                                     RESULT 12
                                                                AAR7169
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A and B chains. This insulin precursor is a component of the chineric proteins insulin precursor is a component of the chineric proteins high-mini-proinsulin (AAY42860) and the chimeric protein diversity and in AAY42861. These chimeric protein additionally contain an N-terminal fragment of human growth hormone (hdh) and a cleavable peptide linker (AAY42857). The hdH portion of the chimeric protein acts as an intranolecular chaperone (IMC) for the insulin precursor.

Combing it to fold correctly. The cleavable peptide linker has a chimeric protein to be removed after folding has taken place. Production of the chimeric protein to be removed after folding has taken place. Production of recombinant human insulin with correctly linked cysteine bridges with fewer necessary procedural steps, and hence resulting in a higher yield for human insulin with correctly linked cysteine bridges with fewer necessary procedural steps, and hence resulting in a higher yield from intracellular degradation by a microordanism host, but also promote the fusion protein and decrease the intermolecular interactions among the fusion proteins, thus allowing folding of the fused insulin precursor, facilitate the solubility of the fusion proteins, thus allowing folding of the fused insulin precursor, the fusion proteins, thus allowing folding of the fused insulin precursor cyanogen bromide cleavage, oxidative sulphitolysis and related purification steps can thus be climinated, along with the use of high concentrations of mercaptan or the use of hydrophobic absorbent resins.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ô
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              This sequence represents a human insulin precursor comprising insulin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     New chimeric proteins containing human growth hormone fragment, used particularly for the production of human insulin \,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    56 FVNQHLCGSHLVEALYLVCGERGFFYTPKTRGIVEQCCTSICSLYQLENYCN 107
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              | FUNDHLCGSHLVEALYLVGERGFFYTPKTRGIVEQCCTSICSI,VQLENYCN 52
                                                                                                                                                                                               conformation; chimeric protein; cleavable; recombinant;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ;
                                                                                                                                                      Insulin; precursor; growth formone; chaperone; intramolecular;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 52,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Indels
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Pred. No. 7.8e-18;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             50.1%; Scor.
160.0%; Pred. No. 7...
'... 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (TONG-) TONGHUA GANTECH BIOTECHNOLOGY LTD.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Claim 12; Page 29-30; 46pp; English.
                                                                               Human insulin precursor, SEC ID 5.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAR04582 standard; protein; 57 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity 160.v...
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              98WO-CN00052
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             98WO-CN00052
(first entry)
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ID AAR0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             This sequence is joined to the C-terminus of an N-terminal frayment. comprising opt. modified tendamistate. This fusion protein may be converted into human insulin using known methods. The synthetic gene was prepared by the phosphoramidite method.
                                                                                                                                                                   /label-Lys residue linking insulin B chain to A chain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GPI: glycosylphophatidylinositol; insulin; hormone; solubilization:
Saccharomyces cerevisiae; anchor; Gasl; plasmid pBY40.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  107
                                                         Proinsulin analogue with a Lys residue I nking the A and B chains.
                                                                                                                                                                                                                                                                                                                                                                                                                                    New insulin fusion proteins comprise pro-insulin analogue linked to tendamistate
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Glycosylphosphatidylinositol-anchored human recombinant insulin.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 55 RFVNOHLCGSHLVEALYLVCGERGFFYTPKTRGIVEQCCTSICSLYQLENYCN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               49.9%; Score 293; DB 11; Length 57; 96.2%; Pred. No. 1e-17; Live 2; Mismatches 0; Indels
                                                                                 insulin fusion protein; pro-insulin analogue; tendamistate;
Lys-Lys bridge; ds
                                                                                                                                                                                                                                                                                                                                                                         Wallmeier H;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          field.)
field.)
                                                                                                                                                                                          /label- Insulin B chain
                                                                                                                                                                                                               /label- Insulin A chain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        on 25-MAR-2003 to correct PR on 25-MAR-2003 to correct PI
                                                                                                                                            Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAR79056 standard; Protein; 160 AA
                                                                                                                                                                                                                                                                                                                                                                          Koller KP, Riess GJ, Uhlmann E,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Disclosure: Page ?; ?pp; German.
                                                                                                                                                                                                                                                                                      89EP-0120056
                                                                                                                                                                                                                                                                                                              88DE-3837273
                                                                                                                                                                                                                                                                                                                           89DE-3927449
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(first entry)
                         (updated)
(first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Best Local Similarity 96.2'
Matches 51; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                 WPI; 1990-141149/19.
                                                                                                                                                                                                                                                                                                                                                   (FARH ) HOECHST AG.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAQ04336
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           57 AA;
                                                                                                                                                                                                                                                                                                                                                                                                               N-PSDB; AAQ04335
                                                                                                                                                      misc-difference
                                                                                                                                                                                                                                                                                        28-OCT-19 9;
                      25-MAR-2003
14-SEP-1990
                                                                                                                                                                                                                                                                                                                03-NOV-1988;
                                                                                                                                                                                                                                                                                                                           19-AUG-1989;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  25-MAR-2003
24-JAN-1996
                                                                                                                                                                                                                                                                09-MAY-1990
                                                                                                                                                                                                                                          EP367163-A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Seguence
                                                                                                                       synthetic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                See also
(Updated
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AAR04582;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (Updated
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
                                                                                                                                                                                Peptide
                                                                                                                                                                                                        Peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Matches
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AAR79056
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Human recombinant insulin may be expressed in Saccharomyces cerevisiae following linkage of the gene to the quycosylphospatidylinositol auchor. This anchoring technique can provide for the release of the product in a highly specific and selective manner. In addition, the recombinant protein will contain an epitope which can be used in its final purification by immunoaffinity. The protein reduced to released by e.g. nitrous (Updated on 25-MAR-2003 to correct PI field.)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              55 RFVNQHI,CGSHLVEALYLVCGERGFFYTPKT-RGIVEQCCTSICSLYQLENYCN 107
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               43 RFVNQHLCGSHLVEALYLVCGERGFFYTPKTKRGIVEQCCTSICSLYQLENYCN 96
                                                                                                                                                                                                                                                                                                                                                             Recombinant prodn. of proteins, e.g. insulin - by producing the protein with a glycosyl:phosphatidyl:inositol anchor followed by selective release
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ä
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  49.1%; Score 288.5; DB 16; Length 160; 98.1%; Pred. No. 6.1e-17; Live 0; Mismatches 0; Indels 1;
                                                                                                                                                                                                                                                                        Cardoso De Almeida ML, Amaral De Castilho Valavicius
Gomes De Amorim Filho A;
                                                                    /note- "anchor attachment site"
                                                                                                                                                                                                                            (ESCO-) ESCOLA PAULISTA MEDICINA.
(FINE-) FINEP FINANCIACORA ESTUDOS & PROJETOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Search completed: September 16, 2003, 12:38:25 Job time : 33.642 secs
                                        Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                               Disclosure, Fig 3; 51pp; English
                                                                                                                                                                95WO-BR00010
                                                                                                                                                                                               94BR-0000600
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Conservative
                                                                                                                                                                                                                                                                                                                      WPI; 1995-302720/39.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity
Matches 53; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       160 AA;
                                                                                                                                                                                                                                                                                                                                      N-PSDB; AAQ99460
                                           Key
Misc-difference
                                                                                                      W09522614-A1
                                                                                                                                                                                               17-FEB-1994;
            Homo sapiens
                                                                                                                                                                .6-FEB-1995;
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Sequence 8, A Sequence 6, A Sequence 3, A Sequence 4, A Sequence 4, A Sequence 5,

Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence 1, Appli

Sequence 4, 7 Sequence 4, 7 Sequence 36,

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51.8%; Score 304; DB 1; Length 63; 94.7%; Pred. No. 7.3e-29; 1ve 0; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 US-08-400-256-15
US-08-468-6748-41
US-08-468-6748-45
US-08-468-6748-45
US-08-46-6748-45
US-08-46-646-3
US-08-46-646-3
US-08-46-646-3
US-08-46-646-3
US-08-46-641-3
US-09-72-1896-3
US-09-72-1896-3
US-09-23-617-3
US-09-134-836-4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ALIGNMENTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER: 1. 18m 380

OPERATING SYSTEM: WINDOWS 3.1

SOFTWARE: WORDPERFECT 5.1

CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/150,376A

FILING DATE: December 1, 1993

CLASSIFICATION DATA:
APPLICATION DATA:
APPLICATION DATA:
APPLICATION DATE: BE 4240420.7

FILING DATE: December 2, 1992

ATTORNEY/AGENT INFORMATION:
NAME: BATDATA V. MAUFER: ESQ.
RECISTRATION NUMBER: 31,287

REFERNCE/COCKET NUMBER: 406 92/F 384

TELECHONE: (908) 231-4079

TELECHONE: (908) 231-4079

TELECHONE: (908) 231-2255

INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 63 AMINO ACID AD
TOROGONE AMINO 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                384
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Best Local Similarity 94.7
Matches 54; Conservative
  COMPUTER: IBM 386
OPERATING SYSTEM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        OPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RESULT 1
US-08-160-376A-6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             US-08-160-376A-6
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     Sequence 39, Appl
Sequence 5, Appl
Sequence 7, Appl
Sequence 6, Appl
Sequence 6, Appl
Sequence 45, Appl
Sequence 48, Appl
Sequence 48, Appl
Sequence 48, Appl
Sequence 7, Appl
Sequence 19, Appl
Sequence 11, Appl
Sequence 11, Appl
Sequence 16, Appl
Sequence 16, Appl
Sequence 17, Appl
Sequence 17, Appl
Sequence 18, Appl
Sequence 18, Appl
Sequence 18, Appl
Sequence 19, Appl
Sequence 18, Appl
                                                                                                                                                                  September 16, 2003, 12:37:10 ; Search time 17.07 Seconds (without alignments) 265.217 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                                                                                                                                                                                                                                             1 MFPTIPLSRLFDNAMLRAHR.....IVEQCCTSICSLYQLENYCN 107
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Description
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                            GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd
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S. 08-291.0608.53
S. 08-126.376.75
S. 08-126.376.75
S. 08-126.376.75
S. 08-139.487.8
S. 08-130.256.48
S. 08-975.365.48
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S. 08-970.574.7
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                              otal number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                                                                                              328717 seqs, 42310858 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SUMMARIES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ost-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                                                                                        - protein search, using sw model
                                                                                                                                                                                                                                                                                                                                                             BLOSUM62
Gapop 10.0 , Gapext 0.5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Issued_Patents_AA:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            inimum DB seq length: 0 aximum DB seq length: 20000000000
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Match Length DB
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rfect score:
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No.
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FILING DATE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ADDRESSEE: No. 57504970 No. 5750497disk of No. 5750497th America, Inc. STREET: 405 Lexington Avenue, 64th Floor
CITY: New York
STATE: New York
COUNTRY: United States of America
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            49 PLGTG------PRFVNQHLCGSHLVEALYLVGERGFFYTPKTRG 87
51 GIGPREVNQHLCGSHLVEALYLVCGERGFFYTPKIRGIVEQCCTSICSLYQLENYCN 1U7
               1 GNSARFVNOHLGGSHLVEALYLVGGERGFFYTPKTHGIVEQCCTSICSLYQLENYCN 63
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sacto
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DB 1; Length 137;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        27; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PREACHIN RELEASE #1.0, VERSION #1.25
CURRENT APPLICATION DATA:
APPLICATION DATA:
RILING DATE: 03-MAR-1995
CLASSIFICATION: 514
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             vry Match 51.5%; Score 302.5; DB 1 t Local Similarity 50.0%; Pred. No. 2 9e-25; ches 70; Conservative 4; Mismatches 27
                                                                                                                                                                                GENERAL INFORMATION:
APPLICANY: Havelund, Svend
APPLICANY: Havelund, John
APPLICANT: JORASSEN, ID
APPLICANT: JORASSEN, ID
APPLICANT: Markussen, Jan
APPLICANT: Markussen, Jan
APPLICANT: Markussen, Jan
APPLICANT: MARKUSSEN, JAN
AVMER OF INVENTION: ACYLATED INSULIN
NUMBER OF SEQUENCES: 49
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ...eER: US/08/400,256
03-MAR-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               88 IVEOCCTSICSLYQLENYCN 107
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ence 39, Application US/08975365
nt No. 6011007
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     118 IVEQCCTSICSLYQLENYCN 137
                                                                                                   SULT 2
-08-400-256-39
Sequence 39, Application US/08400256
Patent No. 5750497
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NAME: Lambiris, Elias J.
REGISTRATION NUMBER: 33-728
REFERENCE/DOCKET NUMBER: 398
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212-867-0123
TELEFAX: 212-889-9655
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TELEFAX: 212-8/8-7003
NFORMATION FOR SEQ ID NO: 39:
SEQUENCE CHARACTERISTICS:
LENGTH: 137 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PPLICANT: Havelund, Svend
PPLICANT: Halstrom, John
PPLICANT: Jonassen, Ib
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       linear
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----- N 48
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STREET: 405 Lexington Avenue, 61th Floor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 5, Application US/08291060B
Patent No. 572843
GENERAL INFORMATION:
APPLICANT: Dorschug, Michael
APPLICANT: Koller, Klaus-Peter
APPLICANT: Marquardt, Rudiger
APPLICANT: Meiwes, Johannes
TITLE OF INVENTION: An Enzymatic Process for the
TITLE OF INVENTION: Conversion of Preprolnsulins Into Insulins
NUMBER OF SEQUENCE: 5
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              39;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Ouery Match 51.5%; Score 102.5; DB 3; Length 137; Best Local Similarity 50.0%; Prod. No. 2.9e-28; Matches 70; Conservative 4; Mismatches 27; Indels 39
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               2 FPTIPLSRLFUNAMLRAHRLHCLAFDTYQEFEEAYIPKEO--KYSFLQ-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ADDRESSEE: Finnegan, Henderson, Farabow, Garrett ADDRESSEE: Dunner, L.L.P. STREET: 1300 I Street, N.W. CITY: Washington STATE: D.C.
                                                                                                                                                                                                                                                                                            MEDIUM TYPE: Floppy disk
COMPUTER: ISM PC Compatible
COMPUTER: ISM PC Compatible
OPERATING SYSTEM: PC-DOS/NS-DOS
SOPTWARE: Patentln Release 1.0. Version #1.25
APPLICATION DATA:
APPLICATION NUMBER: DS/08/y...355
                                                                                                                                                                                                                                                                                                                                                                                                                                                                CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
APPLICATION NUMBER: 08/400.256
FILING DATE: 03-MAR-1995
ATORNEY AGENT INFORMATION:
NAME: Lamblinis, Elias J.
REGISTRATION NUMBER: 33.728
REFERENCE/DOCKET NUMBER: 33.728
TELEPHONE: 212-867-0123
TELEFAX: 212-878-9655
APPLICANT: Andersen, Asser Sloth
APPLICANT: Markussen, Jan
TITLE OF INVENTION: ACYLATE: NSULIN
UNMER OF SEQUENCES: 49
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                               STATE: New York
COUNTRY: United States of America
COMPYTER FRADABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            88 IVEOCCISICSLYQLENYCN 107
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    118 TVEQCCISICSLYQUENYON 137
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             INFORMATION FOR SEQ ID NO: 39:
SEQUENCE CHARACIERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LENGTH: 137 amino acids TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MOLECULE TYPE: protein
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CITY: New York
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Length 56;

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Score 299; DB 1; I
Pred. No. 2.4e-28;
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                                                                                                                                                                                                                                   0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER READABLE FORM:
WEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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NAME: BINGHOLD, CAROLI P.
REGISTRATION NUMBER: 32 220
REFERENCE/DOCKET NUMBER: 024
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FELECOMMUNICATION INFORMATION:
                                                                                                                                                                                      50.9%;
larity 100.0%;
Conservative 0.
(908) 231-4079
               TELEFAX: (908) 231-2255
INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
LENGTH: 56 Amino Acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TELEFAX: 202-408-4400
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 56 amino acids
                                                                                                       ; TYPE: Amino Acid (AA)
; TOPOLOGY: not relevant
US-08-160-376A-7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MOLECULE TYPE: peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FILING DATE:
CLASSIFICATION: 530
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TYPE: amino acid
                                                                                                                                                                                          Query Match
Best Local Similarity
Matches 53; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TOPOLOGY: linear
  TELEPHONE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    US-08-389-487-11
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: Obermeier, Ranier APPLICANT: Cerl, Martin APPLICANT: Ludwig, Jurgen APPLICANT: Ludwig, Jurgen APPLICANT: Sabel, Walter TITLE OF INVENTION: Process For Obtaining Proinsulin TITLE OF INVENTION: Possessing Correctly Linked TITLE OF INVENTION: Cystine Bridges NUMBER OF SEQUENCES: 7
CORRESPONDENCE ADDRESS: ADDRESSE: Renneth A. Genoni, Esq. STREET: Rt. 202-206 No. 5473049th/F.O. Box 2500 CITY: Somerville
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER READABLE FORM:
MEDIUM TYPE: DISKETTE, 3.5 INCH, 1.44 MD STORAGE
COMPUTER: IBM 386
COMPUTER: ISM 386
COMPUTER: WORDPERFECT 5.1
SOFTWARE: WORDPERFECT 5.1
CURRENT APPLICATION DATA:
                  ZIP: 20005-3315
COMPUTER REDABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0. Version #1.30
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                 ATTORNEY/AGENT INFORMATION:
NAME: Einaudi, Carol P.
REGISTRATION NUMBER: 32,20
REFERENCE/DOCKET NUMBER: 02481.1105-02000
TELECOMMONICATION INFORMATION:
TELEPHONE: (202) 408-4366
INFORMATION FOR SEQ ID NO: 5: SEQUENCE CHARACTERISTICS:
LENGTH: 66 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NAME: Barbara V. Maurer, Esq.
REGISTRATION UNDBER: 31,287
REFERENCE/DOCKET UNDBER: 4DE 92/F 384
TELECOMMUNICATION INFORMATION:
                                                                                                                                                               APPLICATION NUMBER: US/08/291,060B
FILING DATE: 08-AUG-1994
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRIOR APPLICATION DATA:
APPLICATION NUMBER: GE P 4240420.7
FILING DATE: December 2, 1992
ATTORNEY/AGENT INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 7, Application US/08160376A Patent No. 5473049 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TOPOLOGY: linear MOLECULE TYPE: peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           single
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'RY: U.S.A.
08876-1258
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tes 55; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
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Matches
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    Gaps
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                                        55 REVNQHICGSHLVEALFILVCGERGFFYTPKTRGIVEQCCTSICSLYQLENYCN 107
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                                          RESULT 6

US-08-389-487-11

US-08-389-487-11

Sequence 11, Application US/0* 1487

Patent No. 563-291

GENERAL INFORMATION:
APPLICANT: Obermeler, Ra.ner
APPLICANT: Ludwig, Jurgen
TITLE OF INVENTION:
TITLE OF INVENTION:
CORRESPONDENCES: 12

CORRESPONDENCE ADDRESS:
ADDRESSEE: Finnegan, Henderson, Farabow, Garrett 6

ADDRESSEE: Dunner
STREET: 1300 I Street, N.W.

CITY: Washington

STATE: D.C.
                                                             4 REVNOHLCGSHEVBALYIV SERGFEYTPKTRGIVEQCCTSICSLYQLENYCH
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SOFTWARE: Patentin Release #1.0, Version #1.25 CURRENT APPLICATION DATA: APPLICATION NUMBER: US/Uc/389,487
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match 50.9%; Score 299; DB 1; 1
Best Local Similarity 100.0%; Pred. No. 2.4e-28;
Matches 53; Conservative 0; Mismatches 0;
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NAME: Lambiris, Elias J.
REGISTRATION NUMBER: 33,728
REFERCE/COCKET NUMBER: 39f
TELECOMMUNICATION:
TELEPHONE: 212-867-0123
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE CHARACTERISTICS:
LENGTH: 145 amino acids
                                                                                                                                                                                                                                                                                                                                                                                     TELEFAX: 202-408-4400
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                            LENGTH: 96 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TELEFAX: 212-878-9655 INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-389-487-8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               single
                      COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TYPE: amino acid
STRANDEDNESS: si
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GENERAL INFORMATION:
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Fatent No. 5663291

GENERAL INFORMATION:

APPLICANT: Obermation

APPLICANT: Sabel, Walten

APPLICANT: Sabel, Walter

TITLE OF INVENTION: Correctly Linked Cystine Bridges

TITLE OF INVENTION: Honderson, Farabow, Garrett & Applicants Prince Correctly Linked Cystine Bridges

NUMBER OF SEQUENCES: 12

CORRESPONDENCE ADDRESS:

ADDRESSEE: Finnegan, Henderson, Farabow, Garrett &
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Ouery Match 50.9%; Score 299; DB 1; Length 96; Best Local Similarity 100.0%; Pred. No. 4.8e-28; Matches 53; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                         TITLE OF INVENTION: Process For Obtaining Proinsulin TITLE OF INVENTION: Possessing Correctly Linked TITLE OF INVENTION: Cystine Bridges
TUBBER OF SEQUENCES: 7
CORRESPONDENCE ADDRESS: ADDRESSE: Renneth A. Genoni, Esq.
STREET: Rt. 202-206 No. 5473049th/P.O. Box 2500 CITY: Somerville
                                                                                                                                                                                                                                                                                                                                                                                                                                ZIP: 08876-1258
COMPUTER READABLE FORM:
MEDIUM TYPE: DISKETTE, 3.5 INCH, 1.44 Mb STORAGE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CLASSIFICATION: 530
PRIOR APPLICATION DATA:
PAPLICATION NUMBER: GE P 4240420.7
FILING DATE: December 2, 1992
ATTORNEY/AGENT INFORMATION:
NAME: BATDARA V. MAUREY: ESQ.
REGISTRATION NUMBER: 31,287
REFERENCE/COCKET NUMBER: 40E 92/F 384
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICATION NUMBER: US/08/160,376A
FILING DATE: December 1, 1993
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                         Sequence 5, Application US/08160376A Patent No. 5473049
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                                                                  GENERAL INFORMATION:
GAPLICANT: Obermeler, Ranier
APPLICANT: GGEL, Martin
APPLICANT: Ludwig, Jurgen
APPLICANT: Sabel, Walter
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TELEPHONE: (908) 231-4079
TELEFAX: (908) 231-2255
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1: 96 Amino Acids
   Amino Acid (AA)
   GY: not relevant
                                                                                                                                                                                                                                                                                                                                                                                        New Jersey
: U.S.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             IBM 386
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         US-08-160-376A-5
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US-08-160-376A-5
                                                                                                                                                                                                                                                                                                                                                                                                               COUNTRY:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 US-08-389-487-8
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E: No. 57504970 No. 5750497disk of No. 5750497th America, Inc. 405 Lexington Avenue, 64th Floor
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COUNTY: United States of America
ZIP: 10174-6401
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPA:DLE
OFFRATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/400,256
FILING DATE: 03-MAR.1995
CLASSIFICATION: 514
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/389.487
                                                                               FILING DATE:
CLASSIFICATION: 530
ATTOREY/AGENT INFORMATION:
NAME: Einaudi, Carol P.
REGISTRATION NUMBER: 32,220
REFERENCE/TOCKET NUMBER: 02481.1424-00000
TELECOMUNICATION INFORMATION:
TELEPHONE: 202-408-4000
TELEFAX: 202-408-4400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: Havelund, Svend
APPLICANT: Halstrom, John
APPLICANT: Andstrom, John
APPLICANT: Andersen, Ib
APPLICANT: Andersen, Asser Sloth
APPLICANT: Markussen, Jan
TITLE OF INVENTION: ACYLATED INSULIN
NUMBER OF SEQUENCES: 49
CORRESPONDENCE ADDRESS:
ADDRESSEE: No. 575049701
STREET: 405 Lexington Avenue, 64th F1
CITY: New York
STATE: New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        3985.220-US
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03-MAR-1995
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TOPOLOGY:
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                                                                                                                                              0; Gaps
                                                                                                                                                                                    55 REVNOHLCGSHLVEALYLVCGERGFFYTPKTRGIVEQCCTSICSLYQLENYCN 107
                                                                                                                                                                                                           93 REVNQHLCGSHLVEALLYCGERGFFYTPKTRGIVEQCCTSICSLYQLENYCN 145
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                                                                                                   Length 145;
                                                                                                                                           Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/975,365
                                                                                                                                              0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Ouery Match 50.9%; Score 299; DB 3; I
Best Local Similarity 100.0%; Pred. No. 7.9e-28;
Matches 53; Conservative 0; Mismatches 0;
                                                                                              Query Match 50.9%; Score 299; DB 1; Best Local Similarity 100.0%; Pred. No. 7.9e-28; Matches 53; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STREET: 405 Lexington Avenue, 64th Floor CIIY: New York STATE: New York COUNTRY: United States of America IP: 10174-6401
                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: Havelund, Svend
APPLICANT: Halstrom, John
APPLICANT: Johnssen, John
APPLICANT: Johnssen, Ib
APPLICANT: Markussen, Jan
APILICAN': Markussen, Jan
APILICAN': Markussen, Jan
APILICAN': Markussen, Jan
APILICAN': AR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     3985.220-US
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                       Sequence 45, Application US/08975365
Patent No. 6011007
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 48, Application US/08400256
Patent No. 5750497
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CLASSIFICATION: 514
PRIOR APPLICATION DATA:
PAPLICATION NUMBER: US 08/400
FILLING DATE: 03-MAR-1995
ATTORNEY/AGENT INFORMATION:
NAME: Lambiris, Elias J.
REGISTRATION NUMBER: 33,728
REFERENCE/OCKET NUMBER: 3985
TELECOMMUNICATION:
TELEPHONE: 212-867-0123
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     145 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TELEFAX: 212-878-9655
INFORMATION FOR SEQ ID NO:
               TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-400-256-45
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       amino acid
amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ADDRESSEE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 US-08-400-256-48
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APPLICANT: Havelund, Svend
APPLICANT: Halstrom, John
APPLICANT: Halstrom, John
APPLICANT: Jonassen, Ib
APPLICANT: Andersen, Asser Sloth
APPLICANT: Markussen, Jan
TITLE OF INVENTION: ACLATED INSULIN
NUMBER OF SEQUENCES: 49
CORRESPONDENCE ADDRESS:
ADDRESSEE: No. 57504970 No. 5750497disk of No. 5750497th America, Inc.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              No. 6011007o No. 6011007disk of No. 6011007th America, Inc.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          94 RFVNQHIGGSHLVEALYLVGGERGFFYTPKTRGIVEQCCTSICSLYQLENYCN 146
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   55 REVNOHLCGSHLVEALYLVCGERGFFYTPKTRGIVEQCCTSICSLYQLENYCN 107
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 299; DB 1; Length 146; Pred. No. 8e-28;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                SOFTWARE: Patentin Release #1.0, version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/400,256
FILING DATE: 03-MAR-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SOFTWARE: PatentIn Release #1.0, Version #1.25 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Ouery Match 80.9%; Score 299; DB Best Local Similarity 100.0% Pred. No. 8e-7 Matches 53; Conservative 0; Mismatches
                                                                                                                                                                                                                           405 Lexington Avenue, 64th Floor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     : 405 Lexington Avenue, 64th Floor
New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NAME: Lambiris, Elias J.
REGISTRATION NUMBER: 33,728
REFERENCE/DOCKET NUMBER: 3985.220-US
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                       STATE: New York
COUNTRY: United States of America
ZIP: 10174 6401
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATION
COMPUTER: IBM PC COMPATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: Jonassen, 1b
APPLICANT: Andersen, Asser Sloth
APPLICANT: Markussen, Jan
ITILE OF INVENTION: ACYLATED INSULIN
NUMBER OF SEQUENCES: 49
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COUNTRY: United States of America ZIP: 10174-6401
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RESULT 12
US-08-975-365-48
Sequence 48, Application US/08975365
Patent No. 6011007
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 INFORMATION FOR SEQ ID NO: 48:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GENERAL INFORMATION:
APPLICANT: Havelund, Svend
APPLICANT: Halstrom, John
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LENGIH: 146 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TELEPHONE: 212-80,
TELEPHONE: 212-878-9655
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        : MOLECULE TYPE: protein US-08-400-256-48
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FILING DATE: 03
CLASSIFICATION:
                                                                                                                                                                                                                                                     New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ADDRESSEE:
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COMPUTER: Integry disk
COMPUTER: Filoppy disk
COMPUTER: Patchfile
COPERATING SYSTEM: PC-DOS/MS-DOS
SOUTWARE: Patchfile Release #1.0, Version #1.25 (EPO)
CUBRENT APPLICATION DATE:
APPLICATION NUMBER: US/08/900,574
FILING DATE: July 24, 1997
CLASSIFICATION DATE: German Application No. 6221837 19630242.0
FILING DATE: July 26, 1996
ATTORNEY/AGENT INFORMATION:
REFERENCE/DOCKET NUMBER: 02481.1499-00000
TELLCOMMUNICATION INFORMATION:
TELLCOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  55 REVNOHLCGSHLVEALYLVCGERGFFYTPKTRGIVEQCCTSICSLYQLENYCN 107
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 57
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Indels
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ADDRESSEE: 6 Dunner, L.i.P.
STREET: 1300 I Street, N.W.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 293; DB 1; L
Pred. No. 1.3e-27;
2; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                            NAME: Kirschner Michael K.
REGISTRATION NUMBER: 34,851
REFERENCE/DOCKET NUMBER: 02481-0593-02000
TELECOMUNICATION INFORMATION:
TELEPHONE: 202-408-4000
TELEFAX: 202-408-4400
                                                                                        FILING DATE: 03 NOV-198
PRIOR APPLICATION DATA:
PRIOR DATE: 19-AUG-1989
PRIOR DATE: 19-AUG-1989
PRIOR APPLICATION DATA:
PRILING DATE: 19-AUG-1989
PRIOR APPLICATION DATA:
FILING DATE: 21-APR-1990
ATTORNEY/AGENT INFORMATION:
                                                              DE P 38 37 273.
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Patent No. 6221837
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Washington : District of Columbia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      49.9%;
96.2%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICA T: Ertl, Johann
APPLICA F: Habermann, Paul
APPLICANT: Geisen, Karl
APPLICANT: Seipke, Gerhard
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (202) 408-4000
(202) 408-4400
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Math
Best Local Similarity 96.29
Matches 51; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TELEFAX: 202-408-4400
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 57 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TOPOLOGY: unknown
MOLECULE TYPE: peptide
US-08-030-731A-44
                             PRIOR APPLICATION DATA:
                                                                  APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    amino acid
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US-08-900-574-3
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STATE:
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US-08-030-731A-44

Sequence 44, Application US/08030731A

Sequence 45, Application US/08030731A

Sequence 45, Application US/08030731A

Sequence 45, Application US-08030731A

APPLICANT: Koller, Klaus-Peter
APPLICANT: Uhlmann, Eugen
APPLICANT: Uhlmann, Eugen
TITLE OF INVENTION: Processes for the Preparation of Forcign
TITLE OF INVENTION: Processes for the Preparation of Forcign
TITLE OF INVENTION: Processes
NUMBER OF SEQUENCES: 48

CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 146;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ADDRESSEE: Finnegan, Henderson, Farabow, Garrett & ADDRESSEE: Dunner STREET: 1300 I Street, N.W., Suite 700 STAIE: D.C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/030,731A
FILING DATE: 12-MAR-1993
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          50.9%; Score 299; DB 3; ilarity 100.0%; Pred. No. 8e-28; Conservative 0; Mismatches 0
                                                                                                                                                                                                                                                                                                             3985.220-US
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APPLICATION NUMBER: US 07/189,840
FILING DATE: 03-MAY-1988
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/430,622
FILING DATE: 01-NOY-1989
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         US 07/687,610
                                                                                               PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/400,256
FILING DATE: 03-MAR-1995
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICATION NUMBER: US 07/735,757
FILING DATE: 29-JUL-1991
APPLICATION NUMBER: US/08/975,365
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                            REGISTRATION NUMBER: 33.728
REGISTRATION NUMBER: 33.728
REFRENCE/COCKET NUMBER: 3985.
TELECOMMUNICATION INFORMATION:
TELEFAK: 212.867-0123
INFORMATION FOR SEQ ID NO: 48: SEQUENCE CHARACTERISTICS:
LENGTH: 146 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FILING DATE: 19-APR-1991
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MOLECULE TYPE: protein US-08-975-365-48
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRIOR APPLICATION DATA:
                             FILING DATE:
CLASSIFICATION: 514
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICATION NUMBER:
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Best Local Similarity
Matches 53; Conserv
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Gaps

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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC-0008AG:DOS
COMPUTER: IBM PC-0008/MS-DOS
CORPATARE: PATENTIN Release #1.0, Version #1.25 (EPO)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/970,574
FILIMG DATE: July 24, 1997
CLASSIFICATION DATA:
APPLICATION NUMBER: German Application No. 6221837 19630242.0
FILING DATE: July 26, 1996
ATTORNEY/AGENT INFORMATION:
NAME: Carol P. Einaudi
REGISTRATION NUMBER: 32,220
REFERENCE/DOCKET NUMBER: 02481.1499-00000
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                  5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GENERAL INFORMATION:
APPLICANT: Ertl. Johann
APPLICANT: Habermann, Paul
APPLICANT: Geisen, Karl
APPLICANT: Geisen, Karl
APPLICANT: Geisen, Karl
APPLICANT: Beipke, Gerhard
TITLE OF INVENTION: Insulin derivatives with increased zinc
TITLE OF INVENTION: binding
NUMBER OF SEQUENCES: 18
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                   Length 65;
                                                                                                                                                                                                                                                                                                                                                                3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ADDRESSEE: Finnegan, Henderson, Farabow, Garrett,
ADDRESSEE: & Dunner, L.L.P.
STREET: 1300 I Street, N.W.
                                                                                                                                                                                                                                                                                                                 Query Match 48.9%; Score 287; DB 3;
Best Local Similarity 91.4%; Pred. No. 7.7e-27;
Matches 53; Conservative 0; Mismatches 3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 5, Application US/08900574 Patent No. 6221837
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           District of Columbia
                                                                                                                                                                                 ORGANISM: Escherichia coli
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ORGANISM: Escherichia coli
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TELEPHONE: (202) 408-4000
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 66 aming acids
INFORMATION FOR SEQ ID NO:
SEGUENCE CHARACTERISTICS:
LENGTH: 65 amino acids
TYPE: Amino acid
STRANDEDNESS: Single
                                                                                                               TOPOLOGY: linear
MOLECULE TYPE: Protein
ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TYPE: Amino acid
STRANDEDNESS: Single
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Protein
                                                                                                                                                                                                                              NAME/KEY: Protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NAME/KEY: Protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CITY: Washington
STATE: District o
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        20005-3315
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TOPOLOGY: line
MOLECULE TYPE: P
ORIGINAL SOURCE:
                                                                                                                                                                                                                                                   LOCATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COUNTRY:
                                                                                                                                                                                                                                                                      US-08-900-574-3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               US-08-900-574-5
                                                                                                                                                                                                      FEATURE:
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GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.
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- protein search, using sw model

55; Search time 33.7237 Seconds (Without alignments) 472.415 Million cell updates/sec September 16, 2003, 12:38:55

Run on:

Mitie: US-09-423-100-6 Perfect score: 587

1 MFPTIPLSRLFDNAMLRAHR......IVEQCCTSICSLYQLENYCN 107 Sednence:

Scoring table: BLOSUM62 Gapop 10.0 , Gapext 0.5

Searched:

Total number of hits satisfying chosen parameters: 556269 seqs, 148893369 residues

Minimum DB seq length: 0 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database: 1. /cgu2_6/ptodata/2/pubpaa/USO7_PUBCOMB.pep:* 2. /cgn2_6/ptodata/2/pubpaa/USO6_NEW_PUB_pep:* 3. /cgn2_6/ptodata/2/pubpaa/USO6_PUBCOMB.pep:* 4. /cgn2_6/ptodata/2/pubpaa/USO6_PUBCOMB.pep:* 5. /cgn2_6/ptodata/2/pubpaa/USO7_NEW_PUB_pep:* 6. /cgn2_6/ptodata/2/pubpaa/USO7_NEW_PUB_pep:* 7. /cgn2_6/ptodata/2/pubpaa/USO7_NEW_PUB_pep:* 8. /cgn2_6/ptodata/2/pubpaa/USO3_NEW_PUB_pep:* 9. /cgn2_6/ptodata/2/pubpaa/USO3_PUBCOMB.pep:* 11. /cgn2_6/ptodata/2/pubpaa/USO3_PUBCOMB.pep:* 12. /cgn2_6/ptodata/2/pubpaa/USO3_PUBCOMB.pep:* 11. /cgn2_6/ptodata/2/pubpaa/USO3_PUBCOMB.pep:* 12. /cgn2_6/ptodata/2/pubpaa/USO3_PUBCOMB.pep:* 13. /cgn2_6/ptodata/2/pubpaa/USO3_PUBCOMB.pep:* 14. /cgn2_6/ptodata/2/pubpaa/USO3_PUBCOMB.pep:* 15. /cgn2_6/ptodata/2/pubpaa/USO3_PUBCOMB.pep:* 16. /cgn2_6/ptodata/2/pubpaa/USO3_PUBCOMB.pep:* 17. /cgn2_6/ptodata/2/pubpaa/USO3_NEW_PUB_pep:* 18. /cgn2_6/ptodata/2/pubpaa/USO3_NEW_PUB_pep:* 18. /cgn2_6/ptodata/2/pubpaa/USO3_NEW_PUB_pep:* 18. /cgn2_6/ptodata/2/pubpaa/USO3_NEW_PUB_pep:* 18. /cgn2_6/ptodata/2/pubpaa/USO3_NEW_PUB_pep:* 18. /cgn2_6/ptodata/2/pubpaa/USO3_NEW_PUB_pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Description	Sequence 6, Appl1		Sequence 5, Appli	18,	Sequence 19, Appl	'n	6		-	Sequence 12, Appl	•		<	Sequence 10, Appl	_
ΔI	US-10-054-873-6	US-10-054-873-7	US-10-054-873-5	US-09-894-711-18	US-09-861-687-19	US-09-858-935B-5	US-10-028-410-3	US-09-280-030-63	US-09-947-563-4	US-09-736-611-12	US-09-740-359-12	US-09-894-711-12	US-09-736-611-10	US-09-740-359-10	US-09-894-711-10
0.0	14	14	14	10	10	11	14	6	10	σ	σ	10	σ	6	10
% Juery Watch Length DB	107	150	52	124	138	51	51	117	96	124	124	124	125	125	125
% Query Match	100.0	9.46	50.1	48.5	48.4	47.4	47.4	47.4	47.2	46.9	46.9	46.9	46.9	46.9	46.9
Score	587	555.5	294	284.5	284	278.5	278.5	278	277	275.5	275.5	275.5	275.5	275.5	275.5
Result No.	<u></u>	7	æ	4	2	φ	7	œ	σ	10	11	12	13	74	15

LENGTH: 107 amino acids TYPE: amino acid

SEQUENCE CHARACTERISTICS

Sequence 8, Appli	Sequence 7, Appli	Sequence 6, Appli	Sequence 5, Appli	Sequence 5, Appl1	Sequence 3, Appli	Sequence 5, Appl1	Sequence 62, Appl	Sequence 1, Appli	4		Sequence 4, Appli	Seguence 125, App	Sequence 3, Appli	Sequence 9, Appl1	Sequence 6, Appli	Sequence 1, Appli	Sequence 2, Appli	Sequence 1, Appli	Sequence 2, Appli	Sequence 23, Appl	_`	Sequence 1, Appli	Sequence 1, Appli	Sequence 1, Appli	Sequence 6, Appli	Sequence 9, Appli	,99	Sequence 7, Appli	Sequence 2, Appli
US-09-736-611-8	US-09-740-359-7	US-09-736-611-6	US-09-740-359-5	US-09-894-711-5	US-10-066-009A-3	US-09-947-563-5	US-09-280-030-62	US-09-878-380-1	US-09-858-935B-4	US-10-028-410-2	US-10-054-873-4	US-09-205-658-125	US-09-815-229-3	US-09-804-409A-9	US-09-969-748C-6	US-10-038-686-1	US-10-328-813-2	US-10-054-873-1	US-10-054-873-2	US-09-984-010-23	US-10-153-207-1	US-10-400-377-1	US-10-400-708-1	US-10-298-148-1	US-10-153-207-6	US-09-929-918-9	US-08-280-030-66	US-09-894-711-7	5-09-853-688-2
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147	147	144	144	146	20	96	130	98	98	98	98	110	110	110	110	110	110	4	95	191	191	191	191	191	214	217	245	144	217
46.9	46.9	46.7	46.7	46.7	46.5	46.2	45.9	45.5	45.5	45.5	45.5	45.5	45.5	45.5	45.5	45.5	45.5	44.3	44.3	43.5	43.5	43.5	43.5	43.5	43.5	43.5	43.5	43.2	42.5
275.5	275.5	274	274	274	273	271	269.5	267	267	267	267	267	267	267	267	267	267	260	260	255.5	255.5	255.5	255.5	255.5	255.5	255.5	255.5	253.5	249.5
16	17	18	19	20	21	22	23	24	25	56	27	28	29	30	31	32	33	34	35	36	37	38	39	40	41	42	43	44	4 5

ALIGNMENTS

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Sequence 6, Application US/10034873
Publication No. US20020164712A1
GENERAL INFORMATION:
APPLICANT: Gan, Zhong Ru
TITLE OF INVENTION: Chimeric Protein Containing an
Intramolecular Chaperone-Like Sequence
                                                                                                                                                                                                                                                                                                                                                          COUNTY: USA
ZIP: 94111-3834
COMPUTER READABLE FORM:
MEDTUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
COMPUTER: DATE: PC-DOS/MS-DOS
SOFTWARE: PATENTIN Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/054,873
FILING DATE: 22-Jan-2002
PRIOR APPLICATION NUMBER: WO PCT/CN98/00052
FILING DATE: 31-MAR-1998
APPLICATION NUMBER: WO 97/23,100
FILING DATE: 31-DEC-2000
ATTORNEYAGENT INFORMATION:
                                                                                                                                                                                                                                      CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew LLP STREET: Two Babarcadero Center, Eighth Floor CITY: San Francisco STATE: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NAME: Mycroft, Frank J
RESISTRATION NUMBER: 46,946
REFERENCE/DOCKET NUMBER: 020167-000130US
INFORMATION FOR SEQ ID NO: 6:
                                                                                                                                                                                                             NUMBER OF SEQUENCES:
RESULT 1
US-10-054-873-6
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61 TPSNREETQQKSNLELLRISLLLIQSWLEPVQLGTGPRFVWQHLCGSHLVEALYLVCGER 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NAME: Mycroft, Frank J
REGISTRATION NUMBER: 46,946
REFERENCE/DOCKET NUMBER: 020167-060130US
INFORMATION FOR SEO ID NO: 5:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/10/054,873
FILING DATE: 22-3ar-2002
CLASSIFICATION: cUnknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: WO PCT/CN98/00052
FILING DATE: 31-MAR-1998
APPLICATION NUMBER: US 09/423,100
FILING DATE: 11-DEC-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             50.1%; Score 294; DB 14; 100.0%; Pred. No. 4.1e-28;
                                                                  121 GFFYTPKTRGIVEQCCTSICSLYQLENYCN 150
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               100.0%; Pred. No. 4.14
tive 0; Mismatches
                                           78 GFFYTPKTRGIVEQCCTSICSLYQLENYCN 107
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TOPOLOGY: Linear
MOLECULE TYPE: proteic
SEQUENCE DESCRIPTION: SEQ 1D NO: 5:
                                                                                                                                                                                                                                                                                                                                                                                                                                                      COUNTRY: USA
ZIP: 94111-3834
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                              Sequence 5, Application US/100',873 Publication No. US20020164712A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STRANDEDNESS: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LENGTH: 52 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                 CITY: San Francisco
STATE: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        52; Conservative
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Matches 52; Conserv
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                                                                                                                                                                            US-10-054-873-5
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                                                                                                                                                                                                                                       ----LGTGPRFVNQHLCGSHLVEALYLVCGER 77
                                                                                                                                                                            Gaps
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                                                                                                                                                                         ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: Gan, Zhong Ru
TITLE OF INVENTION: Chimeric Protein Containing an
Intramolecular Chaperone-Like Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       43;
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                                                                                                                           Length 107;
                                                                                                                                                                                                                                                                                                                          61 LCGSHLVEALYLVCGERGFFYTPKIRGIVEQCCTSICSLYQLENYCN 107
                                                                                                                                                                                                                                                                                                     61 LCGSHLVEALYLVCGERGFFYTPKTRGIVEQUCTSICSLYQLENYCN 107
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                                                                                                                                                                       Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NUMBER OF SEQUENCES: 7
CORRESPONDENCE ADDRESS:
ADDRESSE: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, Eighth Floor
CITY: San Francisco
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NAME: Mycroft, Frank J
REGISTRATION NUMBER: 46,946
REFERENCE/DOCKET NUMBER: 020167-000130US
                                                                                                                           100.0%; Score 587; DB 14; 100.0%; Pred. No. 5.2e-63;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICATION NUMBER: WO PCT/CN98/00052
FILING DATE: 31-AMR-11998
APPLICATION NUMBER: US 09/423,100
FILING DATE: 11-DEC-2000
                                                                                                                                                                       0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICATION NUMBER: US/10/054, EFILING DATE: 22-Jan-2002
CLASSIFICATION: <UNKNOWN>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TOPOLOGY: Linear

MOLECULE TYPE: protein

SEQUENCE DESCRIPTION: SEQ ID NO: 7:
US-10-054-873-7
                    TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 6:
US-10-054-873-6
STRANDEDNESS: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 7, Application US/10054873 Publication No. US20020164712A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LENGTH: 150 amino acids TYPE: amino acid
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STATE: California
                                                                                                                                                Best Local Similarity 100.
Matches 107; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Best Local Similarity 71.3
Matches 107; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COUNTRY: USA
21P: 94111-3834
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                               RESULT 2
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Sequence 18, Application US/09894711
Patent No. US20020137144A1
GNERAL INFORMATION:
GNERAL INFORMATION:
GNERAL INFORMATION:
GNERAL TO. US20020137144A1
APPLICANT:
Ludvigsen, Svend
TITLE OF INVENTION:
TITLE O
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ..
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 FVNQHLCGSHLVEALYLVCGERGFFYTPKTRGIVEQCCTSICSLYQLENYCN 52
blication were very debugged in the containing an altic of invention: Chimeric Protein Containing an IIILE OF INVENTION: Chimeric Protein Containing an Intramolecular Chaperone-Like Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: Patentin Release #1.0, Version #1.30
                                                                                                                                                                                                                                                                                                                                                                                                          NUMBER OF SEQUENCES: 7
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, Eighth Floor
```

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58 STNNGLLFINTTIASIAAKEEGVSLDKRFVNOHLCGSHLVEALYLVCGEKGFFYTPKAAK 117
                                                                                                                                                                                                                 ----PREVNQHLCGSHLVEALYLVCGERGFFYTPK-TR 86
                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: Obbaquie, Yves
APPLICANT: Dubaquie, Yves
APPLICANT: Lowman, Henry B.
IIILE OF INVENTION: METHOD FOR TREATING CARTILAGE DISORDERS
FILE REFERENCE: P1794R1
CURRENT APPLICATION NUMBER: US/09/858,935B
CURRENT FILING DATE: 2002-07-02
PRIOR APPLICATION NUMBER: US 60/248,985
PRIOR APPLICATION NUMBER: US 60/204,490
PRIOR FILING DATE: 2000-05-16
NUMBER OF SEO ID NOS: 153
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 278.5; DB 11; Length 51;
Pred. No. 2.9e-26;
0; Mismatches 0; Indels 1
                                                                                                        Length 138
                                                                                                                                                28; Indels
                                                                                                      Score 284; DB 10;
Pred. No. 2.2e-26;
                                                                                                                                                5; Mismatches
             MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 19:
US-09-861-687-19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: LOWMan, Henry
TITLE OF INVENTION: PROTEIN VARIANTS
TILE REFERENCE: P1712R1-1
CURRENT APPLICATION NUMBER: US/10/028,410
CURRENT FILING DATE: 2001-12-19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRIOR APPLICATION NUMBER: US/09/477,924
PRIOR FILING DATE: 2000-112-19
PRIOR FILING DATE: 2000-01-05
NUMBER OF SEQ ID NOS: 6
SEQ ID NO 3
                                                                                                                                                                                                                                                                                                                                                               87 GIVEQUETSICSLYQLENYCN 107
                                                                                                                                                                                                                                                                                                                                                                                        Sequence 5, Application US/09858935B Publication No. US200300691777 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 3, Application US/10028410
Publication No. US20020160955A1
GENERAL INFORMATION:
APPLICANT: Dubaquie, Yves
APPLICANT: Lowman, Henry
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   47.4%;
98.1%;
                                                                                                    Query Match
Best Local Similarity 48.28;
Matches 68; Conservative
  TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      51; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ORGANISM: Homo sapiens
US-09-858-935B-5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                             49 PLGTG-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        US-09-858-935B-5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           US-10-028-410-3
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TYPE: PRI
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TYPE: PRT
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STREET: 405 Lexington Avenue, 64th Floct
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Ξ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DB 10; Length 124;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SIGNATE: New TOTK
COUNTY: United States of America
ZIP: 10174-6401
COMPUTER READABLE FORM:
WEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
COMPUTER: BM PC COMPATIBLE
SOFTWARE: PATENTIN RELEASE #1.0, Version #1.30
CURRENT APPLICATION DATA:
RTLING DATE: 21-May-2001
CLASSIFICATION: <UNKNOWN>
                                                                                                                                                                                                                                                                                                                                                                                                                     Ouery Match 48.5%: Score 284.5; DB 10;
Best Local Similarity 92.7%; Pred. No. 1.7e-26;
Matches 51; Conservative 2; Mismatches 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  REGISTRATION NUMBER: 33,728
REFERENCE/DOCKET NUMBER: 4341.204-US
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Brandt, Jakob
Kurtzhals, Peter
Hansen, Hertz Per
Kaarsholm. Niels Christian
TITLE OF INVENTION: INSULIN DERIVATIVES
NUMBER OF SEQUENCES: 26
    PRIOR FILING DATE: 2000-03-17
PRIOR FILING DATE: 2000-03-17
PRIOR APPLICATION NUMBER: PA 1999 01869
PRIOR FILING DATE: 1999-12-29
PRIOR FILING DATE: 2000-06-13
PRIOR FILING DATE: 2000-06-13
PRIOR FILING DATE: 2000-06-13
PRIOR FILING DATE: 2000-02-10
PRIOR PRIOR APPLICATION NUMBER: 09/740.359
PRIOR FILING DATE: 2000-12-19
NUMBER OF SEC ID NOS: 20
SOFTWARE: FASLSEQ for Windows Version 4.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICATION NUMBER: 08/932,082
FILING DATE: 16-DEC-1997
PRIOR APPLICATION NUMBER: PA 2000 00443
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  US-09-861-687-19; Sequence 19, Application US/09861687; Publication No. US20020193292A1; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NAME: Lambiris, Elias J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TELEPHONE: 212-867-0123
TELEFAX: 212-878-9655
INFORMATION FOR SEQ ID NO: 19:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LENGTH: 138 amino acids TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: Markussen, Jan
Jonassen, Ib
Havelund, Svend
                                                                                                                                                                                                                                                                                        TYPE: PRT
ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE CHARACTERISTICS
                                                                                                                                                                                                                                                                                                                                                           ; OTHER INFORMATION: Synthetic US-09-894-711-18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CORRESPONDENCE ADDRESS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STATE: New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CITY: New York
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US-09-736-611-12

Sequence 12, Application US/09736611

Patent No. US2001002306941

GENERAL INFORMATION:
ApplicaNT: Kaldsen, Thoras
ApplicaNT: Ludvigsen, Svend
APPLICANT: Raarsholm, Niels
TITLE OF INVENTION: Method For Making Insulin Precursor Analogs
TITLE OF INVENTION: Insulin Precursor Analogs
FILE REFRENCE: 6058-200-05
CURRENT FILING DATE: 2000-12-14
PRIOR PPLICATION NUMBER: 60/781,443
PRIOR FILING DATE: 2000-06-13
PRIOR FILING DATE: 2000-06-13
PRIOR FILING DATE: 1999-12-29
PRIOR APPLICATION NUMBER: 60/211,441

PRIOR FILING DATE: 1999-12-29
PRIOR APPLICATION NUMBER: PA 1999 01868

PRIOR APPLICATION NUMBER: PA 1999 01868

PRIOR APPLICATION NUMBER: PA 1999 01868
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   51 GTGPRFVNQHLCGSHLVEALYLVCGERGFFYTPKT--------------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 96:
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NATA:
FILING DATE: 07-Sep 2001
CLASSIFICATION: <UNKNOWN>
                                                                                                                                                                                                                                                                                                     REFERENCE/DOCKET NUMBER: 02481.1600-00000 TELECOMMUNICATION INFORMATION: TELEPHONE: (202) 408-4400 TELEFAX: (202) 408-4400 INFORMATION FOR SEQ ID No: 4: SEQUENCE CHARACTERISTICS: LENGIH: 96 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
47.2%; Score 277; DB 10;
Best Local Similarity 59.3%; Pred. No. 9.8e-26;
Matches 54; Conservative 0; Mismatches 3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TSICSLYQLENYCN 107
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SOFTWARE: FastSEQ for Windows Version 4.0
                                                                                                                                                PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/134,836
FILING DATE: «UNKNOWN>
ATTORNEY LOSDIE MEDIANCIE!
NAME: LESTIE MEDIANCIE!
REGISTRATION NUMBER: 34,872
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LOCATION: 1..96
SEQUENCE DESCRIPTION: SEQ ID NO: 4:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ORGANISM: Escherichia coli
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TYPE: PRT; ORGANISM: N-terminal extension US-09-736-611-12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NAME/KEY: Protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TOPOLOGY: linear
MOLECULE TYPE: protein
ORIGINAL SOURCE:
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TITLE OF INVENTION: Improved process for obtaining
insulin precursors having correctly bonded cystine bridges
                                                                                                                                                                                                                                                                                        Sequence 63, Application US/09280030A

Sequence 63, Application US/09280030A

Patent No. US2001002151Sal

GENERAL INFORMATION:

APPLICANT: Sato, Selji

APPLICANT: Higashikuni, Naohiko

APPLICANT: Kudo, Toshiyuki

TITLE OF INVENTION: DNAS ENCODING NEW FUSION PROTEINS AND PROCESSES FOR

TITLE OF INVENTION: DNAS ENCODING NEW FUSION PROTEINS OF THE

TITLE OF INVENTION: DNAS

FILE REFERENCE: 382.1026

CURRENT APPLICATION NUMBER: US/09/280.030A

CURRENT APPLICATION NUMBER: US/09/280.030A

CURRENT PILING DATE: 1999-03-26

EARLIER APPLICATION NUMBER: JP10-8739/1998

EARLIER APPLICATION NUMBER: JP10-8739/1998

SOFTWARE: Patentin Ver. 2.0

SOFTWARE: Patentin Ver. 2.0
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                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CTHER INFORMATION: Description of Artificial Sequence: Designated is 'O'THER INFORMATION: an amino acid sequence of CTHER INFORMATION: MWPSP-MWPmpl0.Met-Proinsulin US-09-280-030-63
                                                                                                                             56 FVNQHLCGSHLVEALYLVCGERGFFYTPKTRGIVEOCCT : ICSLYQLENYCN 107
                                                                                                                                                       1 FVNQHLCGSHLVEALYLVCGERGFFYTPKT-GIVEQCCTSICSLYQLENYCN 51
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                               DB 14; Length 51;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       47.4%; Score 278; DB 9; Length 117; 60.0%; Pred. No. 9.5e-26; tive 0; Mismatches 2; Indels
                       Query Match 47.4%; Score 278.5; DB 14; Length Best Local Similarity 98.1%; Pred. No. 2.9e-26; Matches 51; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 4, Application US/09947563
Patent No. US200016534A1
GENERAL INFORMATION:
APPLICANT: RUDroder, Franz-Josef
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STREET: 1300 I Street, N.W.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ORGANISM: Artificial Sequence FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CITY: Washington
STATE: D.C.
COUNTRY: USA
ZIP: 20005-3315
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NUMBER OF SEQUENCES: 7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Best Local Similarity 60.0%
Matches 54; Conservative
                                                                                                                                                                                                                                                                                US-09-280-030-63
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TYPE: PRT
ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                       Ouery Match 46.9%;
Best Local Similarity 90.9%;
Matches 50; Conservative
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Best Local Similarity 90.9%.
Matches 50; Conservative
                                                                                                                        FEATURE:
COTHER INFORMATION: Synthetic
US-09-894-711-12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ) ORGANISM: N-terminal extens. US-09-736-611-10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            US-09-740-359-10
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                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 12, Application US/09740359
Sequence 12, Application US/09740359
Fatent No. US20010041787A1
GENERAL INFORMATION:
THEOFULANT: Ludvigsen, Svend
TITLE OF INVENTION: Method for making insulin precursors and
TITLE OF INVENTION: Method for making insulin precursors and
TITLE OF INVENTION: Method for making insulin precursor analogues having improved fermentation
TITLE OF INVENTION: yield in yeast
FILE REFERENCE: 648.2000.US
CURRENT APPLICATION NUMBER: US/09/740,359
CURRENT FILING DATE: 2000-012-19
PRIOR PILING DATE: 2000-03-17
PRIOR FILING DATE: 2000-03-17
PRIOR FILING DATE: 2000-06-13
PRIOR FILING DATE: 2000-02-10
WUMBER OF SEQ ID NOS: 16
SSOFTWARE: FastSED for Windows Version 4.0
SSO ID NO 12
LENGTH: 124
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,
Query Match 46.9%: Score 275.5; DB 9; Length 124; Best Local Similarity 90.9%; Pred. No. 2.1e-25; Matches 50; Conservative 2; Mismatches 2; Indels 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match 46.9%; Score 275.5; DB 9; Length 124; Best Local Similarity 90.9%; Pred. No. 2.1e-25; Matches 50; Conservative 2; Mismatches 2; Indels 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ; TYPE: PRT
; ORGANISM: TA57 leader fused with N-terminally extended....
US-09-740-359-12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 12, Application US/09894711 Patent No. US20020137144A1 GENERAL INFORMATION: APPLICANT: Kjeldsen, Thomas Borglum APPLICANT: Ludvigsen, Svend
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         US-09-894-711-12
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TOTAL SEQUENCE

PROMISH: NET TOTAL SEQUENCE

PROMISH: NOTE TOTAL SEQUENCE

PROMISH: NOTE TOTAL SEQUENCE

PROMISH: NOTE TOTAL SEQUENCE

OTHER INFORMATION: Syntheir

OF SEQUENCE SIGNIFICATION: Syntheir

MATCHES 50; CONSETTATION: Syntheir

DE TOTAL SEQUENCE SIGNIFICATION: STATE SIGNIFICATION

OF SEQUENCE SIGNIFICATION: STATE SIGNIFICATION

OF SEQUENCE SIGNIFICATION STATE SIGNIFICATION

OF SEGUENCE SIG
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TITLE OF INVENTION: Method for making insulin precursors and TITLE OF INVENTION: Method for making insulin precursors and TITLE OF INVENTION: insulin precursor analogues having improved fermentation: TITLE OF INVENTION: join precursor analogues having improved fermentation: TITLE OF INVENTION: yield in yeast FILE OF INVENTION: UNMBER: US/09/894,711 CURRENT APPLICATION NUMBER: DA: 17 PRIOR PAPLICATION NUMBER: PA 1999 01869 PRIOR PILING DATE: 2000-06.13 PRIOR PAPLICATION NUMBER: 60/211,081 PRIOR FILING DATE: 2000-06.13 PRIOR PELING DATE: 2000-06.13 PRIOR FILING DATE: 2000-02.10 PRIOR FILING DATE: 2000-01.12.19 PRIOR FILING DATE: 2000-01.12.19 PRIOR FILING DATE: 2000-12.19 SURJUBER OF SEQ ID NOS: 20 NUMBER: OF SEQ ID NOS: 20 NUMBER: DA NU
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           46.9%; Score 275.5; DB 10; Length 125; 90.9%; Pred. No. 2.1e-25; tive 2; Mismatches 2; Indels 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
46.9%; Score 275.5; DB 9; Length 125;
Best Local Similarity 90.9%; Pred. No. 2.1e-25;
Matches 50; Conservative 2; Mismatches 2: Indels 1
                                                                                                                                                                                                                                                                                              : TYPE: PRT
: ORGANISM: TA39 leader fused with N-terminally extended
US-09-740-359-10
PRIOR APPLICATION NUMBER: 60/181,450
PRIOR FILING DATE: 2000-02-10
NUMBER OF SEQ ID NOS: 16
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 10
LENGTH: 125
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          . Sequence 10, Application US/09894711; Patent No. US20020137144A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GENERAL INFORMATION:
APPLICANT: Kjeldsen, Thomas Borglum
APPLICANT: Ludvigsen, Svend
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TYPE: PRT ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      OTHER INFORMATION: Synthetic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             50; Conservative
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Matches 50; Conserva
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  US-09-894-711-10
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Search completed: September 16, 2003, 12:52:26 Job time : 34.7237 secs

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GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.
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 protein search, using sw model OM protein September 16, 2003, 12:36:15; Search time 12.4903 Seconds (without alignments) 823.845 Million cell updates/sec Run on:

1 MFPIIPLSRLFDNAMLRAHR.....IVEQCCTSICSLYQLENYCN 107 US-09-423-100-6 587 Fitte: Perfect score: Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

283308 seqs, 96168682 residues Searched: 283308

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Total number of hits satisfying chosen parameters:

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database :

pik_76:* 1: pir1:* 2: pir2:* 3: pir3:* 4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

insulin 1 precurso	insulin - goose	insulin 2 precurso	insulin 2 precurso	insulin 11 - North	insulin I2 - North	insulin precursor	insulin - crested	insalin - turkey (insulin - ostrich	insulin - black-be	insulin - slider t	insulin precursor	insulin - Amphiuma	insulin - duckbill	insulin precursor
IPRT1	INGS	IPRT2	I NMS 2	: 44469	S44470	151221	TNPO	NTK	SONI	A61129	A60414	IPCH	S61361	563590	IPDK
7	٦	-	-	~	~	~	-	_	-	- -	7	_	~	7	-
110	51	110	110	25	52	103	51	51	51	51	51	107	55	51	81
42.4	42.3	42.2	42.2	41.9	41.9	41.7	41.7	41.7	41.7	41.7	41.7	40.8	40.5	40.1	39.8
249	248.5	248	248	246	246	245	244.5	244.5	244.5	244.5	244.5	239.5	238	235.5	233.5

ALIGNMENTS

RESULT 1
PC7082
epidermal growth factor/single chain insulin fusion protein . Bacillus brevis (fragme
C;Species: Bacillus brevis
C;Date: 18-Aug-2000 #sequence_revision 18-Aug-2000 #text_change 31-Mar-2003
C;Accession: PC7082; PC7083
R;Koh, M.; Hanagata, H.; Ebisu, S.; Morihara, K.; Takagi, H.
Biosci. Biotechnol. Biochem. 64, 1079-1081, 2000
A; Title: Use of Bacillus brevis for synthesis and secretion of Des-B30 single-chain h
A; Reference number: PC7082; MUID:20335834; PMID:10879487
A; Accession: PC7082
A;Molecule type: DNA
A; Residues: 1-96 <koh></koh>
A; Accession: PC7083
A; Molecule type: protein
A; Residues: 19-28 <ko2></ko2>
C; Genetics:
A;Gene: eqf-sci
C;Superfamily: insulin
Query Match 46.8%; Score 275; DB 2; Length 96;
Best Local Similarity 94.3%; Pred. No. 1.2e-21;
Matches 50; Conservative 1; Mismatches 0; Indels 2; Gaps 1;
Qy 55 REVNQHLCGSHLVEALXT,VCGERGFFYTPKTRGTVEQCCTSLCSLYQLENYCN 107
Db 46 KEVNOHLGGSHLVEALZLVGGERGFFFFFF GIVEQCGSIGSLFQLENYCN 96

insulin - sperm whale

Cipate: Species: Physelec catodon (sperm whale)
Cipate: 31.Mar-1992 #sequence_revision 31.Mar-1992 #text_change 16.Jul-1999
Cipate: 31.Mar-1992 #sequence_revision 31.Mar-1992 #text_change 16.Jul-1999
Cipate: Sind And 1992 #sequence_revision 31.Mar-1992 #text_change 16.Jul-1999
Cipate: Species 1998
Cipate: Species 1998
A.Title: Structure of sperm- and sei-whale insulins and the:r breakdown by whale peps A.Reference number: A93142
A.Reference number: A93142
A.Residues: 1-30;31-51 <ISH>
R.Harris, J. I.; Sanger, F.; Naughton, M.A.
Arch. Biochem. Biophys. 65, 427-428, 1956
A.Title: Species differences in insulin.
A.Reference number: A90082
A.Accession: A90082 A:Wolecule type: protein
A:Residues: 1-30:31-51 <HAR>
C;Superfamily: insulin
C;Keywords: hormone: pancreas
F;1-30/Domain: insulin chain B #status experimental <BCH> ~

```
C. Accession: J00178
R. Wetckam, W.; Groneberg, J.; Leineweber, M.; Wengenmayer, F.; Winnacker, E.L.
Gene 19, 179-183, 1982
A.Title: The nucleotide sequence of cDNA coding for preproinsulin from the primate Ma
A.Reference number: J00178; MUID:83080474; PMID:6184262
A.Accession: J00178
A.Molecule type: mRNA
A.Residues: 1-110 (WET>
A.Cross-references: GB-J00336; NID:g342121; PIDN:AAA36849.1; PID:g342122
C.Superfamily: Insulin
F:1-24/Domain: signal sequence *status predicted <MAT>
F:25-54,90-110/Product: insulin chain B *status predicted <MAT>
F:25-54,00-110/Product: insulin connecting predicted <AMT>
F:55-89/Dom in: Insulin chain A *status predicted <AMT>
F:55-89/Dom in: Insulin chain A *status predicted <AMT>
F:55-89/Dom in: Insulin chain A *status predicted <AMT>
F:31-96,43-109,95-100/Disulfide b.nds: *status predicted
F:31-96,43-109,95-100/Disulfide b.nds: *status predicted
C;Species: Cercopithecus aethiops (green monkey, grivet)
C;Species: Cercopithecus aethiops (green monkey, grivet)
C;Species: O4-Mar-1993 #Sequence_revision 18-Nov-1994 #text_change 16-Jul-1999
C;Accession: B42179; #Sequence_revision 18-Nov-1994 #text_change 16-Jul-1999
C;Accession: B42179; #Sequence 18-Nov-1994 #text_change 16-Jul-1999
R;Selno, S.; Bell, G.I.; Li, W.H.
A): Ball, G.I.; Li, W.H.
A): Bell, G.I.; Li, W.H.
A): Tile: Sequences of primate insulin genes support the hypothesis of a slower rate on A;Reference number: A42179; MUID:9219953; PMID:1560757
A;Molecule func.
                                                                                                                                                                                                                                                                                                                                                      A:Molecule type: DNA
A:Residues: 1-110 <SEL:
A:Residues: 1-110 <SEL:
A:Residues: 1-110 <SEL:
A:Cross references: EMBL:X61092; NID:922808; PIDN:CAA43405.1: PID:922869
A:Cross references extracted from NCBI backbone (NCBIN:95185, NCBIP:95194)
A:Note: sequence extracted from NCBI backbone (NCBIN:95185, NCBIP:95194)
B:Peterson, J.D.; Nehrlich, S.; Oyer, P.E.; Steiner, D.F.
J. Biol. Chem. 247, 4866-4811, 1372
J. Biol. Chem. 247, 4866-4811, 1372
A:Reference number: 492111; MUID:72288016; PMID:4626369
A:Accession: A0523
A:Accession: A0523
A:Molecule type: protein
A:Residues: 57-87 <PET>
C:Genetics:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   insulin precursor - crab-eating macaque
C:Species: Macaca fascicularis (crab-eating macaque)
C:Date: 07-Sep-1990 #sequence_revision 07-Sep-1990 #text_change 16-Jul-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              23 PAFVNOHLCGSHLVEALYLY "GERGFFYTPKTRREAEDPOVGOVELGGGFGAGSLOPLAL
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C:Superfamily: insulin
C:Keywords: hormone; pancreas
F:1-24/Domain: signal sequence *status predicted <SIG>
F:25-54/Domain: insulin chain # *status predicted <BCH>
F:25-54,90-110/Peroduct: insulin *status predicted <MAT>
F:57-97/Domain: connecting peptide *status experimental
F:90-110/Domain: insulin chain A *status predicted <ACH>
F:31-96,43-109,95-100/Disulfide bonds: *status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         46.5%; Score 273; DB 2;
60.2%; Pred. No. 2.2e-21;
tive 0; Mismatches 1.
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60.2%; Pred. No. 2.2e-21;
tive 0; Mismatches 1;
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Matches 53; Conservative
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Best Local Similarity 60.29
Matches 53; Conservative
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X:Residues: 1-30,31-51 <SMI>
A:Note: the species of elephant is not given, but it is most probably the Indian elephan
C:Superfamily: insulin
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              insulin - finback whale (tentative sequence)
C;Species: Balaenoptera physalus (finback wha'e, common rorqual)
C;Dacte: 31-Mar-1992 *sequence_revision 31-Mar .992 *text_change 16-Jul-1999
C;Accession: A91918
R;Hama, H.; Titani, K.; Sakaki, S.; Narita, K.
J. Blochem. 56, 285-293, 1964
A;Title: The amino acid sequence in fin-whale insulin.
A;Reference number: A91918
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              C;Species: Elephantidae gen. sp. (elephant)
C;Date: 24.Apr-1984 *sequence_revision 30-Sep-1988 *text_change 16-Jul-1999
C;Accession: A01584
                                                                                                                                                                                                                               Gaps
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                                                                                                                                                                                                                                                                                            56 FVNQHLCGSHLVEALYLVCGERGFFYTPKTRGIVEQCCTSICSLYQLENYCN 107
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                                                                                                                                                                                                                                                                                                                              1 FVNQHLCGSHLVEALYLVCGERGFFYTPKA-GIVEQCCTSICSLYQLENYCN 51
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                                                                                                                                                                  51;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 51;
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A; Title: Species variation in the amino acid sequence of insulin.
A; Reference number: A90029; MUID:66160119; PMID:5949593
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1; Indels
                                                                                                                                                                                .7e-22;
1; Indels
                                                                                                                                                                  Length
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    C.Superfamily: insulin
C.Keywords: hormone; pancreas
F;1-30,31-51/Product: insulin chain B *status experimental <BCH>
F;1-30,31-51/Promatin: insulin distatus experimental <MAT>
F;31-51/Domatin: insulin chain A *status experimental <ACH
F;7-37,19-50,36-41/Disulfide bonds: *status predicted
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F:1-30/Domain: insulin chain B *status experimental <BCH>
F:1-30,31-51/Product: insulin *status experimental <MAT>
F:31-51/Domain: insulin chain A *status experimental <ACH>
F:7-37,19-50,36-41/Disulfide bonds: *status predicted
                                 F;1-30,31-51/Product: insulin *status experimental <MAT>F;31-51/Domain: insulin chain A *status experimental <ACIF;7-37,19-50,36-41/Disulfide bonds: *status p;:dlcted
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Pred. No. 8.7e-22;
0; Mismatches 1;
                                                                                                                                                        Score 273.5. E
; Pred. No. 8.7e-
0; Mismatches
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ilarity 96.2%;
Conservative (
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                                                                                                                                                           Query Match
Best Local Similarity 96.2%;
Matches 50; Conservative
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A; Residues: 1-30; 31-51 <HAM>
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Best Local Similarity
Matches 49; Conserv
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es 50; Conserv
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Matches

RESULT 4

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RESULT 5

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Rioliveira, A.E.A.; Machado, O.L.T.; Gomes, V.M.; Xavier-Neto, J.; Pereira, A.C.P.; V Protein Pept. Lett. 6, 15-21, 1999
A; Title: Jack bean seed coat contains a protein with complete sequence lomology to bc A; Reference number: A59151
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A01579;
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A; Cross-references: GB.J00265: NID:q186429; PIDN:AAA59172.1: PID:q386828
R; Bell, G.L.; Swain, W.F.; Pieret, R.; Cordell, B.; Goodman, H.M.; Rutter, W.J.
Nature 282, 525-527, 1979
A; Title: Nucleotide sequence of a CDNA clone encoding human preproinsulin.
A; Reference number: A93216; MJD:80054779; PMID:503234
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C:Date: 23-Oct-1981 #sequence_revision 23-Oct-1981 #text_change 08-Dec 2000
C:Accession: A93222: A94253: A93216; A94251; A93144; A92075; A91166; 15H114;
C:BiBell, G.I.; Pictet, R.L.; Rutter, W.J.; Cordell, B.; Tischer, E.; Gondman, Nature 284, 26-32, 1980
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1; Gans
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A; Residues: 1-110 cREL.>
A; Cross-references: GB:J00265, D:g186429; PIDN:AAA59172.1; P1D:g186824
A; CID:Ch. A.; Dull, T.J.; Gray, A.; Brosius, J.; Sures, 1.
Science 209, 612-615, 1980
A; Title: Genetic variation in the human insulin gene.
A; Reference number: A94253; MUID: 6226313; PMID: 6248962
A; Molecule type: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A)Cross-references: GB:J00265; NID:g186429; PIDN:AAA59172.1; PID:g386828
R;Sures, I:; Goeddel, D.V.: Gray, A.; Ullrich, A.;
Science 208, 57-59, 198.
A;Title: Nucleotide sequence of human preproinsulin complementary DNA
A;Reference number: A94251; MUID:80147417; PMID:6927840
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A:Cross-references: GB:J00265; NID:9186429; PIDN:AAA59172.1; PID:9386628
R:Nicol, D.S.H.W.; Smith, L.F.
Nature 187, 483-485, 1960
                                                                                                                                                                                                                                                                                                                                                                A;Wolecule type: protein
A;Residues: 31-51 <MACA>
C;Comment: The two chains are probably produced from the same precursor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                56 FVNOHLCGSHLVEALYLVCGERGFFYTPKTRGIVEOCCTSICSLYQLENYCN 107
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                F)1-30,31-51/Product: insulin #status experimental <MAT>
F)1-30/Domain: chain B #status experimental <GHB>
F)31-51/Oomain: chain B #status experimental <GHB>
F)31-51/Oomain: chain A #status experimental <GHB>
F)3-37,19-50,36-41/Disulfide bonds: #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A;Title: Sequence of the human insulin genc.
A;Reference number: A93222; MUID:80120725; PMID:6243748
A;Accession: A93222
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A;Molecule type: protein
A;Residues: 25-54;90-110 <NIC>
R;Oyer, P.E.; Cho, S.; Peterson, J.D.; Steiner, D.F.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A; Title: Amino-acid sequence of human insulin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    insulin precursor (validated) - human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      45.6%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  N;Alternate names: preproinsulin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A; Reference number: A93144
                                                                                                                                                                                                                                A; Molecule type: protein
A; Residues: 1-30 <MACB>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A:Molecule type: mRNA
A;Residues: 1-110 <BEL2>
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Best Local Similarity
Matches 48; Conserv
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A; Residues: 1-110 <SUR>
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A:Reference number: A01591; MUD:72189454; PMID:5028210
A:Reference number: A01591; MUD:72189454; PMID:5028210
A:Reference number: A01591; MUD:72189454; PMID:5028210
A:Accession: A01591
A:Molecule type: protein
A:Residues: 1-30.31-51 <BUE>
C:Superfamily: Insulin
C:Reywords: hormone; pancreas
F:1-30.70main: Insulin chain B *status predicted <AMI>
F:31-51/Domain: insulin chain A *status predicted <AMI>
F:31-51/Domain: thulin chain A *status predicted <AMI>
F:31-51/Domain: thulin chain B *status predicted <AMI>
F:31-51/Domain: builin chain B *status bui
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             23 PAFVNQHLCGSHLVEALYLVCGERGFFYTPKTRREAEDPQVGOVELGGGFGAGSLQPLAL 82
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C;Species: Acomys cahirinus (Egyptian spiny mouse)
C;Date: 13-Jul-1981 #sequence_revision 13-Jul-1981 #text_change 31-Mar-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                insulin precursor - jack bean (fragments)
NiAlternate names: hypoglycemic agent; plant insulin
C;Species: Canavalla ensiformis (jack bean)
C;Date: 07-Dec-1999 *sequence_revision 07-Dec-1999 *text_change 10-Dec-1999
C;Accession: B59151; A59151
                                                                                                                                                                                                                                                                                                                                                                                                                                         C;Species: Cricetinae gen. sp. (hamster)
C;Date: 31-Mar-1992 #sequence_revision 31-Mar-1992 #text_change 16-Jul-1999
C;Accession: A91456
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                R;Neelon, F.A.; Delcher, H.K.; Steinman, H.; Lebovitz, H.E.
Fed. Proc. 32, 300, 1973
A;Title: Structure of hamster insulin: comparison with a tumor insulin.
A;Reference number: A91456
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A; Molecule type: protein
A; Residues: 1-30; 31-51 cNEE>
C; Superfamily: insulin
C; Keywords: hormone; pancreas
E; 1-30/Domain: insulin chain B *status experimental <BCH>
F; 1-30, 31-51/Ponnain: insulin chain A *status experimental <ACH>
F; 31-51/Domain: insulin chain A *status experimental <ACH>
F; 31-51/Domain: insulin chain A *status experimental <ACH>
F; 7-37, 19-50, 36-41/Disulfide bonds: *status predicted
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         46.3%; Score 271.5; DB 1 94.2%; Pred. No. 1.4e-21; tive 2; Mismatches 0
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R;Buenzli, H.F.; Humbel, R.E.
Hoppe-Seyler's Z. Physiol. Chem. 353, 444-450, 1972
                                                                                                                                             83 EGSLQKRGIVEQCCTSICSLYQLENYCN 110
                                                                                                    -----RGIVEOCCTSICSLYQLENYCN 107
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Matches 49: Conservative
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C:Species: Balaenoptera borealis (sci whale)
C:Date: 13-01-1981 #sequence_revision 13-01-1981 #text_change 16-Jul-1999
C:Date: 13-01-1981 #sequence_revision 13-Jul-1981 #text_change 16-Jul-1999
C:Accession: A0158
R:Ishihara, Y.; Saito, T.; Ito, Y ; Fujino, M.
Nature: 181, 1488-1469, 1958
A;Tille: Structure of sperm- and sei-whale insulins and their breakdow: by whale peps A;Reference number: A93142
insulin precursor - chimpanzee
C;Species: Pan troglodytes (cl. enzee)
C;Date: 04-Mar-1993 sequence_revision 18-Nov-1994 #text_change 16-Jul 1999
C;Accession: A42179; S22058
R;Selno, S.; Bell, G.I.; Li, W.H.
Mol. Biol. Evol. 9, 193-203, 1992
A;Title: Sequences of primate insulin genes support the hypothesis of a slower rate in R;Reference number: A42179; MuID:92219953; PMID:1560757
A;Accession: A42179
A;Accession: A42179
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 C:Species: Capra aegagrus hircus (domestic goat)
C:Date: 13-Jul-1981 #sequence_revision 13-Jul-1981 #text_change 16-Jul-1999
C:Accession: A01586
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A;Molecule type: DNA'
A;Residues: 1-110 <SEI>A;Residues: 1-110 <SEI>A;Residues: 1-110 <SEI>A;Residues: 1-110 <SEI
A;Cross-references: EMBL:X61089; NID:q38251; PIDN:CAA43403.1; PID:g38252
A;Note: sequence extracted from NCBI backbone (NCBIP:95067)
C;Genetics:
A;Introns: 63/1
C;Superfamily: Insulin
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A;Title: Species variation in the amino acid sequence of insulin.
A;Reference number: A90029; MUID:66160119; PMID:5949593
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A:Residues: 1-30;31-51 <15H>
C:Superfamily: insulin
C:Superfamily: insulin
C:Reywords: hormone: pancreas
F:1-30,31-51/Pomain: insulin chain B #status experimental <ACH>
F:31-51/Pomain: insulin chain A #status experimental <ACH>
F:7-37,19-50,36-41/Pisulfide bonds: #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 257; DB 2; L
Pred. No. 9.3e-21;
0; Mismatches 0;
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92.3%; Pred. No. 9.6e-21;
ive 0; Mismatches 3.
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60.5%;
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Matches 48; Conservative
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Matches 52; Conservative
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A;Residues: 1-30;31-51 <SMI>
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A; Retearch Carle Lype: DNA
A; Status: preliminary; translated from GB/EMBL/DDBJ
A; Status: preliminary; translated from GB/EMBL/DDBJ
A; Motecasion: 158114
A; Residues: 1-59,63-110 <RES>
A; Cross-references: GB:L15440; NID:9307071; PIDN:AAA59179.1; PID:9307072
A; Cross-references: GB:L15440; NID:9307071; PIDN:AA59179.1; PID:9307072
A; Cross-references: GB:L15440; NID:9307071; PIDN:AA59179.1; PID:9307072
A; Title: Totalsynthese von Humaninsulin unter gezielter Bildung der Disulfidbindungen.
A; Reference number: A91636; MULD:7507277; PMID:4443293
A; Note: disulfide-bonded human insulin was synthesized; the synthetic hormone was ident; A; Note: article in German with English abstract
B; Contents: annotation; Synthesis of residues 57-87
B; Contents: a
                                                     J. Biol. Chem. 246, 1375-1386, 1971
A;Title: Studies on human proinsulin. Isolation and amino acid sequence of the human pan A;Feference number: A2075; MUID:71116410; PMID:5101771
A;Accession: A92075
A;Holecule type: protein
B;Residues: 57-87 corps
B;Residues: 57-87 corps
B;Residues: 57-87 corps
B;Residues: 57-87 corps
B;Ro, A: Smyth, D.G.; Markussen, J.; Sundby, F.
Eur. J. Blochem. 20, 190-199, 1971
B;Ro, A: Smyth, D.G.; PMID:71257722; PMID:5560404
B;Reference number: A91186; MUID:71257722; PMID:5560404
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A;Molecule type: protein
A;Residues: 57-87 <KOA>
R;Lucassen, A.M.; Julier, C.; Beressl, J.P.; Boitard, C.; Froguel, P.; Lathrop, M.; Bell
Nature Genet. 4, 305-310, 1993
A;Title: Susceptibility to insulin dependent diabetes mellitus maps to a 4.1 kb segment
A;Reference number: 158114; MUID:93364428; PMID:8358440
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Pred. No. 9.3e-21;
0; Mismatches 0
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56 FVNQHLCGSHLVEALYLVCGERGFFYTPKT--

Match 45.5%; Local Similarity 60.5%; Nes 52; Conservative

Best Loc Matches

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C; Genetics

SLOKRGIVEOCCTSICSLYOLENYCN 110 ----RGIVEQCCTSICSLYQLENYCN 107

RESULT 11 A42179.

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J. Fac. Med. Baghdad 14, 16-28, 1972
A.Title: The isolation and characterization of insulin of camel (Camelus dromedarius).
A;Reference number: A92782
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C.Species: Camelus dromedarius (Arabian camel)
C.Date: 31-Mar-1992 #sequence_revision 31-Mar-1992 #text_change 16-Jul-1999
C:Accession: A92782
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C;Dactes: 2Jun-1981 #sequence_revision 22-Jun-1981 #text_change 16-Jul-1999
C;Accession: A01583; A94572; S16492; A60835; B60835
R;Chance, R.E.; Ellis, R.M.; Bromer, W.W.
Science 161, 165-167, 1968
A;Tkle: Porcine proinsulin: characterization and amino acid sequence.
A;Reference number: A94240; MUID:68286485; PMID:5657063
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C;Superfamily: insulin
C;Keywords: hormone; pancreas
F;1-30,7Domain: insulin chain B *status experimental <BCH>
F;1-30,31-51/Product: insulin *status experimental <MAT>
F;31-51/Domain: insulin chain A *status experimental <ACH
F;7-37,19-50,36-41/Disulfide bonds: *status predicted
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                                                                                                                                                                                          DB 1;
                                                                                                                                                                                       Query Match

44.9%; Score 263.5; DB 1;
Best Local Similarity 90.4%; Pred. No. 9.6e-21;
Matches 47; Conservative 1; Mismatches 3;
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90.4%; Pred. No. 9.6e-21;
tive 1; Mismatches 3;
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A; Residuee: 1.84 <CH2>
R; Brown, H.; Sanger, F.; Kitai, R.
B; Brown, J. 60, 556-565, 1955
A; Ittle: The structure of pig and sheep insulins.
A; Reference number: A90344
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A.Residuce: 1-30,31-51 (-8RO)
R.Shel, L.: Damqaard, U.
HOrm. Metab. Res. 20, 476-480, 1988
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A;Molecule type: protein
R;Residues: 1-34, 'Q', 36-84 <CHA>
R;Chance, RE.
submitted to the Atlas, July 1970
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Best Local Similarity 90.4%
Matches 47; Conservative
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A; Residues: 1-30; 31-51 <DAN>
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A; Accession: A94572
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A; Accession: A92782
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A; Accession: S16492
                                                                                                                                                                                                                                                                                                                                                                                                                                          RESULT 14
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A.Molecule type: protein
A.Residues: 33-38.40.62 <SNE>
A.Residues: 13-38.40.62 <SNE>
A.Residues: the authors report the c.. acterization of a connecting peptide variant lackf
A.Rocession: B60835
A.Molecule type: protein
A.Residues: 33-62 <SNO.
B.Blundell: T.; Dodson, G.; Hodgkin, D.; Mercola, D.
R.Blundell: T.; Dodson Chem. 26, 279-402, 1972
A.Title: Insulin the structure in the crystal and its reflection in chemistry and bi
A.Reference number: A90001
A.Contents: annotation; X-ray crystallography, 1.9 angstroms
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 84;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           us experimental <MAT>
**Status experimental <CPEP>
atus experimental <ACH>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                :tus experimental <BCH>
                                                                                                                                                                                                                                                                                                                                                                                                                                            C; Superfamily: insulin
C; Keywords: hormone; pancreas
F; 1-30,54-84/Product: insulin * : us experimental < BCH:
F; 1-30,54-84/Product: insulin * : us experimental < MAT>
F; 13-53/Domain: connecting pepti * status experimental < ACI
F; 44-84/Domain: insulin chain A atus experimental < ACI
F; 7-70,19-83,69-74/Disulfide bo.d. * status experimental
A:Title: Proinsulin heterogeneity in pigs.
A:Reference number: A60835; MUID:⊬9032178; PMID:3181865
A;Accession: A60835
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     44.8%; Score 263; DB 1;
60.7%; Pred. No. 1.8e-20;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      56 FVNQHLCGSHLVEALYLVCGERGFFYTPKT----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Search completed: September 16, 2003, 12:40:35 Job time : 12.4903 secs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                86 -- RGIVEQCCTSICSLYQLENYCN 107
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity 60.79
Matches 51; Conservative
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GenCore version .1.6
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OM protein - protein search, using sw model

September 16, 2003, 12:33:30; Search time 8.32685 Seconds (without alignments) 604.293 Million cell updates/sec Run on:

fitte: TGS-09-423-100-6
Perfect score: 587
Sequence: 1 MFPTIPLSRLFDNAMLRAHR.....IVEQCCTSICSLYQLENYCN 107

Scoring table:

BLOSUM62 Gapop 10.0 , Gapext 0.5

127863 seqs, 47026705 residues Searched:

127863 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

SwissProt_41:* Database:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

		æ			SUMMARIES	
Result No.	Score	Query Match	Query Match Length	DB	ID	Description
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٠, د	0.00		7.5	٠,	THOUSE ONLY	
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~	273	ė.	110	-	INS_CERAE	P30407 cercopithec
4	273	•	110	_	INS_MACFA	macaca
'n	268.5	٠	51	_	INS_ACOCA	
Q	267		110	Н	INS_HUMAN	P01308 homo sapien
7	267	45.5	110	٦	INS_PANTR	P30410 pan troglod
æ	266	45.3	110	٦	INS_SPETR	~
σ	263.5		5.1		INS_BALBO	4
10	263.5	44.9	51	-	INS_CAMDR	0 camel
11	263.5	44.9	51	-	INS_CAPHI	P01319 capra hircu
12	263	44.8	108	~	INS_PIG	P01315 sus scrofa
13	263		110	-	INS_RABIT	P01311 oryctolagus
14	262.5		51	7	INS_FELCA	
15	262		110	٦	INS_CANFA	P01321 canis famil
	260		110	-	INS_CRILO	P01313 cricetulus
7	258.5	4.	105	٦	INS_BOVIN	P01317 bos taurus
80	257		108	-	INS_AOTTR	P10604 actus trivi
6	257	٠.	110	~	INS_PSAOB	
	256.5	43.7	51	-	INS_DIDMA	
~	255.5		217	н	SOMA_HUMAN	
~	255.5		217	1	SOMA_MACMU	P33093 macaca mula
~	255.5	ω,	217	-	SOMA_PANTR	
4	254.5		105	-	INS_SHEEP	-
2	252	42.9	86	~	INS_HORSE	P01310 equus cabal
56	251.5	42.8	51	~	INS_CHIBR	
27	250	42.6	108	-	INS1_MOUSE	P01325 mus musculu
28	249	42.4	110	٦	INS1_RAT	P01322 rattus norv
58	249	42.4	217	٦	SOMA_CALJA	O9gmb3 callithrix
30	249		217	٦	SOMA_SAIBB	P58343 saimiri bol
31	248.5	42.3	51	7	INS_ANSAN	P07454 anser anser
32	248		110	٦	INS2_MOUSE	32
33	248		110	7	INS2_RAT	P01323 rattus norv

P81423 acipenser 9 P51463 selasphorus	P01328 hystrix cri	P31887 trachemys s	P01332 gallus gall	P58757 pan troglod	Q9tqy7 ornithorhyn	P01333 anas platyr	P12703 alliqator m	P09476 lepisosteus	P12708 zaocys dhum	_
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INS_ACIGUINS SELRE	INS_HYSCH	INS TRAS	INSCHIC	SOM2_PAN	INS_ORNA!	INS_ANAPI	INS_ALLM	INS_LEPSI	INS_ZAODE	SOM2_HUM
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52	51	51	107	217	51	81	51	52	51	217
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41.9	41.	41.	40.	40.	40.	39.	39.	39.	38.	38.
246	244.5	244.5	239.5	236	235.5	233.5	231.5	231	228.5	228
3.4	36	37	38	39	40	4 7	4.2	43	44	5.4

ALIGNMENTS

ond (s). uteleostomi: ti;	OWII TT	THE PENTOSE PHOSPHATE A CHAIN LINKED BY FWO ELAXIN FAMILY.	
PRT; 51 AA. ed) sequence update) annotation update) ack whale) (Common rorqual	Physeter catodon (Sperm whale) (Physeter macrocephalus). Eukaryota; Metazoa: Chordata: Craniata: Vertebrata: Euteleostomn Mammalia: Eutheria: Cetartiodactyla: Cetacea: Mysticeti; Balaenopterides: Balaenoptera. NOBL_TaxID=9770, 9755; [1] SPECIES-B.physalus: Fhama H.r. Titani K Sakaki S., Narita K.; The amino acid sequence in fin whale insulin.*; J. Blochem. 56:285-293(1964) SEQUENCE.	TES-P. catodon; hara Y., Saito T., Ito Y., Fujino M.; hara Y., Saito T., Ito Y., Fujino M.; ucture of sperm- and sel-whale insulins and their breakd e pepsin."; re 181:1468-1469(1958). re 181:1468-1469(1958). 1ES-P. catodon; 1S JI., Sanger F., Naughton M.A.; cies differences in insulin."; 1. Blochem. Biophys. 65:427-438(1956). 1. Blochem. Biophys. 65:427-438(1956). 1. Blochem. Biophys. 65:427-438(1956). 1. Blochem. Biophys. 65:427-438(1956).	FATTY ACIDS. IT ACCELERATES GLYCOLYSIS, THE PENTOSE PHOSPHA CYCLE, AND GLYCOGEN SYNTHESIS IN LIVER. CYCLE, AND GLYCOGEN SYNTHESIS IN LIVER. CYCLE, AND GLYCOGEN SYNTHESIS IN LIVER. DISULTIPE BONDS. SUBGUIT: HETERODIMER OF A B CHAIN AND AN A CHAIN LINKED BY DISULFIDE BONDS. SUBCELLULAR LOCATION: Secreted. SIMILARITY: BELONGS TO THE INSULIN/IGF/RELAXIN FAMILY. A919 18; INWHF. PO1317: INWHP. TP 'O: IPRO04825; Ins/IGF/relax. T: SMO0075: ILGF; I. IT: PSO0262: INSULIN: 1.	ose metabolism. INSULIN B CHAIN. INSULIN A CHAIN. INTERCHAIN. INTERCHAIN.
D; PRT: 51 AA Created) Last sequence update) Last annotation updat (Finback whale) (Comm	whale) (Physical Cranic Triodectyla, prera, prera, narit in fin whal	Y. Bei-wha	LERATES GLY SYNTHESIS II OF A B CHA. : Secreted. TO THE INSUI	· O
STANDARD; (Rel. 01, Cr (Rel. 01, La (Rel. 34, La	codon (Sperm whale) (Physet. Wetazoa: Chordata: Craniata utheria: Ctartiodactyla: C idae: Balaenoptera. 9770, 9755. DENCE. hysalus: Sakak: S., Narita acid Sequence in fin whale 56:285-293(1964)	SPECIES-P. catodon; Ishihara Y., Saito T., Ito Y., Fujino M.; "Structure of sperm- and sei-whale insulins whale pepsin."; Nature 181:1468-1469(1958). [3] SECURICE. SPECIES-P. catodon; Harris J.I., Sanger F., Naughton M.A.; "Species differences in insulin."; "Species differences in insulin."; "Species differences in insulin."; "Species differences in insulin."; "Species Churin Insulin."; "Species	INCREASES CELL PERMISALLITY TO MCNOSACO FATTY ACIDS. IT ACCELERANCES GLYCOLYSIS CYCLE, AND GLYCOGEN SYNTHESIS IN LIVER - SUBGUNT: HETERODIMER OF A B CHAIN AND DISULPIDE BONDS. -! SUBCELLULAR LOCATION: Secreted. -! SIMILARITY: BELONGS TO THE INSULIN/IGE PIR, A991948; INWHF. FIR, A99142; INWHF. HSSP; OO1317; LAPH. InterP O: IPRO04835; Ins/IGF/relax. PROSITE: PS00026: INSULN: 1.	ily; Hormone; 30 31 31 51 7 37 19 50 19 50 36 41
JLT 1 JALPH	Physerer catodon (Sp Eukaryota; Metazoa; Manmalia; Eutheria Baldenopteridae; Bal NCBL_TaxID=9770, 975 1	SPECIES-P. catodon; Ishihara Y., Saito "Structure of sper Whale pepsin."; Nature 181:1468-14 [3] SCOUENCE. SPECIES-P. catodon; Harris J.T., Sarge "Species differenc Arch. Blochem. Blo	INCREASES CELL FATTY CIELL FATTY CIEL, AND GLYC	
RESULT INS_BA INS_BA IDD I AC P DT 2 DT 2 DT 0 DT 0 CN 1	R R R R R R R O O O O O O O O O O O O O	R R R R R R R R R R R R R R R R R R R		KY FT FT FT SO

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Cercopithecinae; Cercopithecus.
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Matches
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                            ä
                           Gaps
                                                                                                                                                                                                                                                       Cercopithecus aethiops (Green monkey) (Grivet).
Eukaryota, Metazoa: Chordata, Craniata; Vertebrata; Euteleostomi;
Mammalia; ?utheria; Primates; Catarrhini; Cercopithecidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     56 FVNQHLCGSHLVEALYLVCGERGFFYTPKTRGIVEQCCTSICSLYOLENYCN 107
                                                                                                                                                                                Elephas maximus (Indian elephant).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Proboscidea; Elephantidae; Elephas.
                                             56 FVNQHLCGSHLVEALYLVCGERGFFYTPKTRGIVEQCCTSICSLYQLENYCN 107
                                                         1 FVNQHLGGSHLVEALYLVGGERGFFYTPKA-GIVEQCCTSICSLYQLENYCN 51
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 FVNQHLCGSHLVEALYLVGGERGFFYTPKT-GIVEQCCTGVCSLYQLENYCN 51
                            1;
                                                                                                                                                                                                                                                                                                                                  -1- SUBCELLULAR LOCATION: Secreted
-1- MISCELLEANEOUS: THE SPECIES OF ELEPHANT IS NOT GIVEN, BUI
MOST PROBABLY THE INDIAN ELEPHANI (ELEPHAS MAXIMUS)
-1- SIMILARITY: BELONGS TO THE INSULIN/IGF/RELAXIN FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 273.5; DB 1; Length 51;
Pred. No. 1.6e-22;
          Length 51;
         Query Match 46.6%; Score 273.5; DB 1; Length EBst Local Similarity 96.2%; Pred. No. 1.6e-22; Matches 50; Conservative 0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1: Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              9007B50CDB457D6D CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     INS_CERAE STANDARD; PRT; 110 AA. P30407; P01309; 01-APR-1993 (Rel. 25, Created) 01-APR-1993 (Rel. 25, Last sequence update) 01-FEB-1996 (Rel. 33, Last annotation update)
                                                                                                                                 21-JUL-1986 (Rel. 01, Created)
21-JUL-1986 (Rel. 01, Last sequence update)
01-FEB-1996 (Rel. 33, Last annotation update)
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INTERCHAIN.
                                                                                                                                                                                                                                                                                                                                                                                                               Hormone; Glucose metabolism
                                                                                                                51 AA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                            INTERCHAIN.
                                                                                                                                                                                                                                                                                                                                                                                IPR004825; Ins/IGF/relax.
                                                                                                                                                                                                                                       MEDLINE-66160119; PubMed-5949593;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               46.68;
                                                                                                                                                                                                                                                                                                                                                                                           SMART: SM00078; IIGF; 1.
PROSITE; PS00262; INSULIN; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            5752 MW:
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                                                                                                                STANDARD;
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es 49; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                          19
36
51 AA;
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                                                                                                                                                                                                           NCBI_TaxID-9783;
                                                                                                                                                                                                                                                                                                                                                                                                               nsulin family:
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                                                                                                                INS_ELEMA
P01316;
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DISULFID
SEQUENCE
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bloinformatics and the EMBL outstation the European Bioinformatics institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for connercial entities requires a license extrement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                              Peterson J.D., Nehrlich S., Oyer P.E., Steiner D.F., ^{\prime} Metermination of the amino acid sequence of the monkey, sheep, and dog proinsulin C-peptides by a semi-micro Edman degradation

    Biol. Chem. 247:4866-4871(1972).
    FUNCTION: INSULIN DECREASES BLOOD GLUCOSE CONCENTRATION. 17
INCREASES CELL PERREABILITY TO MONOSACCHARIDES. AMINO ACIOS AND
FATTY ACIDS. IT ACCELERATES GLYCOLYSIS, THE PENTOSE PHOSPHATE
CYCLE, AND GLYCOGGEN SYNTHESIS IN LIVER.
    SUBGUIT: HETERODIMER OF A B CHAIN AND AN A CHAIN LINKED BY TWO

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                                                                                MEDLINE-92219953; PubMed-1560757:
Seino S., Bell G.I., Li W.;
"Sequences of primate insulin genes support the hypothesis of
slower rate of molecular evolution in humans and apes than in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 110;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        -i. SUB-FELULAR LOCATION: Sereted.
-i. SIMILARITY: BELONGS TO TI : INSULIN/IGE/RELAXIN FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 se metabolism; Signal.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     46.5%; Score 273; DB 1;
60.2%; Pred. No. 4.1e-22;
tive 0; Mismatches 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              54 PRFVNQHLCGSHLVEALYLVCGERGFFYTPKT-----
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                                                                                                                                                                                                                                                                                                                   MEDLINE=72258016; PubMed-4526369;
                                                                                                                                                                                                                                  Mol. Blol. Evol. 9:193-203(1992)
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96
109
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HSSP; P01308; 1AIO.
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es 53; Conserv
                                                                                                                                                                                                                                                                                          SEQUENCE OF 57-87.
                                                       SEQUENCE FROM N.A.
NCBI_TaxID-9534;
                                                                                                                                                                                                                                                                                                                                                                                                                                        procedure."
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DISULFID
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a; Sciurognathi; Muridae; Murinae; Acomys.

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Mammalia; Eutheria; Rode:
NCBL_TaxID=10068;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Nature 284:26-32(1980)
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                                                                                                                                                                                                             HSSP; P01308; 1TYM
                                                                                                                                                                                                                                                                                                                                       51 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               insulin precursor.
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                                   COMPOSITION
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P01308;
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MEDLINE-83080474; Pubmed-6184262;

METEKARM W., Groneberg J., Leineweber M., Wengenmayer F.,

Winnerder E.L.;

The nucleotide sequence of cDNA coding for preproinsulin from the primate Macaca fascicularis.;

Gene 19:179-183(1982).

INCREASES CELL PERMERBILITY TO MONOSACCHARIDES, AMINO ACIDS AND FATTY ACIDS. IT ACCELERATES GLYCOLYSIS, THE PENTOSE PHOSPHATE CYCLE, AND GLYCOGEN SYNTHESIS IN LIVER.

C.: SUBJUIT: HETERODIMER OF A B CHAIN AND AN A CHAIN LINKED BY TWO DISJUININE BONDS.

INCREASE CELLULAR LOCATION: Secreted.

C.: SUBGELLULAR LOCATION: Secreted.

C.: SIMILARIIY: BELONGS TO THE INSULIN/IGF/RELAXIN FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            34; Caps
                                                                                                                                                                          AND
             Macaca fascicularis (Crab eating macaque) (Cynomolgus monkey).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Cercopithecidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Acomys cahirinus (Egyptian spiny mouse).
Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 110;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Pred. No. 4.1e-22;
0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               11991 MW: 83C6E33A80A420F9 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                           Insulin family: Hormone; Glucose metabolism; Signal. SignAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     46.5%; Score 273; DB 1;
60.2%; Pred. No. 4.1e-22;
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Last annotation update)
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INSULIN A CHAIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               51 AA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 -----RGIVEQCCTSICSLYQLENYCN 107
                                                                                                                                                                                                                                                                                                                                       or send an email to license@isb-sib.ch).
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HSSP; P01308; IA10.
InterPro; IPR004825; Ins/IGF/relax.
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21-JUL-1986 (Rel. 01, Last sequo
01-NOV-1997 (Rel. 35, Last anno
                                                                                                                                                                                                                                                                                                                                                                                                     Pram: PF00049; Insulin: 1.
PRINTS; PR00277: INSULINB.
SMART; SM00078: ILGF; 1.
PROSITE; PS00262; INSULIN: 1.
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                                                  Cercopithecinae; Macaca.
NCBL_TaxID=9541;
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96
109
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Matches 53; Conserv
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P01324;
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DISULFID
SEQUENCE
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CHAIN
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Buenzii H.F., Humbel R.E.;

*Isolation and partial structural analysis of insulin from mouse (Musculus) and spiny mouse (Acomys Cabirthus).

*Isolation insulin Deckeases Biodo Glucose Concentration. IT

*INCREASES CELL PERMEABILITY TO MONOSACCHARIDES, AMINO ACIDS AND FRATY ACIDS. IT ACCELERATES GLYCOLYSIS, THE PENTOSE PHUSPHATE CYCLE, AND GLYCOGEN SYNTHESIS IN LIVER.

*ISOLATION BONDS.**

DISCLETOR BONDS.**
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1: Gaps
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Nature 282:525-527(1979).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          56 FVNQHLCGSHLVEALYLVCGERGFFYTPKTRGIVEQCCTSICSLYQLENYCN 107
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Bell G.I., Swain W.F., Pictet R.L., Cordell B., Goodman H.M.,
Rutter W.J.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DB 1; Length 51;
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*Sequence of the human insulin gene.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Indels
                                                                                                                                                                                                                                                                                                                       -1- SUBGELLULAR LOCATION 'C'ECCG'.
-!- SIMILARITY: BELONGS TO THE INSULIN/IGF/RELAXIN FAMILY
PIR: A01591; INMSSP.
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INTERCHAIN (BY SIMILARITY).
BY SIMILARITY.
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Ullrich A., Dull T.J., Gray A., Brosius J., Sures I.;
"Genetic variation in the human insulin gene.";
Science 209:612-615(1980):
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   92BD8B629047D3D CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      core 268.5; DB 1;
Pred. No. 5.5e-22;
3; Mismatches 0;
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21-JUL-1986 (Rel. 01, Last sequence update)
15-SEP-2003 (Rel. 42, Last unnotation update)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             metabolism
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SMART; SM00078; IlGF; 1.
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MEDLINE-80120725; PubMed-6243748;
MEDLINE-72189454; PubMed-5028210;
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Insulin family; Hormone: C. crse
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92.38;
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Best Local Similarity 92...
Acc 48; Conservative
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A MEDLINE-22388257; PubMed-12477932;

A MEDLINE-22388257; PubMed-12477932;

A Klausner R.D., Collins F.S., Wagner L., Shemmen C.M., Schuler G.D.,

A Altaschul S.F., Zeeberg B., Butcow K.H., Schaefer C.F., Bhat N.K.,

A Altschul S.F., Zeeberg B., Butcow K.H., Schaefer C.F., Bhat N.K.,

A Altschul S.F., Jeeberg B., Butcow K.H., Schaefer C.F., Bhat N.K.,

A Altschul S.F., Jeeperg B., Butcow K.H., Schaefer C.F., Bhat N.K.,

A Altschul S.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,

RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,

RA Brownstein M.J., Usdin T.B., Toshhyuki S., Carninci P., Hullahy S.J.,

RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Hullahy S.J.,

RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gubsz R.A.,

RA Richards S., Worley K.C., Hale S., Garcia A.M., Gabs R.A.,

RA Willialon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,

RA Wilting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,

RA Blakesley R.W., Tucchman J.W., Green E.D., Dickson M.C.,

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RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;

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        SEQUENCE FROM N.A.

MEDLINE-8014/417; PubMed-6927840;

Sures I., Goeddel D.V., Gray A., Ullrich A.;

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Science 208:57-59(1980).
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Ko A., Smyth D.G., Markussen J., Sundby F.;
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"Studies on human proinsulin. Isolation and amino acid sequence
the human pancreatic C-peptide.";
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Nicol D.S.H.W., Smith L.F.;
*Amino-acid sequence of human insulin.";
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           e human pancreatic C-peptide.";
Biol. Chem. 246:1375-1386(1971).
                                                                                            SEQUENCE FROM N.A.
MEDLINE-93364428; PubMed-8358440;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDLINE-75040007; PubMed-4803504; Naithani V.K.;
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SYNTHESIS OF 57-87.
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                                                                                                                                                                                                           IISSUE-Pancreas;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TISSUE-Blood;
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of the mutant insulin A3 (V1-1-Neu) isolated from the pancreas.";
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"A mutation in the B chain ce, on gregion is associated with impaired profinsulin conversion in a far.ly with hyperproinsulinemia.";
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MEDLINE-84016053: PubMed-6312455;
Haneda M., Chan S.J., Kwok S.C.M., Rubenstein A.H., Steiner D.F.;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            sequencing of genomic deoxyribonucleic acid amplified by polymerase
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Studies on polypeptides, IV. The synthesis of C-peptide of human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDLINE-9037021; PubMed-2:96279;
Barbetti F., Raben N., Ka Jaki T., Cama A., Accili D., Gabbay K.
Merenich J.A., Taylor S.I., Roth J.,
Two unrelated patients with familial hyperproinsulinemia due to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDLINE-92291307; PubMed-1601997;
Yano H., Kitano N., Morimoto M., Polonsky K.S., Imura H., Scino Y
"A novel point mutation in the human insulin gene giving rise to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Shibasaki Y., Kawakami T., Kanazawa Y., Akanuma Y., Takaku F.; "Fosttranstational cleavage of proinsulin is blocked by a point mutation in familial hyperproinsulinemia."; J. Clin. Invest. 76:378-38*(1985).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          mutation substituting histidine for arginine at position 65 in
proinsulin molecule: Identification of the mutation by direct
                                                                             doppe-Seyler's Z. Physiol. Chem. 354:659-672(1973)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       serine-for-phenylalanine substitution.";
Proc. Natl. Acad. Sci. U.S.A. 80:7390-7394(1983)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        VARIANTS LOS ANGELES SER-48 AND CHICAGO LEU-49
MEDLINE-84170233: Pubmed-6424111;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Clin. Endocrinol. Metab. 71:164-169(1990)
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J. Clin. Invest. 89:1902-1907(1992).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            VARIANI PROVIDENCE ASP-34.
MEDLINE-87175640; Pubmed-3470344;
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MEDLINE-85261996; PubMed-4019786;
                                                                                                                                                                                                  MEDLINE-73161263; PubMed-4698555;
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                                                                                                                                                                SYNTHESIS OF 65-69 AND 70-73
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                                      proinsulin
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or send an email to license@isb-sib.ch).
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31
43 1
95 1
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091XI3;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    84
                                                                                                                                                                                                                                        "Comparative 2D NMR studies of human insulin and des-pentapeptide "Comparative 2D NMR studies of human insulin and des-pentapeptide Insulin: sequential resonance assignment and implications for protein Blochemistry 30:5505-5515(1991).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            25 FVNQHLCGSHLVEALYLVCGERGFFYTPKTRREAEDLQVGQVELGGGPGAGSIQPLALES
                                                                                                 assignment of a desrpentapeptide analogue and comparison with crystal structure.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
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"Two-dimensional Nmr studies of Des-(B26-B30)-insulin: sequence-
"Two-dimensional Nmr studies of service sequence-
specific resonance assignments and effects of solvent composition.";
Blochim. Biophys. Acta 1078:101-110(1991).
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-!- FUNCTION: INSULIN DECREASES BLOOD GLUCOSE CONCENTRATION. 1T INCREASES CELL PERHEABILITY TO MONOSACCHARIDES, AMINO ACIDS AND FATTY ACIDS. IT ACCELERATES GLYCOCYSIS, THE PENTOSE PHOSPHATE CYCLE, AND GLYCOGEN SYNTHESIS IN LIVER.

-!- SUBUNT: HETERODIMER OF A B CHAIN AND AN A CHAIN LINKED BY TWO DISULFIDE BONDS.
                                                                                        'Toward the solution structure of human insulin: sequential 2D 1H
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Pan troglodytes (Chimpanzee).
Eukaryota; Metazoa: Chordata: Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Pan.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           34;
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Seino S., Bell G.I., Li W.;
"Sequences of primate invulin genes support the hypothesis of
slower rate of molecular evolution in humans and apes than in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ch 45.5%; Score 267; DB 1; Length 110; I Similarity 60.5%; Pred. No. 1.8e-21; 52; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     -1- SUBCELLULAR LOCATION: Secreted.
-1- SIMILARITY: BELONGS TO THE INSULIN/IGF/RELAXIN FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  01-APR-1993 (Rel. 25, Created)
01-APR-1993 (Rel. 25, Last sequence update)
15-SEP-2003 (Rel. 42, Last annotation update)
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  [22]
STRUCTURE BY NMR.
MEDLINE-91104966; Pubmed-2271664;
                                                                                                                                                                                                                                                                                                                                                                          STRUCTURE BY NMR.
MEDLINE-91265527; PubMed-1646635;
                                                                                                                                                      Biochemistry 29:10545-10555(1990)
                                                                                                                                                                                                                       MEDLINE-91242467; PubMed-2036420;
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                                                                   Hua Q.-X., Weiss M.A.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   insulin precursor.
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                                                                                                                                                                                                     STRUCTURE BY NMR
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P30410;
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Mol. Biol
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Best Local 9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PROSITE; PS00262; INSULIN;
Insulin family; Hormone; Glatose metabolism; Signal; 3D-structure.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Spermophilus tridecemlineatus (Thirteen-lined ground squirrel).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Sciuridae; Sciurinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 110;
                                                                                                                                                                                                                                                                                                                                                                                                                                                   Indels
                                                                                                                                                                                                                                                                                                                                                             12025 MW; 41EB8DF79837CEF5 CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                        Score 267; DB 1;
Pred. No. 1.8e-21;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         IS-SEP-2003 (Rel. 42, Created)
15-SEP-2003 (Rel. 42, Last sequence update)
15-SEP-2003 (Rel. 42, Last annotation update)
                                                                                                                                                                                                                          INSULIN B CHAIN
                                                                                                                                                                                                                                                C PEPTIDE.
INSULIN A CHAIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                110 AA
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                                                                                                                                                                                                                                                                                             INTERCHAIN.
                                                                                                                                                                                                                                                                                                                  INTERCHAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           95 SLOKRGIVEQCCTSICS: P. LENYCN 110
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      86 ----RGIVEQCCTSICSUM LENYON 107
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                                        PDB: IEFE: 29 WAR-00.
InterPro: IPR004825; Ins/IGF/:elax.
Infam; PF00049; Insulin: 1.
PRINTS; PR00277: INSULINE.
SWART; SM00078: IIGF: 1.
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HSSP; P01308; 1LNP.
                                                                                                                                                                                                                                                                                                                                                                                                        45.58;
EMBL; X61089; CAA43403.1; -
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Best Local Similarity 60.5
Matches 52; Conservative
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96
109
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                                                                                                                                                                                                                                                                                                                                          InterPro; IPR004825; Ins/IGF/relax.
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                                                                      PRT:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                             44,98;
                                                                                                                                                                                                                                                                                                                                                                                                                                            5693 MM;
                                                                                                                                                                                                                                                                                                                                                  SMART; SM00078; 11GF; 1.
PROSITE; PS00262; INSULIN;
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Best Local Similarity 90.4
Matches 47: Conservative
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                                                                      STANDARD;
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36
51 AA:
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P01319;
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INS_CAMDR
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                    -1- FUNCTION: INSULIN DECREASES BLOOD GLUCOSE CONCENTRATION. IT INCREASES CELL PERMEABILITY TO MONOSACCHARIDES, AMINO ACIDS ANY FATTY ACTOS. IT ACCELERATES GLYCOLYSIS, THE PENTOSE PHOSPHATE CYCLE, AND GLYCOGEN SYNTHESIS IN LIVER.

-1- SUBONIT: HETERODIMER OF A B CHAIN AND AN A CHAIN LINKED BY TWO DISULFIDE BONDS.
                                                                                                                                                                                                                                                                                                                                                                                                                                Ishihara Y., Saito T., Ito Y., Fujino M.;
"Structure of sperm- and sei-whale insulins and their breakdown by whale pepsin.";
Nature 181:1468-1469(1958).
                                                                                                                                                                                                                                                                                                                                                            Balaenoptera borealis (Sei whale).
Ekkaryota, Metazoa: Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia: Eutheria: Cetartlodactyla; Cetacea; Mysticeti;
Balaenopteridae; Balaenoptera:
                                                                                                                                                            36;
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                                                                                                                                         Length 110;
                                                                                                                                                                               50 LGTGP--RFVNQHLCGSHLVEALYLVCGERGFFYTPKT------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             -!- SUBCELLULAR LOCATION: Secreted.
-!- SUBLIARITY: BELONGS TO THE INSULIN/IGF/RELAXIN FAMILY.
PIR; A01582; INWHIS.
HSSP; P01317: 1APH.
                                                                                                                                       45.3%; Score 266; DB 1; Length 11 llarity 57.4%; Pred. No. 2.2e-21; Conservative 1; Mismatches 3; Indels
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                                                                             INSULIN A CHAIN.
INTERCHAIN (BY SIMILARITY).
INTERCHAIN (BY SIMILARITY).
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4511768D6+22BEE5 CRC64;
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Pfam; PF00049; Insulin; 1.
PRINTS; PR00277; INSULINB.
SMART; SM0028: IIGF; 1.
PROSITE: PS00262; INSULIN; 1.
Insulin family; Hormone; Glucose metabolism; Signal.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 263.5; DB 1;
Pred. No. 1.9e-21;
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                                                                                                                                                                                                                                                                                                   P01314;
21-JUL-1986 (Rel. 01, Created)
1-JUL-1986 (Rel. 01, Last sequence update)
01-OCT-1996 (Rel. 34, Last annotation update)
                                                          INSULIN B CHAIN. C PEPTIDE.
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INTERCHAIN.
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30 INSULIN B CHAIN.
                                                                                                                                                                                                                                                                                         51 AA
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                                                  BY SIMILARITY
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SMART; SM00078; ILGF; 1.
PROSITE; PS00262; INSULIN; 1.
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92.38;
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87
110
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                                                                                                                                                  Local Similarity
mes 54; Conserv
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SEQUENCE
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PROPEP
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Matches
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INS_BALBO
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Gaps
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J. Fac. Med. Baghdad 14:16-28(1972).
J. Fac. Med. Baghdad 14:15-28(1972).
J. Fac. Med. Baghdad 17:17 Monosaccharides, amino Acids and Fatty Acids. IT Accelerates Glycolysis, THE Pentose Phusphate CYCLE, AND GLYCOGEN SYNTHESIS IN LIVER.

J. SUBUNIT: HEFERDIMER OF A B CHAIN AND AN A CHAIN LINKED BY TWO
                                                                                                                                                                                                                                                                                                                                                                                                                                                      Camelus dromedarius (Dromedary) (Arabian camel).
Welaryota: Metazoa: Chordata; Craniata: Vertebrata; Euteleostomi; Mammalia; Eutheria: Cetartiodactyla; Tylopoda: Camelidae; Camelus.NCBI_TaxID=9838;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Capra hircus (Goat).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi:
Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoldea;
Bovidae; Caprinae; Capra.
56 FVNQHLCGSHLVEALYLVCGERGFFYTPKTRGIVEQCCISICSLYOLENYCN 107
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Danho W.O.;
"The isolation and characterization of insulin of camel (Camelus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ä
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      -:- SUBGELLULAR LOCATION: Secreted.
-:- SIMILARITY: BELONGS TO THE INSULIN/IGE/RELAXIN FAMILY
PIR: A92782; INCMA.
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                                                                                                                                                                                                                                                                                           21-JUL-1986 (Rel. 01, Createu)
21-JUL-1986 (Rel. 01, Last sequence update)
01-FEB-1996 (Rel. 33, Last annotation update)
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21-JUL-1986 (Rel. 01, Last sequence update)
01-FEB-1996 (Rel. 33, Last annotation update)
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  1; Gaps
Comparative sequence analysis of the INS-IGF2-H19 gene cluster in
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Mammalia: Eutheria: Cetartiodactyla; Suina; Suidae; Sus.
NCBL_TaxID-9823;
                                                                                                                                                                                                                      56 FVNQHLCGSHLVEALYLVCGERGFFYTPKTRGIVEQCCISICSLYQLENYCN 107
                                                                                                                                                                                                                              1 FVNQHLGGSHLVEALYLVGGERGFFYTPKA-GIVEQCCAGVCSLYQLENYCN 5.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE OF 25-108.
MEDLINE-68286485; PubMed-5657063;
Chance R.E., Ellis R.M., Bromer W.M.;
Porcine proinsulin: characterization and amino acid sequence.";
                                                                                                                                                                                                                                                                                                                                                                                                                                    Amarger V., Nguyen M., Laere A.S., Braunschweig M., Nezer C.,
Georges M., Andersson L.;
                                                                                                                                                                                       DB 1; Length 51;
                                                            -1- SUBCELLULĀR LOCATION: Secreted.
-1- SUBLIARITY: BELONGS TO THE INSULIN/:GF/RELAXIN FAMILY.
PIR; A01586; INGT.
HSSP: P01317: 1APH.
HSSP: P01317: 1APH.
Interpro: IPROFROG 4825; Ins/IGF/relax.
SNART: SNOONF0 11GF; 1.
PROSITE; PS00262; INSULIN: 1.
                                                                                                                                                                                                      Indels
                                                                                                                                                                                                                                                                                                                                                                             Tuch B.E.;
porcine preproinsalin cDNA sequence.";
(MAY-1998) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                        9007B50CDB4E7DDD CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               X-RAY CRYSTALLOGRAPHY (1.9 ANGSTROMS).
Blundell T.L., Dodson G.G., Hodgkin D., Mercola D.;
                                                                                                                                                                                Score 263.5; DB 1;
Pred. No. 1.9e-21;
                                                                                                                                                                                                                                                                                         21-JUL-1986 (Rel. 01, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
                                                                                                                           INSULIN B CHAIN.
                                                                                                                                          INSULIN A CHAIN.
                                                                                                                                                                                                                                                                           108 AA.
                                                                                                                   Insulin family; Hormone; Glucose metabolism
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                                                                                                                                                INTERCHAIN.
INTERCHAIN.
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                                                                                                                                                                                                                                                                                                                                                                                                                    STRAIN-Large white;
MEDLINE-22135958; PubMed-12140686;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Mamm. Genome 13:388-398(2002).
                                                                                                                                                                                       44.98;
                                                                                                                                                                        5692 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Science 161:165-167(1968).
                                                                                                                                                                                     Query Match
Best Local Similarity 90.41
Matches 47; Conservative
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                                                      DISULFIDE BONDS
                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
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SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                   Insulin precursor
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P01315; Q9TSJ5;
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between the Swiss Institute of Biotiformatics and the EMBL outstation the European Bioinformatics institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                 Baker E.N., Blundell T.L., Cutfield J.F., Cutfield S.M., Dodson E.J., Dodson G.G., Crowtoot Hodykin D.M., Hubbard R.E., Isaacs N.W., Reynolds C.D., Sakabe N., Vijayan N.M.; "The structure of 2n pig insulin crystals at 1.5-A resolution."; Philos. Trans. R. Soc. Lond., B, Biol. Sci. 119:369-456(1988).
                                                                                                                                                                                           *Experience with fast Fourier least squares in the refinement of the crystal structure of rhombohedral 2-zinc insulin at 1.5-A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    insulin at 1.65-A resolution...

Acta Crystallogr. D 53:507-512(1997).

-!- FUNTION: INSULIN DECREASES BLOOD GLUCOSE CONCENTRATION. IT INCT : ASES CELL PERMEMBILITY TO MONOSACCHARIDES, AMINO ACTOS AND FATTY ACIDS. IT ACCELFRATES GLYCOCLYSIS, THE PENTOSE PHUSPHATE CYCLE. AND GLYCOGEN SYNTHESIS IN LIVER.

-!- SUBDMIT: HEITERDDIMER OF . B CHAIN AND AN A CHAIN LINKED BY INC. DISULFIDE BONDS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Diao J.-S., Wan Z.-L., Chang W.-R., Liang D.-C.;
"Structure of monomeric porcine DesBl-B2 despentapeptide (B26-B46)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WWW-"http://www.expasy...rd/spotlight/articles/sptlt009.html"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDLINE-91222450, PubMed-2025410;
Badger J., Harris M.R., Reynolds C.D., Evans A.C., Dodson E.J.,
Dodson G.G., Worth A.C.T.,
"Structure of the pag insulin dimer in the cubic crystal.";
Acta Crystallogr. B 47:127-136(1991).
"Insulin. The structure in the crystal and its reflection in chemistry and biology.": Adv. Protein Chem. 26:279\cdot402(1972).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Balschmidt P., Hansen F.B., Dodson E., Podson G., Korbe: F. "Structure of porcine insulin cocrystallized with clupeine Acta Crystallogt, 8 47:975-986(1991).
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SIMILARITY: BELONGS TO THE INSULIN/IGE/RELAXIN FAMILY
DATABASE: NAME-Protein Spotlight:
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MEDLINE-92126280; Pubmed-1772633;
                                                                                                                                  X-RAY CRYSTALLOGRAPHY (1.5 ANGSTROMS)
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EMBL; AY044828; AAL69550.1; -.
                                                                                                                                                                                                                                                                                                     Acta Crystallogr. A 34:782-791(1978).
                                                                                                                                                                                                                                                                                                                                                                                                        MEDLINE-89099318; PubMed-2905485;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NOTE-Issue 9 of April 2001;
                                                                                                                                                                      Isaacs N.W., Agarwal R.C.
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28-FEB-97.
16-FEB-99.
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31-JAN-94.
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2TCI;
1MPJ;
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STRAIN-New Zealand white; IISSUE-Pancreas:
MEDLINE-94179230; PubMed-8132571;
Devaskar S.U., Giddings S.J., Rajakumar P.A., Carnaqhi L.R.,
Menon R.K., Zahm D.S.;
*Insulin gene expression and insulin synthesis in mammalian neuronal
                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
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Giddings S.J., Carnaghi L.R., Devaskar S.U.;
Submitted (APR-1991) to the EMBL/GenBank/DDBJ databases.
I- FUNCTION: INSULIN DECREASES BLOOD GLUCOSE CONFIRENTRATION. IT
INCREASES CELL PERMEABILITY TO MONOSACCHARIDES. AMINO ACIDS AND
FAITY ACIDS. IT ACCELRAISES CLYCOLYSIS, THE PENTOSE PHOSPHATE
CYCLE, AND GLYCOGEN SYNTHESIS IN LIVER.
I- SUBUNIT: HETERODIMER OF A B CHAIN AND AN A CHAIN LINKED BY TWO
                                                                                                             Glucose metabolism; Signal; 3D-structure.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Oryctolagus cuniculus (Rabbit).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi;
Manmalla, Eutheria, Lagomorpha, Leporidae; Oryctolagus.
                                                                                                                                                                                                                                                                                                                                                                                                                                32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Smith L.F.; "Species variation in the amino acid sequence of insulin."; Am. J. Med. 40:662-666(1966).
                                                                                                                                                                                                                                                                                                                                                                                            Length 108;
                                                                                                                                                                                                                                                                                                                                                                                                                                1; Indels
                                                                                                                                                                                                                                                                                                                                                       11671 MW; CB4491B429858EBE CRC64;
                                                                                                                                                                                                                                                                                                                                                                                        44.8%; Score 263; DB 1;
ilarity 60.7%; Pred. No. 4.6e-21;
Conservative 0; Mismatches 1;
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INSULIN A CHAIN.
INTERCHAIN.
INTERCHAIN.
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01-FEB-1996 (Rel. 33, Last sequence update)
01-OCT-1996 (Rel. 34, Last annotation update)
                                                                                                                                                  INSULIN B CHAIN.
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PDB; 1ZNI; 28-JAN-98.
PDB; 1ZNJ; 28-JAN 98.
InterPro; IPRO04825; Ins/IGF/relax.
PERM; PF00049; Insulin; 1.
SMART; SM00078; ILOF; 1.
PROSITE; PS00262; INSULIN; 1.
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-1- SUBCELLULAR LOCATION: Secreted.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE OF 25-54 AND 90-110.
MEDLINE-66160119; Pubmed-5949593;
                                                                                                               Insulin family; Hormone;
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es 51; Conserv
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation. the European Bloinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to licenseeisb-sib.ch).
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Characterization of cat insulin.:
Arch. Biochem. Biophys. 247:20-27(1986).
-!- FUNCTION: INSULIN DECREAS S BLOOD GLUCOSE CONCENTRATION. IT
INCREASES CELL PERMEMBLIL Y TO MONOSACCHARIDES, AMINO ACIDS AND
FATTY ACIDS. IT ACCELEMALLS GLYCOLYSIS, THE PENTOSE PHOSPHATE
CYCLE, AND GLYCOGEN SYNTHESIS IN LIVER.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         -:- SUBUNIT: HETERODIMER OF A B CHAIN AND AN A CHAIN LINKED BY TWO DISULFIDE BONDS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutherla; Carnivora; Fissipedia; Felidae; Pelis.
NCBL_TaxID-9685;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 110;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 263; DB 1; Lengtu ... Pred. No. 4 6e-21; Ored. No. 4.00-21;
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-!- SIMILARITY: BELONGS TO THE INSULIN/IGF/RELAXIN FAMILY.
PIR; A01588; INCT.
-! - SIMILARITY: BELONGS TO THE INSULIN/IGF/RELAXIN FAMILY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               -> Y (IN REF. 3).
8202975885077FA8 CRC64;
                                                                                                                                                                                                                                                                                                                                              Pfam: PP00049; Insulin: 1.
SMART: SM00078; IIGF: 1.
PROSITE; PS00262: INSULIN: 1.
Insulin family; Hormone: Glucose metabolism: Signal.
SIGNAL.
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C PEPTIDE.
INSULIN A CHAIN.
INTERCHAIN.
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(Rel. 40, Last annotation update)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDLINE-86214076; PubMed-3518635;
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01-JAN-1988 (Rel. 06, Last Seyy
16-0CT-2001 (Rel. 40, Last anno
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      11838 MW;
                                                                                                                                                                                                                                        EMBL; U03610; AAA19033.1; -. EMBL; M61153; AAA17540.1; -.
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59.3%;
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PRINTS; PR00277; INSULINB.
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HSSP; P0~308; ITYM.
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Matches 51; Conserv
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HSSP; P01317; IAPH.
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                                                                                                                                                                                                       ;
                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      "Species variation in the amino acid sequence of insulin.";
Am. J. Med. 40:662-666(1966).
-!- FUNCTION: INSULIN DECREASES BLOOD GLUCOSE CONCENTRATION. IT
INCREASES CELL PERMEABILITY TO MONOSACCHARIDES, AMINO ACITS AND
FATTY ACIDS. IT ACCELERATES GLYCOLYSIS, THE PENTOSE PHOSPHATE
CYCLE, AND GLYCOGEN SYNTHESIS IN LIVER.
-!- SUBBNIT: HETERODIMER OF A B CHAIN AND AN A CHAIN LINKED BY TWO
DISULPIDE BONDS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDLINE-83119971: PubMed-6296142:
Kwok S.C.M., Chan S.J., Steiner D.F.;
*Cloning and nucleotide sequence analysis of the dog insulin gene.
Coded amino acid sequence of canine preproinsulin predicts an
additional C-peptide fragment.*;
J. Biol. Chem. 258:2357-2363(1983).
                                                                                                                                                                                                                                  56 FVNQHLCGSHLVEALYLVCGERGFFYTPKTRGIVEQCCTSICSLYQLENYCN 107
                                                                                                                                                                                                                                                                                                                                                                                                                                               Canis familiaris (Dog).
Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria: Carnivora; Fissipedia; Canidae; Canis.
                                                                                                                                                                                                                                                    1 FVNQHLCGSHLVEALYLVCGERGFFYTPKA-G1VEQCCASVCSLYQLEHYCN 51
                                                                                                                                                                       Score 262.5; DH 1; Length 51;
Pred. No. 2.4e-21;
2; Mismatches 2; Indeis
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PIR; A92413; IPDG.
HSSP; P01317; 1APH.
HTGFPO; IPR004625; Ins/IGF/relax.
Pfam; PF00049; Insulin; 1.
SMART; SM00078; ILGF; 1.
PROSITE; PS00762; INSULIN; 1.
Insulin family; Hormone; Glucose metabolism; Signal.
SIGNAL.
24
                                                                                                                                            9007B5096A0A7DDD CRC64;
                                                                                                                                                                                                                                                                                                                                                                       21-JUL-1986 (Rel. 01, Created)
21-JUL-1986 (Rel. 01, Last sequence update)
11-FEB-1996 (Rel. 33, Last annotation update)
Insulin precursor.
SMARI: SM00078: 11GF: 1.
PROSITE: PS00262: INSULIN: 1.
Insulin family: Hormone: Glucose metabolism.
1 30 INSULIN B CHAIN.
                                                                                   INSULIN A CHAIN
                                                                                                                                                                                                                                                                                                                                          110 AA
                                                                                                                                                                                                       2; Mismatches
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                                                                                                 INTERCHAIN.
INTERCHAIN.
                                                                                                                                                                                                                                                                                                                                          PRT;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE OF 25-54 AND 90-110.
MEDLINE-66160119; PubMed-5949593;
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5745 MW:
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Best Local Similarity 90.4'
Matches 47; Conservative
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                                                                                                                  Length 110
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54 INSULIN B CHAIN.
87 CEPTTIDE.
110 INSULIN A CHAIN.
96 INTERCHAIN.
109 INTERCHAIN.
1100
1. 12190 M.. A574791864A4FB98 CRC64;
                                                                                                                  44.6%; Score 262; DB 1; 59.3%; Pred. No. 5.9e-21;
                                                                                                                                                0; Mismatches
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Best Local Similarity 59.33
Matches 51; Conservative
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Search completed: September 16, 2003, 12:38:51 Job time : 9.32685 secs

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O14644 homo sapien
Q918q7 rana pipien
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GenCore version 5.1.6 Copyright (c) 1993 - 2003 Compugen Ltd.
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sp_unclassified:*
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191.5 189.5 187.5	1/1.3 161 159.5 159.5 159.5	156 154 152 149.5	1488 1488 1488 1488 15	· •	147.5 147.5 147.5 147.5
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ALIGNMENTS

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                                                                                                   Pongo pygmaeus (Orangutan).
Bukaryola: Metazoa: Chordata: Craniata: Vertebrata; Euteleostomi;
Mammalia: Eutheria: Primates: Catarrhini: Businidae; Pongo.
NCRI_PaxID=96(0).
                                                                                                                                                                                                                                                                                 34;
                                                                                                                                                                                                                                                       Length 110,
                                                                                                                                                                                                                                                                                 Indels
                                                                                                                                                                          Stead J.D.H., Jeffreys A.J.; Haplotype diversity at the insulin region ": Submitted (JUL-2002) to the EMBL/GenBank/DDBJ databases. EMBL, AY137503; AAN06937.1; SEQUENCE 110 AA; 12038 MM: 22D2B32B94F520FB CRC64;
                                                  Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                         45.5%; Score 267; DB 6; Le
60.5%; Pred. No. 6.6e-24;
Mismarches 0;
             110 AA
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                                        Created)
            PRT;
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                                    01-MAR-2003 (TrEMBLrel, 23, 01-MAR-2003 (TrEMBLrel, 23, 01-MAR-2003 (TrEMBLrel, 23,
                                                                                                                                                                                                                                                                  Best Local Similarity 60.59
Matches 52; Conservative
             PRELIMINARY;
                                                                            Insulin precursor.
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                  ----RGIVEQCCTSICSLYQLENYCN 107
                                                                                                                                                                                                                   Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Pfam: PF00103; hormone; 1.
PROSITE; PS00266; SOMATOTROPIN_1; 1.
                                                                                                                                                                       PHT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRI:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              interPro; IPR001400; Somatotropin.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity 97.99
Matches 47; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRELIMINARY;
                                                                                                                                                                         PRELIMINARY;
                                                                                                                                                                                                              01-MAR-2002 (TrEMBLrel.
01-MAR-2002 (TrEMBLrel.
01-MAR-2003 (TrEMBLrel.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Home sapiens (Haman)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         245 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NCB1_Tax1D-9606;
                                                                                                                                                                                                                                                                                                                                                                                          NCBI_TaxID-9509;
                                                                                                                                                                                                                                                                                    Growth hormone.
                    86
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE
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014644
                                                                                                                                                  08WNE0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
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                                                                                                                                                                                                                                 Spermophilus tridecemlineatus (Thirteen-Lined ground squirrel).
Eukaryota: Metuzoa: Chordata: Craniata: Vertebrata: Euteleostomi;
Mammalia: Eutheria: Rodentia: Sciurognathi; Sciuridae: Sciurinae:
Spermophilus:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Felis silvestris catus (Cat.).
Eukaryota, Metazoa, Chordata: Craniata; Vertebrata; Eutoleostomi;
Mammalia, Eutheria, Carnivora; Fissipedta; Felidae; Felis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        36;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             34;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 110;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 110;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    "Cart insulin.";
Submitted (MAY-2000) to the EMBL/GenBank/DDBJ databases.
-i- SUBCELLULAR LOCATION: SECRETED (BY SIMILARITY).
-i- SIMILARITY: BELONGS TO THE INSULIN/IGF/RELAXIN FAMILY.
EMBL; AB04355; BAB84110.1; --
InterPro; IPR04825: Ins/IGF/relax.
PRINTS: PR00277: INSULINB.
SMART; SM00078; I1GF; I.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            42.8%; Score 251; DB 6; Length 11
55.8%; Pred. No. 5.3e-22;
tive 2; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Indels
                                                                                                                                                                                                                                                                                                                                                                                                          Pfam: PF00049; Insulin; 1.
PRINTS: PR00277; INSULINB.
SMART; SM0(078: 11GF). 1.
PROSITE: P: 10262; INSULIN: 1.
SEQUENCE: 110 AA: 12004 MH; 4511768D6622BEE5 CHC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    95FB6E170C7BECA4 CRC64;
01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  01-MAR-2002 (TrEMBLrel. 20, Created)
01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 266; DB 11;
Pred. No. 8.7e-24;
1; Mismatches 3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        56 FVNQHLCGSHLVEALYLVCGERGFFYTPKT----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             110 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRI;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PROSITE; PS00262; INSULIN; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            45.38;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   0uery Match
Best Local Similarity 57.44
Matches 54; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TISSUE-Pancreas;
Okamoto S., Morimatsu M.;
*Cat insulin.*;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        48; Conservative
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                    01-MAR-2003 (TrEMBLrel.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Local Similarity
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                                                                                                                                                                                              SECUENCE FROM N.A.
                                                                                                                                                  NCBI_TaxID-43179;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NCBI_TaxID+9685;
                                                                                                                                                                                                                       TISSUE-Pancreas;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Preproinsulin.
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Gaps
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Mammalia, Eutheria, Primates, Platyrrhini, Gebidae, Atelimae, Ateles.
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MEDLINE-9837373; PubMed-9709963;
Boguszewski C.L., Svensson P.A., Jansson T., Clark R.,
Carlsson L.M.S., Carlsson B.;
"Cloning of two novel growth hormone transcripts expressed in human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Eukaryota, Metazoa, Chordata, Craniala, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
                                                                                                                                                                                                                                                                                                                Revol A., Esquivei D., Santiago D., Barrera Saldona H.:
"Independent duplication of the growth hormone gene in three
Anthropoidean lineages."
Submitted (APR-2001) to the EMHL/GenBank/DDBJ databases.
BMBL. AFR7424; AAL7286.1:
InterPro.; IPR001400: Somatoiropin.
Pfam: PF00103; hormone: 1.
PROSITE; PS00266: SOMATOTROPIN.1: 1.
PROSITE; PS00388: SOMATOTROPIN.2: 1.
SEQUENCE 217 AA: 24894 MW; 425829FF41EEAAE6 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      2 FPTIPLSRLFDNAMLRABKLHQLAFDTYQEFEEAYIPKEQKYSFLQNP 49
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 217;
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27101 MW: 14CC7F8CD75D91C8 CRC64:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       01-JAN-1998 (ITEMBLEEL. 05, Greated)
01-JAN-1998 (ITEMBLEEL. 05, Last sequence update)
01-DEC-2001 (ITEMBLEEL. 19, Last annotation update)
Placental growth hormone isoform hGB V3 precensor.
Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  42.4%; Score 249; DB 6; 97.9%; Pred, No. 2e-21;
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J. Clin. Endocrinol. Metab. 81:2878-2885(1998).
HSSP: P01241; 1A22.
                                                                                                                                Ateles geoffroyi (Black-handed spider monkey).
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Length 245;

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EMBL; L16553; AAA18840.1; -.
HSSP; P01241; 1AXI.
InterPro; IPR001400; Somatotropin.
                                                                                                            Best Local Similarity 78.7%
Matches 37; Conservative
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Matches 37, Conservative
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                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Golos T.G., Durning M., Fisher J.M., Fowler P.D.;
"Cloning of four growth hormone/chorionic somatchmanmotropin-related complementary deoxyribonucleic acids differentially expressed during pregnancy in the rhesus monkey placenta.";
Endocrinology 133:1744-1752(1993).
                                                                                                                                                                                                                                                 01-0CT-2000 (TrEMBLrel. 15, Last sequence update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
Preproinsulin.
mana pipiens (Northern leopard frog).
Eukaryota: Metazoa: Chordata; Craniata; Vertebrata; Euteleostomi;
Amphibia: Batrachia: Anura; Neobatrachia; Ranoidea; Ranidae: Rana.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    01-NOV-1996 (TrEMBLrel. 01, Created)
01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
Somatotropin 2 precursor (Growth hormone 2) (Fragment).
Macaca mulatta (Rhesus macaque).
Eukaryota: Metazoa; Chordata: Craniata: Vertebrata; Euteleostomi:
Mammalia: Eutheria; Primates; Catarrhini; Cercopithecidae;
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                                            49
                                                      27 FPTIPLSRLFDNAMLRARRLYQLAYDTYQEFEEAYILKEQKYSFLQNP 74
                                            2 FPTIPLSRLFDNAMLRAHRLHQLAFDTYQEFEEAYIPKEQFFSFLQNP
                      Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                       Indels
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                                                                                                                                                                                                                                                                                                                                                                                               PROSITE; PS00262; INSULIN; 1.
SEQUENCE 106 AA: 12183 MM; 3A870EEC70217F92 CRC64;
7.?e-19;
2;
                                                                                                                                                                                                                                                                                                                                                                                                                              37.4%: Score 219.5; DB 13;
49.4%: Pred. No. 2.8e-18;
tive 7; Mismatches 4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 212 AA
                                                                                                                       106 AA
           Pred. No. 7.26
2; Mismatches
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01-OCT-2000 (TrEMBLrel. 15, Last seq
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      87 -- GIVEQCCTSICSLYQLENYCN 107
                                                                                                                      PRT:
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                                                                                                                                                                                                                                                                                                                                                      InterPro; IPR004825; Ins/IGF/relax.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDLINE-94008724; PubMed-8404617;
                                                                                                                                                                                                                                                                                                                                                              Pfam: PF00049; Insulin; 1
PRINTS: PR00277; INSULINB.
SMART; SM00078; IlGF; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                 Ouery Match 37.4
Best Local Similarity 49.4
Matches 41; Conservative
                      44; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRELIMINARY:
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                                                                                                                       PRELIMINARY;
             Similarity
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                                                                                                                                                                                                                      NCBI_TaxID-8404;
            Best Local
Matches 4
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                                                                                                  RESULT 6
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MEDLINE-94008724; PubMed-9404617;
Golos T.G., Durning M., Fisher J.M., Fowler P.D.;
Golos T.G., Fisher J.G., Fisher J.G., Fowler P.D.;
Forganicy of four growth hormone/Chhorionic somatcommunotropin-related
complementary deoxyribonucleic acids differentially expressed during
pregnancy in the rhesus m key placenta.";
Endocrinology 133:1744-17 [1993],
Endocrinology 133:1744-17 [1993],
Fisher J.G., F
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
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Mammalia; Eutheria; Primates; Catarrhini; Cercopithecidae;
Cercopithecinae; Macaca.
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Actinopterygii; Neopterygii; Teleostel; Osteoglossomorpha;
Osteoglossiformes; Pantodontidae; Pantodon.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 212;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Indels
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Al-Mahrouki A.A., Irwin D.M., Graham L.C., Touson J.H.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRINTS: PR00836; SOMATOTROPIN.
PROSITE; PS00338; SOMATOTROPIN_2; 1.
SEQUENCE 217 AA; 24942 MW: FF5AA8915131F2BC CRC64;
                                                                                                                                                                                 SEQUENCE 212 AA; 24525 MW; 27BC91106256E6F5 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               01.NOV-1996 (TrEMBLrel. 01, Created)
01.NOV-1996 (TrEMBLrel. 01, Last sequence update)
01.NAR-2003 (TrEMBLELEL. 23, Last annotation update)
Chorionic somatomamnofropin-1.
Macaca mulatta (Rhesus macaque).
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01-JUN-2001 (TrEMBLrel. 17, L st sequence update)
01-MAR-2003 (TrEMBLrel. 23, L st annotation update)
                                                                                                                                                                                                                                                                                     36.3%; Score 213; DB 6; 78.7%; Pred. No. 3.7e-17;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                36,3%; Score 213; DB 6; 78,7%; Pred; No. 3.8e-17; Live 9; Mismatches 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 110 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            217 AA
                                                                                                                                                                                                                                                                                                                                                                                                      9; Mismatches
Pfam; PF00103; hormone; 1.
PROSITE; PS00338; SOMATOTROPIN_2; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Pantodon buchholtzi (Butterflyfish)
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Pfam; PF00103; hormone; 1.
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33.69
Query Match
Best Local Similarity 80.09
Matches 36; Conservative
                                                                                                                                                       Genomics 4:479-497(1989).
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                  Homo sapiens (Human).
                                                                                                                                                                                  SEQUENCE FROM N.A.
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                                                                               SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                     TISSUE-Placenta;
                                                      NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                               HSSP; P01241;
                                                                                                                                                                                                                                                                                                  Strausberg R.
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                                                                                                                                                                                                                                    014407;
01-NOV-1996 (TrEMBLrel. 01, Created)
01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
Chorlonic somatomammotropin CS-2 (Chorlonic somatomammotropin hormone
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TISSUE-Midpregnancy placenta;
MEDLINE-94008724: PubMed-8404667;
Golos T.G., Durning M., Fisher J.M., Fowler P.D.;
"Cloning of four growth hormone/chorionic somatcomanmotropin-related complementary deoxyribonucleic acids differentially expressed during pregnancy in the rhesus monkey placenta.";
Endocrinology 13:1744-1752(1993).
                                                                                                                                                                                                Gaps
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                                                                                                                                                                                                                                                                                                                                                                   007369;
01-NOV-1996 (TEMBLrel. 01, Created)
01-NOV-1996 (TEMBLrel. 01, Last sequence update)
01-NOV-1996 (TEMBLrel. 03, Last sequence update)
01-MAR-2003 (TEMBLrel. 23, Last annotation update)
01-MAR-2003 (TEMBLrel. 23, Last annotation update)
Chorionic somatomammotropin.3.
Macaca mulatta (Rhesus macaque).
Macaca mulatta (Rhesus macaque).
Macaca mulatta (Rhesus macaque).
Charitata (Rheria; Primates: Caniata: Vertebrata; Euteleostomi: Cercopithecidae; Macaca.
VCBL_TAXID-9544:
                                                                                                                                                                                              35;
                                                                                                                                                                   34.3%; Score 201.5; DB 13; Length 110; 43.5%; Pred, No. 4e-16;
*Molecular cloning of preproinsulin cDNAs from several osteoglossomorphs and a cyprinid.*;

L. Cell. Endocrinol. 174:51-58(2001).

L. SUBCELLULAR LOCATION: SECRETED (BY SIMILARITY).

-: SUBCELLULAR LOCATION: SECRETED (BY SIMILARITY).

-: SIMILARITY: BELONGS TO THE INSULIN/IGF/RELAXIN FAMILY.

R. EMBP., AR199589; AAK28712.1; -...

R. HSSP. PO1308: JAR28712.1; -...

R. HSSP. PO1308: JAR28712.1; -...

R. PFART: PRO0495; Insulin; 1.

SMART: SMO0078: Insulin; 1.

R. PROSITE: PSO0262: INSULIN; 1.

SEQUENCE 110 AA; 12324 MM; BDECCD659D872E06 CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    34.2%; Score 201; DB 6; Length 217; 74.5%; Pred. No. 1e-15; Live 8; Mismatches 4; Indels
                                                                                                                                                                                                                      58 NQHLCGSHLVEALYLVCGERGFFYTPKT------------
                                                                                                                                                                                             5; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              F1EB6AFDBBA1B185 CRC64;
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Pfam: PF00103; hormone: 1.
PR051TE; PS00266; SOMATOTROPIN.1; 1.
SEQUENCE 217 AA; 24874 MH; FIEB6A
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                                                                                                                                                                                  Best Local Similarity 43.59
Matches 37, Conservative
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                                                                                                                                                                                                                                                                                                                                                               PRELIMINARY;
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                                                                                                                                                                      Query Match
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Q07369
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Q14407
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Chen E.Y., Liao Y.C., Smith D.H., Barrera-Saldana H.A., Gelinas R.E.,
Seeburg P.H.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
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Eukaryota: Metazoa: Chordata; Craniata: Vertebrata; Euteleostomi:
Actinopterygii; Neopterygii; Teleostel; Ostariophysi; Cyprinitormes:
Cyprinidae; Danio.
                                                                                                                                                                                                                                                         "The human growth hormone locus: nucleotide sequence, biology, and evolution.";
                                                                                                                                                                                                                                                                                                                                                                                                         MEDLINE-91102558; PubMed-1 .158; Vnencak-Jones C.L., Phillips J.A. 111.; Het spots for growth hormone gene deletions in homologous regions outside of Alu repeats. Science 250:1748-1748(1990).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi.
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
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Argenton F., Zecchin E., Bortolussi M.;
"Early appearance of pancreatic hormone-expressing cells in the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ..
O
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      zebrafish embryo.";
Mech. Dev. 87:217-221(1999).
-!- SUBCELLULAR LOCATION: SECRETED (BY SIMILARITY).
-!- SIMILARITY: BELONGS TO THE INSULIN/IGF/RELAXIN FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        4 TIPLSRLFDNAMLRAHRLHQLAFDTYQEFEEAYIPKEQKYSFLQN 48
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              4: Indels
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Strausberg R.:
Submitted (JUL-2002) to the 1M i./GenBank/DDBJ databases.
EMBL: J03071; AAA52553.1:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Submitted (JAN-2002) to the EM J./GenBank/DDBJ databases
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01-MAR-2001 (TIEMBLrel. 16, Last sequence update)
01-MAR-2003 (TIEMBLrel. 23, Last annotation update)
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80.0%; Pred. No. 3e-15;
tive 5; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   108 AA
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Pfam: PF00103; hormone; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EMBL; BC022044; AAH22044 1;
EMBL; BC035965; AAH35965.1;
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Signal. SIGNAL

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26 NQHLCGSHLVEALYLVCGERGFFYNPKMDKRDAEPLLGFLSPKSGLENEVDEYPFKLVGD
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Eukaryota: Metazoa: Chordata: Craniata; Vertebrata: Futeleostomi:
Mammalia; Butheria; Primates; Platyrrhini; Celidae; Atelinae; Atèles.
                   01-JUN-2001 (TrEMBLrel. 17, rated)
01-JUN-2001 (TrEMBLrel. 17, st sequence update)
01-MAR-2003 (TrEMBLrel. 23, t annotation update)
01-MAR-2003 (TrEMBLrel. 23, t annotation update)
Preproinsulin (Fragment).
Chitala chitala (clown kniferish) chitala (clown kniferish) action to make year ebratas Euteleustomi;
Eukaryotas Metacas Chordan Clamata; Vertebrata; Euteleustomi;
Actinopterygii: Neopterygii: Cloostel; Osteoglossomorpha;
Osteoglossiformos; Notopteridue; Chitala,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Revol A., Esquivel D., Santiago D., Barrera-Saldana H.
Revol A., Esquivel D., Santiago D., Barrera-Saldana H.
"Independent duplication of the growth hormone gene in three
Anthropoidean lineages.";
EMBL, AF374235, AAL72287.1;
L. Submitted (APR-2001) to the EMBL/GenBank/DDBJ databases.
R. EMBL, AF374235, AAL72287.1;
R. Pfam., PF00103; hormone; 1.
R. PRINT: PRO0103; hormone; 1.
R. PRINT: PS00266; SOMATOTROPIN.]: 1.
R. PROSITE; PS00266; SOMATOTROPIN.]: 1.
R. PROSITE; PS00308; SOMATOTROPIN.]: 0.
SEQUENCE 217 AA: 25293 WW; 741745A1B75C053E CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          33.2%; Score 195; DB 13; Length, 11;; 44.2%; Pred. No. 2.4e-15;
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                                                                                                                                                                                                                                                                 58 NQHLCGSHLVEALYLVCGERGFFYIPK-------
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TED (BY SIMILARITY).
:NSULIN/IGF/RELAXIN FAMILY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       9: Indels
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SEQUENCE 111 AA: 12483 MW; 247CA4431376329F CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        est sequence update)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       86 VKMKRGIVEOCCHRPCNIFIXONOYCN 111
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Best Local Similarity 44.29
Matches 88; Conservative
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                                                                                                                                                                                                     NCBI_TaxID-112163;
                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                         59 QHLCGSHLVEALYLVCGERGFFYTPK
                                                                                                                                                                                                                                                                                                                                                                                                                                 59 QHLCGSHLVEALYLVCGERGFFYTPK------T 85
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       33; Gaps
                                                                                                                                                                                                                                                                                                                                                              33; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Catla catla (catla).
Eukaryota: Metazoa: Chordata: Craniata: Vertebrata: Euteleostomi:
Actinopterygii: Neopterygii: Teleostei: Ostariophysi: Cypriniformes;
Cyprinidae: Catla.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A Bhattacharya S., Roy S.S., Dasgupta S., Ravikumar L., Mukherjee M., A Bhattacharya S., Roy S.S., Dasgupta S., Ravikumar L., Mukherjee M., A Bhattacharya I., Wakabayasi K.;
A new cell secreting insulin.
I. Submitted (APR-2001) to the EMBL/GenBank/DDBJ databases.
I. SUBCELLULAR LOCATION: SECRETED (BY SIMILARITY).
I. SIMILARITY: BALONGS TO THE INSULIN/ICF/RELAXIN FAMI:Y.
REMBL: AF373021; AAX51558 I.;
REMBL: AF373021; ANSULINB.
REMBL: AF3002062; INSULINB.
REMBL: PS002062; INSULIN: I.
REMBL: PS002062; INSULIN: I.
REMBL: PS002062; INSULIN: I.
REMBL: AF3002062; INSULIN: I.
REMBL: AF3002062; INSULIN: I.
                                                                                                                                                                                                                                                                                                              33.3%; Score 195.5; DB 13; Length 108;
45.1%; Pred. No. 2e-15;
tive 5; Mismatches 7; Indeis 33;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    33.3%; Score 195.5; DB 13; Length 108;
45.1%; Pred. No. 2e-15;
tive 5; Mismatches 7; Indels 33;
                                                                                                                                                                                                                                                                                                                                                         7; Indeis
                                                                                                                                                                                                   POTENTIAL.
INSULIN B CHAIN.
INSULIN A CHAIN.
3195289E72AD6D25 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       01-DEC-2001 (TrEMBLrel. 19, Last sequence update) 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       108 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  111 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         86 RGIVEQCCTSICSLYQLENYCN 107
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      86 RGIVEOCCTSICSLYQLENYCN 107
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                                                             InterPro; IPR004825; Ins/IGF/relax.
Pfam; PF00049; Insulin; 1.
PRNTS; PR00277; INSULINB.
SMART; SMO07078; IldF: 1.
PROSITE: PS00262; INSULIN; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRT;
                                                                                                                                                                                                     1 23 PC
24 53 IP
86 108 II
108 AA; 11904 MW;
EMBL; AJ237750; CAC20109.1; -. HSSP; P01308; 1LPH, ZPB-GENE-980526-110; ins
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       0uery Match
Best Local Similarity 45.18
Matches 37; Conservative
                                                                                                                                                                                                                                                                                                                   Query Match 33.39
Best Local Similarity 45.19
Matches 37; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRELIMINARY;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                        SEQUENCE
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RESULT 13 Q902N4

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85

19:

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Gaps

098TB0

RESULT 14 0987B0

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27 FPRIPLSRLFGDAMLRAHQLHQVAFDTYQELEENCIPKKQKYFFLKNP 74

Search completed: September 16, 2003, 12:40:00 Job time: 27.8132 secs

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GenCore version f 1.6
Copyright (c) 1993 - 2003 (umpugen Ltd.
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OM protein - protein search, using sw model

September 16, 2003, 12:31:20 ; Search time 44.358 Seconds (without alignments) 536.746 Million cell updates/sec Run on:

1 MFPTIPLSRLFDNAMLRAHR.....IVEQCCTSICSLYQLENYCN 150 US-09-423-100-7 Title: Perfect score: Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

1107863 seqs, 158726573 residues Searched: 1107863 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database

 کم	A_Geneseq_19Jun03:*
1:	/SIDS1/gcgdata/geneseq/geneseqp-emb1/AA1980.DAT:*
:	/SIDS1/gcgdata/geneseg/genesegp-emb1/AA1981.DAT:*
٠ ::	/SIDS1/gcqdata/geneseg/genesegp-emb1/AA1982.DAT:*
 	/SIDS1/gcgdata/geneseg/genesegp-embl/AA1983.DAT:*
	/SIDS1/gcgdata/geneseg/genesegp-embl/AA1984.DAT:*
, 9	/SIDS1/qcgdata/geneseq/yeneseqp-embl/AA1985.DAT:*
7:	/SIDS1/gcgdata/geneseq/geneseqp-emb1/AA1986.DAT:*
 80	/SIDS1/gcgdata/geneseq/geneseqp-embl/AA1987.DAT:*
	/SIDS1/gcgdata/geneseg/genesegp-embl/AA1988.DAT:*
10:	/SIDS1/gcgdata/geneseg/genesegp-embl/AA1989.DAT:*
11:	/SIDS1/gcgdata/geneseq/geneseqp-embl/AA1990.DAT:*
12:	/SIDS1/gcgdata/geneseq/geneseqp-embl/AA1991.DAT:*
13:	/SIDS1/gcgdata/geneseq/genesegp-embl/AA1992.DAT:*
14:	/SIDS1/gcgdata/geneseq/geneseqp-embl/AA1993.DAT:*
15:	/SIDS1/gcgdata/geneseq/geneseqp-embl/AA1994.DA1:*
16:	/SIDS1/gcgdata/geneseq/geneseqp-embl/AA1995.DAT:*
17:	/SIDS1/gcgdata/geneseg/geneseqp-embl/AA1996.DAT:*
18:	/SIDS1/gcgdata/geneseg/geneseqp.emb1/AA1997.DAT:*
19:	/SlDS1/gcgdata/geneseg/genesegp-emb1/AA1998.DAT:*
20:	/SIDS1/qcqdata/geneseq/geneseqp-embl/AA1999.DAT:*
21:	/SIDS1/gcgdata/geneseq/geneseqp-emb1/AA2000.DAT:*
22:	/SIDSI/gcgdata/geneseq/geneseqp-embl/AA2001.DAT:*
23:	/SIDS1/gcgdata/geneseq/geneseqp-emb1/AA2002.DAI:*
24:	/SIDS1/gcgdata/geneseq/geneseqp-embl/AA2003.DAT:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

SOUTHWITES			Description	2861 Chimeric protein.	AAY42860 hGH-mini-proinsuli			94861 Human growth hormo				
			ore Match Length DB ID	20	20	20	20	23	10	50	10	10
			Length	150	107							. •
	æ	Query	Match	100.0	69.7	59.0	59.0	59.0	58.5	58.5	58.3	58.3
			Score	797	555.5	470	470	470	466	466	465	465
		Result	NO.		8	e	4	S	9	7	80	6

Human growth hormo Fusion protein of		growth	Human growth hormo	Segment of B-cell	Human growth hormo	Human growth hormo	Human beta-nerve g	Protein sequence o	Natural human 22kD	Human growth hormo		_	Human growth hormo	Human growth hormo	Human growth hormo	Humas growth hormo	Human growth hormo	Heman growth hormo	growth	_	Human growth hormo													
AAR11740 AAR03255	ABG31862		ABG94977			ABC94976	AAP51033	AA020110	AAY 04396	AAY78425	AAO17485	AAO17486	ABG94863	ABG94864	ABG94907	ABG94908	ABG94909	ABG94910		ABG94912	ABG94913	ABG94914	ABG94915	ABG94916		ABG94918	ABG94919	ABG94920	ABG94921	ABG94922	ABG94923	ABG94924	ABG94925	ABG94926
12	23	53	53	11	23	23	۲	18	20	21	22	5.5	53	23	53	23	?	5.3	53	23	23	23	23	23	53	23	23	23	23	23	23	53	7	5
262 310	191	191	191	144	191	191	762	191	191	191	191	191	191	191	161	191	191	141	191	191	191	191	191	191	191	191	191	191	191	191	191	191	191	191
58.3	ന	ന	CC)	ന	30	æ	20	r-	^	\sim	\sim	^	7	~	~	7	7	7	7	~	~	7	7	~	~	7	7	7	~	2	7	7	7	~
465	464	463	463	462	462	462	462	461	461	461	461	461	461	461	461	461	461	461	461	461	461	461	461	461	461	461	461	461	461	461	461	461	461	461
10	12	13	14	15	16		18		20	21	22	23	24	25	26	27	28	58	30	31	32	33	34	35	36	37	38	39	40	4.1	42	43	44	45

ALIGNMENTS

AAY42861 standard; protein; 150 AA. 19-JAN-2000 (first entry) AAY42861; RESULT 1

Chimeric protein, SKQ 10 7.

Insulin; precursor; growth hormone; chaperone; intramolecular; folding; conformation; chimeric protein; cleavable; recombinant; production; yield.

Synthetic. Homo sapiens.

WO9950302-A1.

07-0CT-1999.

98WO-CN00052. 98WO-CN00052 31-MAR-1998; 31-MAR-1998; (TONG-) TONGHUA GANTECH BIOTECHNOLOGY LTD.

Gan Z;

WPI; 1999-610839/52.

New chimeric proteins containing human growth hormone fragment, used

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                                                                                                         of the chimeric protein acres as an intramplecular chaperone (IMC) for the insulin precursor, enabling it to fold correctly. The cleavable peptide linker has a C-terminal Arq residue which enables the high protein to frecombinate human insulin with enables the high portion of the chimeric protein can provide human insulin with correctly linked cysteine bridges with fewer necessary procedural steps, and hence resulting in a higher yield of human insulin. The IMC sequences not only protect insulin sequences from intracellular degradation by a microorganism host, but also promote the folding of the fused insulin precursor, facilitate the solutions protein among the fusion proteins of the sequences the intranolecular interactions among the fusion proteins, thus allowing folding of the fusion proteins and cerease the internolecular procedural steps of cyanogen bromide cleavage, oxidative sulphitolysis and related purification steps can thus be eliminated, along with the use of high concentrations of mercaptan or the use of hydrophobic absorbent
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    61 TPSNREETQQKSNLELLRISLLLIQSWLEPVQIGTGPRFVNQHLCGSHLVEALY:UCGER 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     61 TPSNREETQQKSNLELLRISLLLIQSWLEPVQLGTGPRFVNQHLCGSHLVEALYLVCGER 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 MFPTIPLSRLFDNAMLRAHRLHQLAFDTYQEFEEAYIPKEQKYSFLQNPQTSLSFSESIP 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           This sequence represents a chimeric protein, which contains an N-terminal fragment of human growth hormone (ADH) of the sequence given in AAY42855, a cleavable peptide linker (AAY42857), and a human insulin precursor comprising insulin A and B chains (AAY42859). The hGH portion
                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              conformation; chimeric protein; cleavable; recombinant;
                                                                                                                                                                                                                                                                                                                                                                                                                                 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Insulin; precursor; growth hormone; chaperone; intramolecular;
                                                                                                                                                                                                                                                                                                                                                                                               100.0%; Score 797; DB 20; Length 150; 100.0%; Pred. No. 1e-42; Live 0; Mismatches 0; Indels 0
particularly for the production of human insulin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           121 GFFYTPKTRGIVEQCCTSICSLYQLENYCN 150
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GFFYTPKTRGIVEQCCTSICSLYQLENYCN 150
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (TONG-) TONGHUA GANTECH BIOTECHNOLOGY LID.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  hGH-mini-proinsulin chimeric protein.
                           Claim 14; Page 30-31; 46pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAY42860 standard; protein: 107 AA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    19-JAN-2000 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                  Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                  Similarity
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production; yield.
                                                                                                                                                                                                                                                                                                                                                                        150 AA
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                                                                                                                                                                                                                                                                                                                                                                                                                               150;
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                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
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This Sequence Tepresents a Collimetric process.

This Sequence (ARM) of the sequence given in AAV42855, a cleavable peptide hormone (AGM) of the sequence given in AAV42855, a cleavable peptide in the content of the chimetric protein across compressing insulin.

A and B chains (AAV42895), and a human insulin precursor compension in state of the content of the chimetric protein acts as an intramolecular chapterone (IMC) for the insulin precursor.

C enabling it to fold correctly. The cleavable peptide linker has a clearant of the correctly. The cleavable peptide linker has a clearant of the content of the correctly in the insulin protein can provide human insulin via an AGM profitsulin of the compinant human insulin via an AGM profitsulin a higher yield of recombinant human insulin via an AGM profitsulin sequences from intracellular degradation by a microorganism host, but also promote the folicing of the fused insulin precursor, facilitate the solubility of the fusion proteins, thus all wing folding of the fused insulin precursor at commercially useful high concentrations. The procedural steps of cyanically useful high concentrations in the fuse of high concentrations steps can thus be eliminated, along with the use of high purification steps can thus be eliminated, along with the use of high concentrations of mercaptan or the use of hydrophobic absorbent resins.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              61 TPSNREETQQKSNLEHRISHLLIQSWLEPVQLGTGPRFVNQHLCGSHLVEALYLVCGER 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 MEPTIPLSRLFDNAMLRAHRLHQLAFDTYQEFEEAYIPKEQKYSFLQNPQTSLSFSESIP 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                        New chimeric proteins containing human growth hormone fragment, used particularly for the production of human insulin
                                                                                                                                                                                                                                 hGH-mini-proissulin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Growth hormone; chaperone; intramolecular; insulin; precursor; folding; conformation; chimeric protein; cleavable; recombinant;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 555.5; DB Pred. No. 8e-28;
                                                                                                                                                                                                                                 This sequence represents a chimeric protein,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             121 GEFYTPKIRGIVEQCCTSICSLYQLENYCN 150
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                0; Mismatches
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                                                                                                                                                       Claim 13; Page 30; 46pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         69.7%;
71.3%;
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Best Local Similarity 71.39
Matches 107, Conservative
WPI; 1999-610839/52.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               31-MAR-1998;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               07-0CT-1999.
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19-NOV-1998
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                                                                                                                                                                         This sequence represents an archimente protein (AAV42861) which also contains a human insulin precursor (AAV42859). The hGH portion of the chimeric protein acts as an intramolecular chaperone (IMC) for the insulin precursor, enabling it to fold correctly. A cleavable peptide insulin precursor, enabling it to fold correctly. A cleavable peptide linker with a C-terminal Arg residue (AAV42857) enables the hGH portion of the chimeric protein to be removed after folding has taken place. Production of recombinant human insulin with correctly linked cysteine bridges with fewer necessary procedural steps, and hence resulting in a higher yield of human insulin with correctly linked cysteine bridges yield of human insulin. The IMC sequences not only protect insulin sequences from intracellular degradation by a microorganism host, but also promote the folding of the fuscon protein and decrease the intermolecular interactions among the fusion proteins, thus allowing folding of the fusion protein and decrease the intermolecular interactions among the fusion proteins, thus allowing folding of the fusion protein and decrease the intermolecular corrections and related purification steps can thus be eliminated, along with the consentrations of mercaptan or the use of hydrophobic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Human; anti-anglogenic; prolactin; placental lactogen; hPL; anglogenesis; growth hormone; hGH; hGH-V; capillary endothelial cell proliferation; placental vascularisation; pregnancy; treatment; anglogenic disease;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 tumour; inhibitor; malignant; angiofibroma; arteriovenous malformation; arthritis; atherosclerotic plaques; corneal graft neovascularisation; wound healing; proliferative retinopathy; macular degeneration; trachoma; granulation; glaucoma; ocular; uveitis; fracture; Osher-Weber syndrome; psoriasis; fibroplasia; scleroderma; Kaposi's sarcoma; vascular adhesion; ulcer; leukaemia; reproductive disorder; contraceptive agent; gene therapy; pre-eclampsia; intrauterine growth retardation; placental dysfunction;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    sequence represents an N-terminal fragment of human growth hormone
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                    New chimeric proteins containing human growth hormone fragment, used particularly for the production of human insulin \,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ..
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 470; DB 20;
Pred. No. 1.5e-22;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   59.0%; Scor.
100.0%; Pred. No. 1...
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  61 TPSNREETQQKSNLELLRISLLLIQSWLEPVQ 92
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(TONG-) TONGHUA GANTECH BIOTECHNOLOGY LTD.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAW92265 standard; Protein: 134
                                                                                                                                    Claim 5; Page 28; 46pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Conservative
                                                         WPI; 1999-610839/52.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Local Similarity
les 92; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   92 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                      absorbent resins.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sednence
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requirings can be used to provide the arthritic such as the control arthritis, atherosclerotic plaques, corneal graft neovascularisation, delayed wound healing, proliferative retinopathy who as diabetic retinopathy, macular degeneration, granulations such as those occurring in haemophilic joints, inappropriate vascularisation in wound healing such as hypertrophic scars or keloid scars, neovascular glaucoma, ocular tumour, uveitis, non-union fractures, Osler-Weber syndrome, psoriasis, pyogenic glaucoma, retrolental fibroplasia, scleroderma, solid tumours, kaposi's sarcoma, trachoma, vascular adhesions, chronic varicose ulcers, leukaemia, and reproductive disorders such as follicular and ulveal cysts and choriocarcinoma. They can also be used as contraceptive agents. DNA encoding the poptides can be used in gene therapy. The measurement of abnormal levels of Nuterminal Iraqments of hell, hGH+, prolacitin or hPL can be used in assays for impairment of vascular development associated with pre-eclampsia, intrauterine growth retardation, and placental
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          This invention describes novel human anti-angiogenic peptides derived from 10 to 150 consecutive amine acids selected from the N-terminal end of human placental lategore. Purl, human growth hormone (htm), growth hormone bariant (htm), or he an productin. Such peptides (ii) inhibit capillary endothelial cell preliferation and organisation (ii) inhibit angiogenesis in chick choricallantoic membrane and (iii) binds to at least one specific receptor which does not bind an intact full length hGH, hPL, prolactin or hGH-V. The invention also describes a method for diagnosing a probable abnormality of placental vascularisation during pregnancy. The peptides can e used for treating an angiogenic disease in modulating vascularisation of patient's placenta. In particular, the peptides can be used for preventing or treating e.g. malignant tumours,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 MFPT1PLSRLFDNAMLRAHRLHQLAFDTYQEFEEAY1PKEQKYSFLQNPQTSLSFSES1P 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 MFPI1PLSRLFDNAMLRAHRL4QLAFDTYQEFEEAYIPKEQKYSFLQNPQTSLSFSESIP 60
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Indels
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                                                                                                                                                                                                   Weiner RI;
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                                                                                                                                                                                                   Taylor R,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Claim 4; Page 49-50; 87pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ABG94861 standard; Protein; 191
98WO-US09691.
                                                                                                                                                                                                                                                                                                                                                                                                       human placental lactogen, variant or human prolactin
                                                                                                                                                                                                                                                                                                                                                                           New anti-angiogenic pepti
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Ouery Match
Bost Local Similarity 100..
Thies 92; Conservative
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                                                                                                                                                                                                Struman I,
                                                                                                                            (REGC ) UNIV CALIFORNIA
                                                                                                                                                                                                                                                                    WPI; 1999-045192/04
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                                                                                                                                                                                                                                                                                                       N-PSDB; AAX01707
12-MAY-1998;
                                                                13-MAY-1997;
                                                                                                                                                                                                   Martial JA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ABG94861;
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61 PSNREETQQKSNLELLK1SLLLIQSWLEPVQF-LKSVFANSLVYGASDSNVVDILEQLKR 119

109 LVEALYLVCGERGFFYTPKTRGIVEQ 134

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(first entry) (updated) (revised)

62 PSNREETQQKSNLELLRISLILIQSWLEPVQLGTCPRFVNQHLCGS--

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Growth hormone; placental lactogen; prolactin; active domain; hGH: structure-function relationship; segment-substituted polypeptide;
           mutant; mutein.
                                                    26-OCT-1989;
27-APR-1992;
13-OCT-1992;
02-FEB-1994;
28-OCT-1988;
                   Homo sapiens.
Synthetic.
                              US6428954-B1
                                             06-JUN-1995;
                                     06-AUG-2002
                                                                                   Wells JA,
                                                                                                                                                                                                                                                Sequence
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Human growth hormone; fusior protein; recombinant
                             AAP90129 standard; protein; 192
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    growth hormone or deriv. lig. and high yield.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (WAKI ) WAKUNAGA SEIYAKU KK
                                                                                                                                                                                                                   Human growth hormone.
                                                                                                                                                                                                                                                                                                                                         Homo sapiens (Human)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WPI; 1989-209284/29.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               02-DEC-1987;
                                                                                                                                                                                                                                                                                                                                                                                     JP01144981-A
                                                                                                                                                                       01-NOV-1989
                                                                                                                                                                                                                                                                                                                                                                                                                                     07-JUN-1989
                                                                                                                          25-MAR-2003
                                                                                                                                              06-FEB-1996
                                                                          AAP90129;
                                                                                                                                                                                                                                                                                            vector.
AAP90129
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 of known amino acid sequence in a parent polypeptide e.g. human growth hormone (hGH) which has been cloned and has a pre-identified biological activity, where the active domain interacts with a target when the parent polypeptide is in its native-folded form and the interaction is responsible for the biological activity comprising: (a) comparing the amino acid sequence of polypeptide structure in the region of known amino acid sequence or polypeptide structure in the region of known amino acid sequence of an analogue polypeptide (e.g. prolactin, placental lactogen or porcine growth hormone) which has at least 15% homology with hGH alpha-carbon coordinates within about 2-3.5 angstroms of hGH alpha-carbon coordinates for about 60% of the analogue sequence, where any interaction of the analogue with the target is different from target interaction with hGH;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (b) substituting DNA encoding an analogous polypoptide segment from the analogue into DNA encoding the full length hGH, and expressing a manalogue into DNA encoding the full length hGH, and expressing a polypoptide (c) contacting the segment-substituted polypoptide (c) contacting the segment assequent of the pand (c) with a second analogous polypoptide segment; and segment-substituted polypoptides as an indication of the location of the unknown active domain in hGH. The method is useful for determining the relationship between structure and function of known polypoptide segmences. The present sequence is that of human growth hormone
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                The invention relates to identifying an unknown active domain in a region
                                                                                                                                                                                                                                                                                                                                                                                                         acid sequence by substituting analog segments into the parent polypeptide is useful to determine the relationship between structure and function
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                mutant substituted with residues from an hGH analogue (prolactin, placental lactogen or porcine growth hormone).

Note: The present sequence is not shown in the specification but was created by the indexer using the mature hGH sequence and information contained in the specification.
                                                                                                                                                                                                                                                                                                                                                                                   Identifying active domains within cloned polypeptides of known amino
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 191;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  59.0%; Score 470; DB 23; 69.2%; Pred. No. 2.6e-22;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Example 1; Page -; 86pp; English.
                                                                                         89US-0428066.
92US-0875204.
92US-0960227.
                                               95US-0483039
                                                                                                                                                                    94US-0190723
88US-0264611
                                                                                                                                                                                                                                                                                    Cunningham BC;
                                                                                                                                                                                                                                          (GETH ) GENENTECH INC.
                                                                                                                                                                                                                                                                                                                                    WPI; 2002-696875/75.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   191 AA;
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protein - consisting of human i to foreign protein, for stability

87JP-0304937 87JP-0304937

61 TPSNREETQQKSNLELLRISLLLIQSWLEPVQLGTGPRFVNQHLCGS------HLV 110 61 TPSNREETQQKSNLELI SLLLIQSWLEPVQF-LRSVFANSLVYGASDSNVYDLLKDLE 119 The invention consists of a vector contg. a fusion protein which is formed by ligating, downstream of a promoter. hGH or a deriv. (pref. formed by subtstn. of Met-14 with Leu) and a foreign protein. Stability of the vector in the host is greatly increased so the protein yield is higher. (Updated on 25-MAR-2003 to prect PA field.) 16; 58.5%; Score 466; DB 10; Length 192; illarity 70.5%; Pred. No. 4.6e-22; Conservative 7; Mismatches 20; Indels 19 120 EGIQTLMGRLEDG---SPRTGQIFKQ 142 111 EALYLVCG -- ERGFFYTPKTRGIVEQ 134 Disclosure: Fig 1; 19pp; Japan se. Query Match Best Local Similarity Matches 103; Conserv 192 AA; Seguence ò 61 18;

1 FPTIPLSKLFDNAMLRAHRLHQLAFDTYQEFEEAYIPKEQKYSFLQNPQTSLCFSESIPT 60 2 FPTIPLSRLFDNAMLRAHRLHQLAFDTYQEFEEAYIPKEQKYSFLQNPQTSLSFSESIPT

19; Indels

8; Mismatches

Matches 101; Conservative

õ

Similarity

Local

RESULT 7 AAW92264

Length 192;

Score 466; DB 20; Pred. No. 4.6e-22;

58.5%; 70.5%;

192 AA;

Sequence

7; Mismatches

This invention describes novel human anti-anglogenic peptides derived from 10 to 150 consecutive amino acids selected from the N-terminal end of from 10 to 150 consecutive amino acids selected from the N-terminal end of human placental lactogen (hPL), human growth hormone (hGH) growth hormone variant (hGH-V), or human prolactin. Such peptides (i) inhibit capillary endothelial cell proliferation and organisation (ii) inhibit capillary endothelial cell proliferation and organisation (ii) inhibit consists of a probable abnormality of placental vacularisation during pregnancy. The peptides can be used for treating an angiogenic disase in a subject, for inhibiting tumour formation or growth in a patient or for modulating vacularisation of a patient's placenta. In particular, the peptides can be used for preventing or treating e.g. malignant tumours, contacting a subject, for inhibiting tumour formation arthritic such as rheumatoid a subject, for inhibiting tumour formation arthritic such as rheumatoid carthritis, atherosclerotic plaques, conneal graft necessorial and a contaction, celayed wound healing, proliferative retinopathy such as diabetic contactional placental placental placental placental glaucoma, sociar memophilic joints inappropriate vascularisation in wound healing, contactorial such as hypertrophic scars or keloid scars, necessariant, sold tumours, coular tumour, uveitis, non-union fractures, Osler-Weber syndrome, psoriasis, placender and choiccarchoma. Tetrolental fibroplasis, scheroderma, solid tumours, conditions the peptides can also be used as contraceptive agents. DNA encoding the peptides can be used in gene therapy. The measurement of abnormal levels of N-terminal fragments of hGH, hGH-V, prolactin or hPL very business intracellangs and placental and placental account of vascular daveloner, and placental account of vascular daveloner, and placental angelian proverse impairment of vascular daveloner, and placental angeliance of managements and reproductive discounts of vascular daveloner, and pl

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Best Local Similarity 70.5
Matches 103; Conservative
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                                                                                                                                                                                                                  Human; anti-anglogenic; prolactin; placental lactoden; hPL; anglogenesis; growth hormone; hGH; hGH-V; capillary endothelial cell proliferation; blacental vascularisation; pregnancy; treatment: anglogenic disease; tumour; inhibitor; malignant; anglofibroma; arteriovenous malformation; arthritis; atherosclerotic plaques; corneal graft neovascularisation; granulation; glaucoma; coular; uveitis; fracture; Osler-Weber syndrome; psoriasis; fibroplasia; scleroderma; Mapc i's sarcoma; vascular adhesion; uler: lackaemia; reproductive disorder; contraceptive agent; gene therapy; pre-eclampsia; intrauterine growth retardation; placental dysfunction.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            New anti-angiogenic peptides - comprise N-terminal fragments of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     human placental lactogen, human growth h\varepsilon mone, growth hormone variant or human prolactin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Weiner RI;
                                                                                                                                                                       Human anti-angiogenic peptide hGH Met-1Phe191.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Taylor R,
   AAW92264 standard; Protein; 192 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Example 3; Page 49; 87pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 98WO-US09691.
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                                                                                                                     (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Struman I,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (REGC ) UNIV CALIFORNIA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WPI; 1999-045192/04.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  N-PSDB; AAX01706
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         HOMO sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              W09851323-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 12-MAY-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        13-MAY-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Martial JA,
                                                                                                                  08-JUN-1999
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                                                        61 TPSNREETQQKSNLELLRISLLLIQSWLEPVQLGTGPRFVNOHLCGS------HLV 110
                                                                         1 MFPTIPLSRLFDNAMLRAH: HQLAFDTYQEFEEAYIPKEQKYSFLQNPQTSLSFSESIP 60
               1 MFPTIPLSRLFDNAMLRAHRLHQLAFDTYQEFEEAYIPKEQKYSFLQNPQTSLSFSESIP 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   protein, which contains a thrombin recognition site, and human beta n growth factor (beta-NGF) at the C-terminal. Beta-NGF can be used to control geriatric dementia and other nervous disorders, and can be released from the fusion protein by incubation with thrombin (see AAN90577-8, AAP91034, AAP91299).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             New human nervo growth factor gene encoding fusion protein - having cleavage site for thrombin, useful for treating generation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Human growth hormone segment, used at the N-terminal of a fusion
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ö
                                                                                                                                                                                                                                                                                                                                                           geriatric dementia; nervous d sorders; human nerve factor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      58.3%; Score 465; DB 10; 98.9%; Pred. No. 4.2e-22;
                                                                                                                                                                                                                                                                                                                                             Human growth hormone; fusion (lotein; thrombin;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             61 TPSNREETQQKSNLELLRISLLLIQSWLEPVQ 92
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     0; Mismatches
                                                                                                                                     | : : | | | : | : | : | EGIOTLMGRLEDG --- SPRTGQ1FKQ 142
                                                                                                                    111 EALYLVCG -- ERGFFYTPKTRGIVEQ 134
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Disclosure; page 21; 38pp; English.
                                                                                                                                                                                                                       AAP91041 standard; protein: 40
                                                                                                                                                                                                                                                                                                               Human growth hormone segment
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               89EP-0102795
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                                                                                                                                                                                                                                                                                    (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                         Homo sapiens (human).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WPI; 1989-243092/34
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (TOYJ ) TOSOH CORP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 140 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           dementia, etc.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               17-FEB-1989;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          19-FEB-1988;
                                                                                                                                                                                                                                                                                   14-DEC-1989
                                                                                                                                                                                                                                                                                                                                                                                                                                                 23-AUG-1989
                                                                                                                                                                                                                                                                                                                                                                                                                    EP329175-A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Ohtsuka E;
                                                                                                                                                                                                                                                     AAP91041;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Matches
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(first entry)
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Matches 91; Conservative
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                                                                                                                                        (TOYJ ) TOSOH CORP.
                                                                                                                                                                                                                                                                                                262 AA;
                                                                                                                                                                 N-PSDB; AAQ11578
                                                                   JP03067598-A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      JP02013375-A.
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                                                    Homo sapiens
                                                                                                      07-AUG-1989;
                                                                                                                       07-AUG-1989;
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25-JUN-1991
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                                                                                                                                                                                                                                                                                                                                                                       Fusion protein consisting of human growth hormone at the tremnial end (1st region), a 3 amino acid sequence representing thrombin recognition site, and human beta nerve growth factor (4eta-WEY) at the C-terminal. Beta-NGF can be used to control geriatric generating and other nervous disorders, and can be released from the fusion protein by incubation with thrombin (see AAN90577-8, AAP91034.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 MFPTIPLSRLFDNAMLRAHRLHQLAFDTYQEFEEAYIPKEOKYSFLQNPQTSLSFSESIP 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                         New human nerve growth factor gene encoding fusion protein - having cleavage site for thrombin, usefil for treating geriatric
                                                                                              Human nerve growth factor and human growth hormone fusion protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ;
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                                                                                                              Human nerve growth factor; fusion protein: thrombin; gerlatric dementia; nervous disorders; human growth hormone.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 465; DB 10;
Pred. No. 6.8e-22;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           61 TPSNREETQQKSNLELLRISLLLIQSWLEPVQ 92
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                0; Mismatches
                                                                                                                                                                                                                                                                                                                                                         Claim 36; page 31-32; 38pp; English.
                                                                                                                                                         Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAR11740 standard; Protein; 262 AA.
                                          AAP91299 standard; protein; 261
                                                                                                                                                                                                                                                                                                                                                                                                                                                             58.38;
98.98;
                                                                                                                                                                                                                                                     88JP-0035042
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                                                                             14-DEC-1989 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               91; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (updated)
                                                                                                                                         Homo sapiens (human).
                                                                                                                                                                                                                                                                                                        WPI; 1989-243092/34
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                              261 AA;
                                                                                                                                                                                                                                                                                                                                           dementia, etc.
                                                                                                                                                                                                                                                                      HOSOT ( LYOT)
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                                                                                                                                                                                                                                                                                                                                                                                                                                              Seguence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAR11740;
                                                            AAP91299;
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                                                                                                                                                          Key
Region
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                                    AAP91299
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A recombinant human nerve growth factor beta subunit-conty. protein can be produced as this fusion protein. It is purified by contacting a qel having a cation exchange qp. with the fusion protein, in the presence of urea. The purified protein is useful in a medicament for treating disorders of the nervous system, eg dementia.

(Updated on 25-MAR-2003 to correct PF field.)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    B-cell stimulatory factor-2; interleukin-6; B-cell differentiation; interleukin-5; fusion protein.
Human growth hormone/human nerve growth factor beta fusion protein
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                                 Fusion protein of B-cell stimulatory factor-2 and B-cell differentiation factor.
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11 - 111111-11111-11111-1
6) TPSNREETQOKSNLEDAK(SILDAGSMLEFVO 92
                                                                                                                                                                                             hGH; hNGF; nervous system diseases; dementia
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mutant; mutein.
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28-OCT-1988;
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                                                                                                                                                                                                                     Query Match
                                                                                                                                                     hormone.
                                                                                                                                                                                                                                                                                                                                                                                    RESULT 13
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                                                                                                                                                                                                  1 MFPTIPLSRLFDNAMLRAHRLHQLAFDTYQEFEEAYIPKEQKYSFLQNPQTSLSFSESIP 60
                                                                                                                                                                                                           New conjugates exhibiting growth hormone activity, useful for treating a disease or for manufacturing a medicament for treating a disease, e.g. Turner's syndrome, growth hormone deficiency, achondroplasia, AIDS wasting or cachexia -
                                                                                                                                                                                                                                                                                                                                                                                Human: growth hormone; hGH: Turner's syndrome; achondroplasia:
growth hormone deficiency in adults; GHDA; chroni: renal insufficiency;
renal failure in children; acquired immune deficit ocy syndrome; AIDS;
AIDS wasting; cachexia; mutant; mutein.
                                                                                                     DNA encoding BDF (IL-) with DNA the product into an expression vector
                                                                                                                                                                                Gaps
                                            Prepn. of human B-cell differentiation factor - from specified DNA sequence segment, by recombinant DNA technique, gives protein of specified amino acid sequence.
                                                                                                                                                                               ·.
                                                                                                                                                              Length 310;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /note= "Wild type Arg substituted by Lys"
                                                                                                                                                                               Indels
                                                                                                                                                            58.3%; Score 465; DB 11; 98.9%; Pred. No. 7.7e-22; iive 0; Mismatches 1;
                                                                                                                                                                                                                                     Mature human growth hormone (hGH), mutant #4.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Andersen KV, Drustrup J, Christiansen J;
                                                                                                                                                                                                                                                                                                                                                                                                                                                           Location/Qualifiers
                                                                                                                                                                                                                                                                                                       ABG31862 standard; Protein; 191 AA
                                                                                                   The protein is produced by fusing encoding BSF-2 (IL-5)and ligating See also AAR05311 and AAR05313.
                                                                                   Claim 31; Page 9; 17pp; Japanese
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (MAXY-) MAXYGEN APS.
(MAXY-) MAXYGEN HOLDINGS LTD.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         11-JAN-2001, 2001DK-0000042.
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                                                                                                                                                                                                                                                                                                                                             (first entry)
                                                                                                                                                                      Best Local Similarity 98.9
Matches 91; Conservative
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                 WPI: 1990-062207/09
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Misc-difference 134
(TOYJ ) TOSOH CORP.
                                                                                                                                           310 AA;
                            N-PSDB; AAQ02028
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                                                                                                                                                                                                                                                                                                                                                                                                                                 Homo sapiens
Synthetic.
                                                                                                                                                                                                                                                                                                                                            05-NOV-2002
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                                                                                                                                            Sequence
                                                                                                                                                                                                                                                                                                                          ABG31862;
                                                                                                                                                             Query Match
                                                                                                                                                                                                                                                                                      RESULT 12
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                                                    The invention relates to new conjugates, which exhibit growth hormone (GH) activity and comprise at least one non-polypeptide group covalently attached to a GH polypeptide. The amino acid sequence of the conjugates differs from that of wild type human GH in at least one introduced and at least one removed amino acid residue comprising an attactment group for the first non-polypeptide group. The conjugate or pharmaccutical composition is useful for treating a disease or for manufacturing a medicament for treating a disease, e.g. Turner's syndrome. GH deliciency in adults (i.e. GHDA), achondroplasia, chronic renal insufficiency or failure (including renal failure in children), acquired immune deliciency syndrome (ALDS) wasting, cachexia in AIDS patients, or cachexia associated with other diseases. The conjugates are useful if the treating a variety of disorders caused by growth hormone inadequacy. The present
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          61 PSNREETQQKSNLELLRISLLLIQSWLEPVQF-LRSVFANSLVYGASDSNVYDLLKDLEE 119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             62 PSNREETQQKSNLELLRISLILIQSWLEPVQLGTGPRFVNOHLCGS------HLVE 111
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Note: The present sequence is not shown in the specification but is derived from the wild type human growth hormone sequence given in SEO No.2 (see ABG31857).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     2 FPTIPLSRLFDNAMLRAHRLHQLAFDTYQEFEEAYIPKEQKYSFLQNPQTSLSFSESIPT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 FPTIPLSRLFDNAMLRAHRLHQLAFDTYQEYEEAYIPKEQKYSFLONPQTSLCFSESIPT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Growth hormone; placental lactoden; prolactin; active domain; hGH; structure-function relationship; segment-substituted polypeptide:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 16;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          core 464; DB 23;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 6: Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Human growth hormone mutant het. (109-112)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               112 ALYLVCG--ERGFFYTPKTRGIVEO 134
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        JOILMGRLEDG --- SPKTGQIFKQ 141
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AA.
Claim 10; Page -; 74pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ABG94860 standard; Protein; 1/1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          58.2%;
71.6%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           95US-0483039.
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92US-0960227
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88US-0264611
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Best Local Similarity 71.0
Matches 103; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 191 AA;
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95US-0483U39

US6428954-B1

Synthetic.

06-AUG-2002

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of known amino acid sequence in a parent polypeptide e.g. human growth bromone (hds) which has been cloned and has a pre-identified biological activity, where the active domain interacts with a target when the polypeptide is in its native-cloded form and the interaction is responsible for the biological activity coorprising; (a) comparing the amino acid sequence of polypeptide structure in the region of known amino acid sequence of hdH with the amino acid sequence or polypeptide structure in a region of known amino acid sequence of an analogue polypeptide (e.g. prolactin, placental lactogen or portine growth hormone) which has at least 15% homology with hdH alpha-carbon coordinates within about 2.3.5 angstroms of hdH alpha-carbon coordinates for about 60% of the analogue sequence, where any interaction of the analogue with the target is different from target interaction with hdH.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (b) substituting DNA encoding an analogous polypeptide segment from the manalogue into DNA encoding the full length hGH, and expressing a segment substituted polypeptide; (c) contacting the segment-substituted polypeptide (c) contacting the segment-substituted polypeptide with the target to determine interaction; (d) repeating steps
                                                                                                                                                                                                                                                                    the invention relates to identifying an unknown active domain in a region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (b) and (c) with a second analogous polypeptide segment, and (e) comparing the difference between activity of the first and second segment-substituted polypeptides as an indication of the location of the unknown active domain in helf. The method is us ful for determining the relationship between structure and function of known polypeptide sequences. The present sequence is that of human growth hormone
                                                     Identifying active domains within cloned polypeptifes of known amino acid sequence by substituting analog segments into the parent polypeptide is useful to determine the relationship between structure
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         mutant substituted with residues from an hGH analogue (prolactin, placental lactogen or porcine growth hormone).

Note: The present sequence is not shown in the specification but was created by the indexer using the mature hGH sequence and information contained in the specification.
                                                                                                                                                                                                        Example 1; Page -; 86pp; English
MPI; 2002-696875/75
                                                                                                                                                      function
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191 AA; Sednence

61 PSNREETQQKSNLELLRISLLLIQSWLEPVQF-LRSVFANSLVYGASDSUDYHLLKDLEE 119 62 PSNREETQQKSNLELLRISLLLIQSWLEPVQLGTGPRFVNQHLCGS-----HLV----E 111 2 FPTIPLSRLFDNAMLRAHRLHQLAFDTYQEFEEAYIPKEQKYSFLUNPQTSLSFSESIPT 61 Gaps 16; 18; Indels 58.1%; Score 463; DB 23; 71.0%; Pred. No. 7.1e-22; 8; Mismatches 112 ALYLVCG--ERGFFYTPKTRGIVEQ 134 120 GIQTLMGRLEDG---SPRTGQIFKQ 141 Matches 103; Conservative Local Similarity Query Match qq ò q ò

Growth hormone; placental lactogen; prolactin; active domain; hGH; structure-function relationship; segment-substituted polypeptide; mutant; mutein. ABG94977 standard; Protein; 191 AA Human growth hormone mutant Y103A. (first entry) 03-DEC-2002 ABG94977; RESULT 14 ABG94977

Homo sapiens.

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The invention relates to identifying an unknown active domain in a region of known amino acid sequence in a parent polypeptide e.g. human growth hormone (hGH) which has been cloned and has a pre-identified biological activity, where the active domain interacts with a target when the polypeptide is in its native-folded form and the interaction is responsible for the biological activity comprising: (a) comparing the amino acid sequence or polypeptide structure in the region of known amino acid sequence of hGH with the amino acid sequence or polypeptide structure in a region of known amino acid sequence of an analogue polypeptide (e.g. prolact: placental lactogen or porcine growth hormone) which has at leas 18% homology with hGH alpha-carbon coordinates within about 2 % angstroms of hGH alpha-carbon coordinates
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              polypeptide with the target to determine interaction; (d) repeating steps (b) and (c) with a second and rous polypeptide segment; and (e) comparing the difference between activity of the first and second
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  62 PSNREETQQKSNLELLRISLLLIQSWLEPVQLGTGPRFVNQHLCGS------HLVE 111
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         61 PSNREETQQKSNLELLKISLLLIQSWLEPVQF-LRSVFANSLVAGASDSNVYDLLKDLEE 119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (b) substituting DNA encoding an analogous polypeptide segment from the analogue into DNA encoding the ^{+}-11 length hGH, and expressing a segment-substituted polypeptide; (c) contacting the segment-substituted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      for about 60% of the analogue, sequence, where any interaction of the analogue with the target is different from target interaction with hGH;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    the unknows active domain in hGH. The method is useful for determining the relationship between structure and function of known polypeptide sequences. The present sequence is that of human growth hormone mutant substituted at functionally important residues and used in
                                                                                                                                                                                                                                                                                                                                                                                                                           Identifying active domains within cloned polypeptides of known amino acid sequence by substituting analog segments into the parent polypeptide is useful to determine the relationship between structure
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Note: The present sequence is not shown in the specification but was created by the indexer using the mature hGH sequence and information contained in the specification.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                segment-substituted polypeptides as an indication of the location of
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Example 16; Page -; 86pp; English.
                                                                                                                                                                  89US-0428066.
92US-0875204.
92US-0960227.
94US-0190723.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      the method of the invention.
                                                                                                                                                                                                                                                        88US-0264611
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                                                                                                                                                                                                                                                                                                 (GETH ) GENENTECH INC.
                                                                                                                                                                                                                                                                                                                                                                                WPI; 2002-696875/75.
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es 102; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            and function
                                                                                                                          06-JUN-1995;
                                                                                                                                                                                                               13 · OCT - 1992;
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120 GIQTLMGRLEDG---SPRTGQIFKQ 141

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The sequence encoding this protein can be fused with DNA encoding B-ceil differentiation factor (IL-6) and ligated into an expression vector tor prodn. of a fusion protein. See also AAR05311.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                 Prepn. of human B-cell differentiation factor - from specified DNA sequence segment, by recombinant DNA technique, gives protein of specified amino acid sequence.
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                                                                                        Segment of B-cell stimulatory factor-2 (IL-5).
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                      AAR05313 standard; protein; 144 AA
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                                                                                                                                                                                                   88JP-0162556.
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                                                                  (first entry)
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N-PSDB; AAQ02028.
                                                                                                                                                                                                                                             (TOYJ ) TOSOH CORP.
                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 144 AA;
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                                                                                                                                   Homo sapiens.
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GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.
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3: /cgn2_6/ptodata/1/laa/6A_COMB.pep:*
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Sequence 2, Appli	Patent No. 5424199	Sequence 5, Appli	Š		Sequence 5, Appli		6	Sequence 39, Appl	Sequence 48, Appl	Sequence 48, Appl	Sequence 45, Appl	Sequence 45, Appl	Sequence 8, Appli	Sequence 1, Appli	4	ç	7,
US-08-990-774-2	5424199-3	US-08-187-756C-5	US-08-710-324A-5	US-09-411-657-5	US-08-160-376A-5	-08-389-487-8	U:-68-400-256-39	US-08-975-365-39	US-C8-400-256-48	US-CR-975-365-48	US: 08-400-256-45	US-08-975-365-45	US-08-468-824-8	08-09-105-651-1	US-U7-963-331D-4	US-08-160-376A-6	US-08-388-267C-2
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176	168	198	198	198	96	96	137	137	146	146	145	145	191	216	191	63	190
45.1	4 3.0	42.0	42.0	42.0	39.7	39.7	39.4	39.4	38.8	38.8	38.8	38.8	38.5	38.5	38.2	38.1	37.8
359.5	343	334.5	334.5	334.5	316.5	316.5	314	314	309.5	309.5	309	309	306.5	306.5	304.5	304	301.5
28	67	30	31	32	33	34	35	36	37	38	39	40	41	42	43	44	4 5

ALLGNMENTS

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APPLICANT: DeBoor, Herman A.
APPLICANT: Heyneker, Herbert L.
APPLICANT: Seeburg, Peter H.
AITLE OF INVENTION: DNA for Expression of Bovine Growth Hormone NUMBER OF SEQUENCES.
                                                                                                                                                                                                                                                                                                                                                           COMPUTER READBLE FORM:
MEDIUM TYPE: 5.25 inch, 360 Kb 110ppy disk
COMPUTER: 15M PC COMPUTER:
OPENATING SYSTEM: PC-DUSZWS DAS
SOFTWARE: patin (Generated)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/OH/US4:88:
FILING DATE: 14-JUL-1993
CLASSIFICATION: 435
                                                                                                                                                                                          ....urrbs:

STREET: 460 Point San Bruco blvd

CITY: South San Francisco

STATE: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRIOR APPLICATION 1439
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/619827
FILING DATE: 28 NOV-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/198824
PRIOR APPLICATION DATA:
APPLICATION DATA:
APPLICATION DATA:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 06/632361
FILING DATE: 19-JUL-1984
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 06/303687
FILING DATE: 18-SEP-1981
ATTORNEY/AGENT INFORMATION:
                       Sequence 1, Application US/08093383
Patent No. 5489529
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         P35,910
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TELEFAX: 415/92.
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 192 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 REFERENCE/DOCKET NUMBER: 460
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NAME: Johnston, Sean A. REGISTRATION NUMBER: P3
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US-08-093-383-1
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US-08-791-728-2

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TELEPHONE:
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APPLICANT: Saldana, Hugo Barrera
APPLICANT: Saldana, Hugo Barrera
APPLICANT: Salvado, Jose Maria Viader
APPLICANT: Salvado, Jose Maria Viader
TITLE OF INVENTION: Genetically Modified Methylotrophic P. pastoris Yeast for the
TITLE OF INVENTION: Production and Secretion of the Human Growth Hormone
FILE REFERENCE: 1829.0010000
CURRENT APPLICATION NUMBER: US/09/284,878
CURRENT FILING DATE: 1999-07-21
PRIOR APPLICATION NUMBER: PCT/MX97/00033
PRIOR APPLICATION NOWBER: PCT/MX97/00033
PRIOR FILING DATE: 1997-10-24
NUMBER OF SEQ ID NOS: 9
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 61 PSNREETQQKSNLELLRISLLIQSMLEPVQF-LRSVFANSLVYGASOSNVYDLLKDLEE 119
                                                                                                                                                                                                                                          62 PSNREETQQKSNLELLRISLLI, IQSMLEPVQLGTGPRFVNQHLCGS------ HLVE 111
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 MFPTIPLSRLFDNAMLRAHRLHQLAFDTYQEFEEAYIPKEQKYSFLONPQTSLSFSESIP 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          16; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TITLE OF INVENTION: Stabilization Of Somatotropins And Other TITLE OF INVENTION: Proteins By Modification Of Cysteine Residues
                                                                                                          16;
                                                           Ouery Match 58.5%; Score 466; DB 1; Length 192; Best Local Similarity 70.5%; Pred. No. 1.1e-42; Matches 103; Conservative 7; Mismatches 20; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match 57.8%; Score 461; DB 4; Length 191; Best Local Similarity 70.3%; Pred. No. 3.7e-42; Matches 102; Conservative 7; Mismatches 20; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 112 ALYLVCG--ERGFFYTPKTRGIVEQ 134
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Patent No. 5951972
GENERAL INFORMATION:
APPLICANT: Daley, Michael J.
APPLICANT: Cady, Susan M.
APPLICANT: Cady, Susan M.
APPLICANT: Shieh, Hong-Ming
APPLICANT: Shieh, Peter
APPLICANT: Soldon, Andrew P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 5, Application US/09284878
Patent No. 6342375
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TYPE: PRT
ORGANISM: Homo saptens
US-09-284-878-5
; TOPOLOGY: linear
US-08-093-383-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GENERAL INFORMATION:
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US-08-383-621-4
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US-09-284-878-5
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62 PSNREETQQKSNLELLRISLLLIQSWLEPVQLGTGPRFVNQHLCGS------------HLVE 1111
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           2 FPTIPLSRLFDNAMLRAHRLHQLAFDTYOEFEEAYIPKEQKYSFLQNPQTSLSFSESIPT 61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: Dalcy, Michael J.
APPLICANT: Buckwalter, Brian L.
APPLICANT: Buckwalter, Brian L.
APPLICANT: Gady, Susan M.
APPLICANT: Shich, Hong-Ming
APPLICANT: Boblen, Peter
APPLICANT: Boblen, Peter
APPLICANT: Seddon, Andrew P.
TITLE OF INVENTION: Stabilization of Somatotropins and Other
TITLE OF INVENTION: Proteins by Modification of Cysteine Residues
NUMBER OF SEQUENCES: 11
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          16;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 194:
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70.3%; Pred. No. 3.8e-42;
tive 7: Mismatches 20; Indels
                                                                                                                                                             COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                       E: Dr. Estelle J. Tsevdos
1937 West Main Street, P.O. Box 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          7; Mismatches
                                                                                                                                                                                                                                                                                                           APPLICATION NUMBER: US/08/383,621
FILING DATE: 06-FEB-1995
CLASSPICATION S14
PRIOR APPLICATION S14
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/766,142
FILING DATE: 25-SEP-1991
ATTORNEY/AGENT INFORMATION:
NAME: TSEVGOS, ESCELLE J.
REGISTATION NUMBER: 31,145
REFERENCE/DOCKET NUMBER: 31,278-01
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ADDRESSEE: American Cyanamid Company
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     112 ALYLVOS - ERGFFYTPKTRGIVEG 134
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 4, Application US/08459906 Patent No. 6010999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       One Cyanamid Plaza
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TELEFAX: 203-321-2971
TELEX: 203-710-474-4059
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          203-321-2756
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1: 194 amino acids
amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match 57.8 Best Local Similarity 70.3 Matches 102; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ) MOLECULE TYPE: protein US-08-383-621-4
CORRESPONDENCE ADDRESS:
ADDRESSEE: Dr. Estel
                                                             CITY: Stamford
STATE: Connecticut
COUNTRY: U.S.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CITY: Wayne
STATE: New Jersey
COUNTRY: U.S.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    linear
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Score 461; DB 3;
Pred, No. 4.46-42;
                                                                                                                                                                                                                                                                                                                                                                  7; Mismatches
                  NAME: Highlander, Steven L
REGISTRATION NUMBER: 47.642
REFERENCE/DOCKET NUMBER: UTSD:426\HYL
TELECOMMUNICATION INFOHMATION:
TELEFAX: (512) 418-3000
TELEFAX: (512) 444-7577
INFORMATION FOR SEQ ID NO: 10:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               112 ALYLVCG -- ERGFFYTPKTRGIVEO 134
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: Newgard, Chr.L. Ther B. APPLICANT: Halban, Philip, A. APPLICANT: No 6110707minquon, Karl APPLICANT: Clark, Samuel A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/: :4,582
FILING DATE: Concurrently Herewith
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICATION NUMBER: US 60/028,427 FILING DATE: 15-0CT-1996 PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/589,028 FILING DATE: 19-JAN-1996 ATTORNEY AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 White & Durkee
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 10, Application US/08784582 Patent No. 6110707 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER: Floppy disk
COMPUTER: IBM PC COMpatible
OPERATING SYSTEM: PC-DOS // SOFTWARE: Patent
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NAME: Highlander, Steven L. REGIS RATION NUMBER: 37,642
                                                                                                                                                                                                                                                                                                                           57.8%; 70.3%;
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                          LENGTH: 217 amino acids TYPE: amino acid
                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity 70.3%
Matches 102; Conservative
                                                                                                                                                                          SEQUENCE CHARACTERISTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       P.O. BCX 4433
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COUNTRY: USA
ZIP: 77210
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy O
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NUMBER OF SEQUENCES: 7
CORRESPONDENCE ADDRESS:
ADDRESSEE: Arnold, W
                                                                                                                                                                                                                                                                incar
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                                                                                                                                                                                                                                                                , TOPOLOG :
US-08-589-028-10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RESULT 6
US-08-784-582-10
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       64 PSNREETQQKSNLELLRISLLLIQSWLEPVQF.LRSVFANSLVYGASDSNVYDLLKDLEE 122
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     4 FPTIPLSRLFDNAMLRAHRLHQLAFDIYQEFEEAYIPKEQKYSFLQNPQTSLCFSESIPT 63
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 2 FPTIPLSRLFDNAMLRAHRLHQLAFDTYQEFEEAYIPKEQKYSFLQNPQTSLSFSESIPT 61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          57.8%; Score 461; DB 3; Length 194;
70.3%; Pred. No. 3.8e-42;
tive 7; Mismatches 20; Indels 16;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: Newgard, Christopher H.
APPLICANT: Newgard, Christopher H.
APPLICANT: Halban, Philippe
APPLICANT: No. 6087129mington, Karl D.
APPLICANT: Clark, Samuel A.
APPLICANT: Thippen, Anice E.
APPLICANT: Thippen, Anice E.
APPLICANT: Wisse, Fred
TITLE OF INVENTION: Recombinant Expression of Proteins From TITLE OF INVENTION: Secretory Cell Lines
NUMBER OF SEQUENCES: 50
                                                                                                 CURRENT APPLICATION DATA:
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/459,906
FILING DATE: 02-JUN-1995
CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: Webster, Darryl L.
REGISTRATION NUMBER: 31,278-03
TELECOMMUNICATION NUMBER: 31,278-03
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION 1978-1931-3247
TELEPHONE: 201-831-3247
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       112 ALYLVCG - - ERGFFYTPKTRGIVEQ 134
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICATION NUMBER: US/08/589,028
FILING DATE: Concurrently Herewith
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CORRESPONDENCE ADDRESS:
ADDRESSEE: Arnold, White & Durkee
STREET: P. O. Box 4433
CITY: HOUSTON
                    COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
CMEDIUM TIBM PC compatible
OPERATING SYSTEM: PC DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 10, Application US/08589028 Patent No. 6087129
                                                                                                                                                                                                                                                                                                                                                                             TYPE: amino acids
TYPE: amino acids
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                  INFORMATION FOR SEQ ID NO: 4: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity 70.39
Matches 102; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MOLECULE TYPE: protein US-08-459-906-4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COUNTRY: USA
ZIP: 77210-4433
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GENERAL INFORMATION:
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· HI.VE 111
                                                                                                                                   1) FPIIPLSRLEDNAMLRAHRIHQLAFDTYQEFEEAYIPKEQKYSFLQNPQTSLCFSESIPT 86
                                                                                                       2 FPTIPLSRLFDNAMLRAHRLHQLAFDTYQEFEEAYIPKEQKYSFLONPQISLSFSESIPT 61
                                                20; Indels 15; Gaps
                                                                                                                                                                                                                 62 PSNREETQQKSNLELLKISLLLIQSWLEPVQLGTGPRFVNQHLCGS----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: Thigpen, Anice E.
APPLICANT: Quaade, Christian
APPLICANT: Kruse, Fred
APPLICANT: MCGATTY, Dennis
TITLE OF INVENTION: RECOMBLAGNE EXPRESSION OF PROTEINS FROM
TITLE OF INVENTION: SECRETORY CELL LINES
Length 217;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SYSTEM: PC-DOS/MS-DOS
PatentIn Release #1.0, Version #1.30
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HLVE 111

Saps

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2 FPTIPLSRLFDNAMLRAHRLHQLAFDTYQEFEEAYIPKEQKYSFLQNFQTSLSFSFSIFT 61
                                                                                                                                                                                                                                                                                                                    Score 461; DB 3; Length 217;
Prod. No. 4.4e-42;
7; Mismatches 20; Indels 16;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 11, Application US/08759626
Parent No. 6225446
Parent No. 6225446
APPLICANT Altmann, Scott W. APPLICANT Rock, Fernando L. APPLICANT Rastelein, Robert C. TITLE OF INVENTION MUTATIONAL VARIANIS OF MAMMLIAN PROTEINS NUMBER OF SEQUENCES: 11
COMMESSORINGE ADDRESS: 1

                                                                                                                                                                                                                                                                                                                                                                                                              62 PSNREETQQKSNLELLM LLIQSWLEPVQLGTGPRFVNQHLCGS-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-OOS/MS:NOS
SOFTWARE: PALEMILIN Release #1.0, Version #1.30
CURENT APPLICATION DATA:
APPLICATION NUMBER: US/08/754,628
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 112 ALYLVCG--ERGFFYTPKTRGIVEG 134
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                E: DNAX Research Institute
901 California Averue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FILING DATE: 05 DEC-1946
CLASSIFICATION: 4.5
PRIOR APPLICATION DAIA:
PRIOR DATE: 05-0008,5/4
FILING DATE: 06-000-1995
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NAME: Ching, Edwin P.
REGISTRATION NUMBER: 34,090
REFERENCE/DOCKET NUMBER: DX055
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-496-1200
INFORMATION FOR SEQ ID NO: 11:
SEQUENCE CHARACITERISTICS:
LENGTH: 217 amino acids
                                                                                                                                                        57.8%;
                                                                                                                                                               Query Match
Best Local Similarity 70.33
Matches 102; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        single
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Z1P: Z1D4
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STREET: 901 Califo
CITY: Palo Alto
STATE: California
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94..115
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         TYPE: amino acid STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TYPE: amino acid
STRANDEDNESS: sin
TOPOLOGY: linear
                                                                     ; TOPOLOGY: linear
US-08-785-271-10
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LOCATION:
FEATURE:
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US-08-759-628-11
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    57.8%; Score 461; DB 3; Length 217;
70.3%; Pred. No. 4.4e-42;
tive 7; Mismatches 20; Indels 16; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: NewGard, Christopher B.
APPLICANT: NewGard, Christopher B.
APPLICANT: Halban, Philippe A.
APPLICANT: Clark, Samuel A.
APPLICANT: Clark, Samuel A.
APPLICANT: Thigpen, Anice E.
APPLICANT: Thigpen, Anice E.
APPLICANT: Thigpen, Ered
TITLE OF INVENTION: RECOMBINANT EXPRESSION OF PROIEINS FROM
TITLE OF INVENTION: SECRETORY CELL LINES
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER: REACHER FOR MEDIUM TYPE: FIPOPY disk COMPUTER: IBM PC COMPATIBLE FOR SOFTMANE FOR SOFTMANE: PC-DOS/MS-DOS SOFTMANE: PATENTIN Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/785,271
FILING DATE: CONCURRENTLY HERWITH CASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/589,028
FILING DATE: 19-JAN-1996
ATORNEY/AGENT INFORMATION:
NAME: Highlander, Steven L.
RESTSRATION NUMBER: 37.642
REFERENCE/COCKET NUMBER: 37.642
REFERENCE/COCKET NUMBER: 37.642
REFERENCE/COCKET NUMBER: USDS:313
FELECOMMUNICATION INFORMATION:
REFERENCE/DOCKET NUMBER: UTSD:514
TELECOMMUNICATION INFORMATION:
TELEPHONE: 512/418-3000
TELEFAX: 512/474-7577
INFORMATION FOR SEQ ID NO: 10:
SEQUENCE CHARACTERISTICS:
LENGTH: 217 amino acids
TYPE: amino acids
STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          112 ALYLVCG -- ERGFFYTPKTRGIVEQ 134
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ADDRESSEE: Arrold, White & Durkee STREET: P.O. Box 4433 CITY: Houston
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 10, Application US/08785271 Patent No. 6194176 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TELEFAX: 512/474-7577
INFORMATION FOR SEQ ID NO: 10:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TELEPHONE: 512/418-3000
TELEFAX: 512/474-7577
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                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity 70.33
Matches 102; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                          linear
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US-08-784-582-10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          US-08-785-271-10
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TITLE OF INVENTION: Process for preparing recombinant profess using highly efficient expression vector from Sacharomyres resevisiae
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 66, Application US/09280030A

Patent No. 6506595

GENERAL INFORMATION:
APPLICANT: Higashikuni, Nachiko
APPLICANT: Higashikuni, Nachiko
APPLICANT: Kondo, Masaki
TITLE OF INVENTION: DREFARING USEFUL POLYPEPTIDES THROUGH EXPRESSION OF THE
FILLE OF INVENTION: DATE: 1999-03: 6
CURRENT APPLICATION NUMBER: US/09/280,030A
CURRENT FILLNG DATE: 1999-03: 6
ERRLIER FILLNG DATE: 1999-03: 3
NUMBER OF SEQ ID NOS: 66
CONTANTO DATE: 1998-03: 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     62 PSNREETQQKSNLELLKISI: LIGSWLEPVQLGTGPRFVNQHLCGS-----------HLVE 111
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                2 FPTIPLSRLFUNAMLRAHRLHULAFUTYQEFEEAYIPKEQKYSFLQNPQTSLSFSESIPF 61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sal is
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 57.8%; Score 461; DB 4; Length 241
70.3%; Pred. No. 5e-42;
Live 7; Mismatches 20; Indels
                                                                                                                                                                                                                                                                                                                                                                3.5 inch, 1.44 Mb storage
                                                                                                                                                                                 CORRESPONDENCE ADDRESS:
ADDRESSEE: BACHMAN & IAPOINTE, P.C.
STREET: Suite 1201, 900 Chapel Street
                                                                                                                                                                                                                                                                                                                                                                                                       OPERATING SYSTEM: h.n.-wS 95/98
SOFTWARE: MS WORD
CURRENT APPLICATION DATA
APPLICATION NUMBER: US/09/424.620B
INFORMATION FOR SEQ 100. 6391585-1999
INFORMATION FOR SEQ 1D NO: 25.
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             : LENGTH: 241 amino icids
: TYPE: amino acid
: TYPE: amino acid
: TOPOLOGY: lincar
: MOLECULE TYPE: PROTEIN
: SEQUENCE DESCRIPTION: SEQ 11: NO: 25:
US-09-424-620B-25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              112 ALYLVCG--ERGFFYTPKT: IVEU 134
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEONG, Baik-Lin
                                                                                                                                                                                                                                                                                             COUNTRY: U.S.A.
ZIP: 06510-2802
COMPUTER READABLE FORM:
MEDIUM TYPE: DISKET:
                     BAE, Cheon-Soc
YANG, Doo-Suk
                                             Doc-Suk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ORGANISM: Artificial Sequence
                                                                     Jee-Won
                                                                                                                                                            NUMBER OF SEQUENCES: 25
                                                                                                                                                                                                                                                                          STATE: Connecticut
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity 70.39
Matches 102; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SOFTWARE: Patentin Ver. 2.0
                                                                                                                                                                                                                                                       CITY: New Haven
                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER: IBM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  US-09-280-030-66
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQ ID NO 66
LENGTH: 245
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: Olazaran, Martha Guerrero
APPLICANT: Saldana, Hugo Barrera
APPLICANT: Saldana, Hugo Barrera
APPLICANT: Saldana, Hugo Barrera
APPLICANT: Saldana, Hugo Barrera
TITLE OF INVENTION: Genetically Modified Methylotrophic P. pastoris Yeast for the
TITLE OF INVENTION: Genetically Modified Methylotrophic P. pastoris Yeast for the
TITLE OF INVENTION: Production and Secretion of the Human Growth Hormone
FILE REPERENCE: 1829.0010000
CURRENT APPLICATION NUMBER: US/09/284,878
CURRENT FILING DATE: 1999-07-21
PRIOR FILING DATE: 1999-10-24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       62 PSNREETQQKSNLELLRISLLLIQSWLEPVQLGTGPRFVNQHLCGS------HLVE 111
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                                                                                                                                                                                                                                                                                                                                                                                                              27 FPIIPLSRLFDNAMLRAHRLHQLAFDTYQEFEEAYIPKEGKYSFLONPQISLCFSESIPT 85
                                                                                                                                                                                                                                                                                                2 FPTIPLSRLFDNAMLRAHRLHQLAFDTYQEFEEAYIPKEQKYSFLQNPQISLSFSESIPT 61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 2 FPTIPLSRLFDNAMLRAHRLHQLAFDTYQEFEEAYIPKEQKYSFLQNPQTSLSFSESIPT 61
                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      16;
                                                                                                                                                                                                                                                       16;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match 57.8%; Score 461; UB 4; Length 217; Best Local Similarity 70.3%; Pred. No. 4.4e-42; Matches 102; Conservative 7; Mismatches 20; Indels
                                                                                                                                                                                                         Length 217;
                                                                                                                                                                                                                                                       20; Indels
                                                                NAME/KEY: Peptide
LOCATION: 192..210
COTER INFORMATION: /note- "The peptides above are
COTER INFORMATION: depicted in Figure 1"
US-08-759-628-11
                                                                                                                                                                                                       57.8%; Score 461; DB 3; 70.3%; Pred. No. 4.4e-42; tive 7; Mismatches 20,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 25, Application US/09424620B
Patent No. 6391585
GENERAL INFORMATION:
APPLICANT: HANIL SYNTHETIC FIBER CO., LTD.
JANG. KI-Ryong
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               112 ALYLVCG -- ERGFFYTPKTRGIVEQ 134
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     146 GIQTLMGRLEDG---SPRTGOIFKO 167
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                112 ALYLVCG--ERGFFYTPKTRGIVEQ 134
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 1, Application US/09284878 Patent No. 6342375
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NUMBER OF SEQ ID NOS: 9
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 1
                                                                                                                                                                                                    Query Match
Best Local Similarity 70.3 Matches 102; Conservative
  Peptide
133..153
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TYPE: PRT
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RESULT 10
US-09-424-620B-25
NAME/KEY:
LOCATION:
FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   US-09-284-878-1
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NAME: Highlander Steven L. REGISTRAIION NUMBER: 37,642 REFERENCE/DOCKET NUMBER: UTTELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TELEFAX: 512/474-7577
INFORMATION FOR SEQ ID NO: 73:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           57.8%;
70.3%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            : 360 amino acids
amino acid
                        Query Match 57.8°
Best Local Similarity 70.3°
Matches 102; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    21P: 77210
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Houston
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Texas
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TELEPHONE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              US-08-784-582-73
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                                                                                                                                                                           2 FPTIPLSRLFDNAMLRAHRLHQLAFDTYQEFEEAYIPKEQKYSFLQNPQTSLSFSESIPT
                                                                                                                                  Gaps
; OTHER INFORMATION: Description of Artificia Sequence: Designated is ; OTHER INFORMATION: an amino acid sequence of MWPsp-MWPmp20-TEV-C-GH US-09-280-030-66
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: Halban, Philippe A.
APPLICANT: Halban, Philippe A.
APPLICANT: Halban, Philippe A.
APPLICANT: Halban, Philippe A.
APPLICANT: Clark, Samuel A.
APPLICANT: Clark, Samuel A.
APPLICANT: Clark, Samuel B.
APPLICANT: Thigpen, Anice E.
APPLICANT: McGarry, Dennis
APPLICANT: McGarry, Dennis
TITLE OF INVENTION: RECOMBINANT EXPRESSION OF PROTEINS FROM TITLE OF INVENTION: SECRETORY CELL LINES
NUMBER OF SEQUENCES: 79
CORRESPONDENCE ADDRESS:
                                                                                                                                  16;
                                                                                   Query Match 57.8%; Score 461; DB 4; Length 245; Best Local Similarity 70.3%; Pred. No. 5.2e-42; Matches 102; Conservative 7; Mismatches 20; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC Compatible
COMPUTER: IBM PC Compatible
COMPUTER: Patentin Release #1.6, Version #1.30
SOFTWARE: Patentin Release #1.6, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/784,582
FILING DATE: CONCURRENTLY Herewith
CLASSIFICATION NUMBER: US/08/028,427
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/028,427
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/589,028
FILING DATE: 19-JAN-1996
ATORNEY/AGENT INFORMATION:
NAME: Highlander, Steven L.
REGISTRATION NUMBER: 37,642
REBERRENCE/POCKET NUMBER: USD:514
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                               112 ALYLVCG - - ERGFFYTPKTRGIVEQ 134
                                                                                                                                                                                                                                                                                                                                                                        E: Arnold, White & Durkee P.O. Box 4433
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 71, Application US/08784582 Patent No. 6110707
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            INFORMATION FOR SEQ ID NO: 71:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE CHARACTERISTICS:
LENGTH: 274 amino acids
TYPE: amino acid
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GENERAL INFORMATION:
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STREET: P.(
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US-08-784-582-71
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62 PSNREETQQKSNLELLRISLLLJQSWLEPVQLGTGPRFVNQHLCGS········HLVE 111
                                                                                                                                                                                                                                               2 FPTIPLSRLFDNAMLRAHRL JLAFDTYQEFEEAYIPKEQKYSFLQNPQTSLSFSESIPT 61
                                                                                                                                       27 FPTIPLSRLFDNAMLRAHRU QLAFOTYQEFEEAYIPKEQKYSFLQNPQTSLCFSESIPT 86
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: Newgard, Christop or B.
APPLICANT: Halban, Philippe A.
APPLICANT: No 6110707minq m. Karl D.
APPLICANT: No 6110707minq m. Karl D.
APPLICANT: Clark, Samuel A.
APPLICANT: Thigpen, Anice E.
APPLICANT: Thigpen, Anice E.
APPLICANT: Trise or Christian
APPLICANT: Truse, Fred
APPLICANT: McGarry, Dennis
TITLE OF INVENTION: RECOMBINANT EXPRESSION OF PROTEINS FROM
TITLE OF INVENTION: SECRETORY CELL LINES
NUMBER OF SEQUENCES: 79
CORRESPONDENCE ADDRESS:
                                                         16;
57.8%; Score 461; DB 3; Length 274; 70.3%; Pred. No. 6e-42;
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                                                      20; Indels
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OPERATING SYSTEM: PC-DOS/MS:EXS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT PAPLICATION DATA:
APPLICATION NUMBER: 35/08/384,582
FILING DATE: CONCULTERILLY HETCHICH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 461; DB 3;
Pred. No. 8.5e-42;
                                                      7: Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CLASSIFICATION: 455
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE: 15-CAT-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/589,028
FILING DATE: 19-JAN-1996
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                   112 ALYLVCG--ERGFFYTPKTRGIVEQ 134
                                                                                                                                                                                                                                                                                                                                                                : : | : | : : | : : | 146 GIQILMGRLEDG---SPRTGQIFKQ 167
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               E: Arnold, White & Durkee P.O. Box 4433
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; Sequence 73, Application US/0878 +82
; Patent No. 6110707
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62 PSNREETQQKSNLELLR1SLLL1QSWLEPVQLGTGPREVNQHLGGS-------HLVE 111
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              2 FPTIPLSRLFUNAMLRAHRLHQLAFDTYQEFEEAYIPKEQKYSFLQNPQTSLSFSESIPT 61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                27 PPITPLSRLFUMASLRAHRLHQLAFOTYQEFEBAYIPKEQKYSFLONPQTSLCFSESIPI 86
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           16;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 455; DB 1; Length 217;
Pred. No. 2e-41;
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Job time : 24.93 sers
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            CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/187,756C
FILING DATE: January 27, 1994
                                                                                                                                                                                            36,134
IR: 325800-55
                                                                                                                                                                          NAME: FERRARO, GREGORY U. REGISTRATION NUMBER: 36,134 REFERENCE/DOCKET NUMBER: 32 TELECOMMUNICATION: 1NFORMATION: 201-994-1766
WORD PERFECT 5.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity 69.7%;
                                                                                                                                                                                                                                                                        TELEFAX: 201-994-1744
INFORMATION FOR SEQ ID NO: 4:
                                                                                                                                                        ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                            SEQUENCE CHARACTERISTICS:
LENGTH: 217 AMING ACIDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Matches 101; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                            MOLECULE TYPE: PROTEIN
                                                                                           PRIOR APPLICATION DATA:
APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                     AMING ACID
                                                                                                                                                                                                                                                                                                                                                                                           LINEAR
                                                        FILING DATE: Ja CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                   STRANDEDNESS
                                                                                                                                      FILING DATE:
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APPLICANT: C APPEL, SCOTT
TITLE OF INVENTION: Human Growth Hormone to stimulate humatopoiesis and immune recons
TITLE OF INVENTION: after hematopoietic stem cell transplantation in humans
FILE REFERENCE: CHAPPEL-6.1
CURRENT APPLICATION NUMBER: us/09/465.461
RIOR REPLIAND DATE: 1999-12-17
PRIOR APPLICATION NUMBER: 60/112,668
RIOR FILING DATE: 1998-12-17
NUMBER OF SEO ID NOS: 1
SOFTWARE: Patentin version 3.1
SEO ID NO 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      62 PSNREETQQKSNLELLRISLLLIQSWLEPVQLGTGPRFVNQHLCGS······ ···HLVE 111
                                                                                                                                        2 FPTIPLSRLFDNAMLRAHRIHQLAFDTYQEFEKAYIPKEQKYSFLQNPQTSLSFSESIPT 61
                                                        2 FPTIPLSRLFDNAMLRAHKLHQLAFOTYQEFEEAYIPKFOKYSFLQNPQTSLSFSESIPT 61
  16: Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                57.1%; Score 455; DB 4; Length 191; 69.7%; Pred. No. 1.7e-41;
  Indels
  20;
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Patent No. 5597709
GENERAL INFORMATION:
TITLE OF INVENTION: Human Growth Hormone
NUMBER OF SEQUENCES:
CORRESPONDENCE ADDRESS:
ADDRESSEE: CARELLA, BYRNE, BAIN, GILFILLAN,
ADDRESSEE: CACCHI, STEWART & OLSTEIN
STRET: 6 BECKER FARM ROAD
CITY: ROSELAND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     7; Mismatches
  7; Mismatche
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                                                                                                                                                                                            112 ALYLVCG - - ERGFFYTPKTRGIVEO 134
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                                                                                                                                                                                                                                                                                                                               Sequence 1, Application US/09465461
Patent No. 6348444
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 OPERATING SYSTEM: MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity 69.7%
Matches 101; Conservative
    Matches 102; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STATE: NEW JERSEY
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ZIP: 07068
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US-08-187-756C-4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LENGTH: 191
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                                                                                                                                                                                                                                                                                            RESULT 14
US-09-465-461-1
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GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.
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OM protein - protein search, using sw model

September 16, 2003, 12:38:55; Search time 47.2763 Seconds (without alignments) 472.415 Million cell updates/sec Run on:

1 MFPTIPLSRLFDNAMLRAHR.....IVEOCCTSICSLYQLENYCN 150 US-09-423-100-7 797 Title: Perfect score: Sequence:

Scoring table:

556269 seqs, 148893369 residues BLOSUM62 Gapop 10.0 , Gapext 0.5 Searched: Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 2000060000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database

1. /cgn2_6/ptodata/2/pubpaa/US07_PUBCOMB.pep: 2. /cgn2_6/ptodata/2/pubpaa/US07_PUBCOMB.pep: 3. /cgn2_6/ptodata/2/pubpaa/US06_NEW_UBB.pep: 4. /cgn2_6/ptodata/2/pubpaa/US06_PUBCOMB.pep: 5. /cgn2_6/ptodata/2/pubpaa/US07_NEW_PUB.pep: 6. /cgn2_6/ptodata/2/pubpaa/PCTUS_PUBCOMB.pep: 7. /cgn2_6/ptodata/2/pubpaa/US08_NEW_PUB.pep: 8. /cgn2_6/ptodata/2/pubpaa/US08_NEW_PUB.pep: 10. /cgn2_6/ptodata/2/pubpaa/US08_PUBCOMB.pep: 11. /cgn2_6/ptodata/2/pubpaa/US09_PUBCOMB.pep: 12. /cgn2_6/ptodata/2/pubpaa/US09_PUBCOMB.pep: 13. /cgn2_6/ptodata/2/pubpaa/US09_PUBCOMB.pep: 14. /cgn2_6/ptodata/2/pubpaa/US09_PUBCOMB.pep: 14. /cgn2_6/ptodata/2/pubpaa/US09_PUBCOMB.pep: 15. /cgn2_6/ptodata/2/pubpaa/US10A_PUBCOMB.pep: 16. /cgn2_6/ptodata/2/pubpaa/US10B_PUBCOMB.pep: 17. /cgn2_6/ptodata/2/pubpaa/US10B_PUBCOMB.pep: 18. /cgn2_6/ptodata/2/pubpaa/US10B_PUBCOMB.pep: 17. /cgn2_6/ptodata/2/pubpaa/US10B_PUBCOMB.pep: 18. /cgn2_6/ptodata/2/pubpaa/US10B_PUBCOMB.pep: 17. /cgn2_6/ptodata/2/pubpaa/US00_PUBCOMB.pep: 18. /cgn2_6/ptodata/2/pubpaa/US00_PUBCOMB.pep: 18. /cgn2_6/ptodata/2/pubpaa/US60_PUBCOMB.pep: Published_Applications_AA:* ••

Pred. No. is the number of results predicted by charce to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

No. Score Match Length DB ID 1 797 100.0 150 14 US-10-054-873-7 Sequence 7, Appli 2 555.5 69.7 107 14 US-10-054-873-5 Sequence 2, Appli 4 4 61 57.8 191 12 US-10-054-873-2 Sequence 2, Appli 5 461 57.8 191 12 US-10-153-207-1 Sequence 1, Appli 6 461 57.8 191 12 US-10-153-207-1 Sequence 1, Appli 7 461 57.8 191 12 US-10-400-708-1 Sequence 1, Appli 12 US-10-400-708-1 Sequence 1, Appli 12 US-10-298-148-1 Sequence 6, Appli 14 US-10-298-148-1 Sequence 6, Appli 15 US-10-298-148-1 Sequence 6, Appli 16 461 57.8 214 12 US-10-298-148-9 Sequence 6, Appli 17 US-10-298-148-1 Sequence 6, Appli 18 455 57.1 217 9 US-09-289-148-9 Sequence 2, Appli 18 455 57.1 217 12 US-09-89-148-4 Sequence 2, Appli 18 455 57.1 217 12 US-09-89-148-4 Sequence 4, Appli 18 454 57.0 217 10 US-09-894-16 Sequence 16, Appli 19 US-09-893-688-4 Sequence 4, Appli 19 US-09-893-688-4 Sequence 6, App	Result		Query				
100.0 150 14 US-10-054-873-7 59.7 107 14 US-10-054-873-5 59.8 191 12 US-10-1054-873-1 57.8 191 12 US-10-1053-207-1 57.8 191 12 US-10-400-708-1 57.8 191 12 US-10-400-708-1 57.8 191 12 US-10-208-148-1 57.8 214 12 US-10-298-148-1 57.8 217 9 US-09-280-030-65 57.1 217 9 US-09-853-688-2 57.1 217 12 US-09-853-688-2 57.1 217 12 US-09-853-688-2 57.1 217 12 US-09-853-688-2	NO.	Score		Length	DB	ID	Description
69.7 107 14 US-10-054-873-6 59.0 92 14 US-10-054-873-2 57.8 191 12 US-10-10-23 57.8 191 12 US-10-400-377-1 57.8 191 12 US-10-400-708-1 57.8 191 12 US-10-208-1 57.8 214 12 US-10-298-148-1 57.8 214 12 US-10-298-148-1 57.8 217 9 US-09-229-918-9 57.8 27 1 217 9 US-09-853-688-2 57.1 217 9 US-09-853-688-2 57.1 217 12 US-10-834-16 57.2 217 10 US-09-803-68-2 57.3 217 10 US-09-803-68-2	1	797		150	14	US-10-054-873-7	
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57.8 191 11 0S-09-984-010-23 57.8 191 12 US-10-153-207-1 57.8 191 12 US-10-400-708-1 57.8 191 12 US-10-400-708-1 57.8 214 12 US-10-298-148-1 57.8 217 9 US-09-99-918-9 57.8 247 9 US-09-280-030-65 57.1 217 9 US-09-835-688-2 57.1 217 12 US-09-804-409A-16 56.2 217 9 US-09-853-688-4	e	470	59.0	92	14	US-10-054-873-2	7
57.8 191 12 US-10-153-207-1 57.8 191 12 US-10-400-377-1 57.8 191 12 US-10-400-708-1 57.8 191 12 US-10-298-148-1 57.8 214 12 US-10-298-148-9 57.8 217 9 US-09-280-030-66 57.1 217 9 US-09-853-688-2 57.1 217 12 US-09-853-688-2 57.1 217 12 US-09-853-688-2 57.1 217 12 US-09-853-688-2 57.1 217 12 US-09-853-688-4	4	461	57.8	191	11	US-09-984-010-23	23.
57.8 191 12 US-10-400-377-1 57.8 191 12 US-10-400-708-1 57.8 191 12 US-10-298-148-1 57.8 217 9 US-09-289-918-9 57.8 245 9 US-09-280-036-6 57.1 217 9 US-09-853-688-2 57.1 217 12 US-09-865-468-4 57.0 217 10 US-09-864-409A-16 56.2 217 9 US-09-853-688-4	'n	461	57.8	191	12	US-10-153-207-1	Sequence 1, Appli
57.8 191 12 US-10-400-708-1 57.8 191 12 US-10-298-148-1 57.8 214 12 US-10-153-207-6 57.8 245 9 US-09-928-9 57.1 217 9 US-09-280-030-66 57.1 217 12 US-09-969-748C-4 57.0 217 10 US-09-969-748C-4 56.2 217 9 US-09-804-409A-16	9	461	57.8	191	12	US-10-400-377-1	Sequence 1, Appli
57.8 191 12 US-10-298-148-1 57.8 214 12 US-10-153-207-6 57.8 217 9 US-09-229-918-9 57.8 245 9 US-09-2280-030-66 57.1 217 9 US-09-969-788-2 57.1 217 12 US-09-969-748C-4 57.0 217 10 US-09-868-4409A-16 56.2 217 9 US-09-853-688-4	7	461	57.8	191	12	US-10-400-708-1	Sequence 1, Appli
57.8 214 12 US-10-153-207-6 57.8 245 9 US-09-9289-918-9 57.1 217 9 US-09-853-688-2 57.1 217 12 US-09-8651-688-2 57.0 217 10 US-09-8684-409A-16 56.2 217 9 US-09-863-688-4	89	461	57.8	191	12	US-10-298-148-1	Sequence 1, Appli
57.8 217 9 US-09-929-918-9 57.8 245 9 US-09-280-030-66 57.1 217 9 US-09-953-688-2 57.1 217 12 US-09-969-748C-4 57.0 217 10 US-09-804-409A-16 56.2 217 9 US-09-893-688-4	σ	461	57.8		12	US-10-153-207-6	Sequence 6. Appli
57.8 245 9 US-09-280-030-66 57.1 217 9 US-09-853-688-2 57.1 217 12 US-09-969-748C-4 57.0 217 10 US-09-804-405A-16 56.2 217 9 US-09-803-688-4	10	461	57.8		σ	US-09-929-918-9	Sequence 9, Appli
57.1 217 9 US-09-853-688-2 S 57.1 217 12 US-09-969-748C-4 57.0 217 10 US-09-9804-409A-16 56.2 217 9 US-09-853-688-4 S	11	461	57.8		σ	US-09-280-030-66	Sequence 66, Appl
57.1 217 12 US-09-969-748C-4 57.0 217 10 US-09-804-409A-16 56.2 217 9 US-09-853-688-4	12	455	57.1		6	US-09-853-688-2	Sequence 2, Appli
57.0 217 10 US-09-804-409A-16 56.2 217 9 US-09-853-688-4 S	13	455	57.1		12	US-09-969-748C-4	Sequence 4, Appli
56.2 217 9 US-09-853-688-4 S	14	454	57.0		10	US-09-804-409A-16	Sequence 16, Appl
	15	448	56.2		σ	US-09-853-688-4	Sequence 4, Appli

Sequence 12, Appl Sequence 1, Appl Sequence 3, Appl Sequence 3, Appl Sequence 350, Appl	Sequence 2, Appli Sequence 411, App Sequence 18, Appl Sequence 3, Appli	Sequence 19, Appl Sequence 5, Appli Sequence 8, Appli Sequence 7, Appli	E	Sequence 5, Appli Sequence 5, Appli Sequence 53, Appli Sequence 63, Appli Sequence 4, Appli	Sequence 12, Appl Sequence 12, Appl Sequence 10, Appl Sequence 10, Appl Sequence 10, Appl	S
12 US-09-824-200-12 12 US-10-300-822-1 12 US-10-289-845-3 9 US-09-861-887-3 15 US-10-043-487-350	12 US-10-153-207-2 15 US-10-103-313-411 15 US 10-188-246-18 12 US-10-153-207-3	10 US-09-861-687-19 14 US-10-054-873-5 4 US-09-736-511-8 1:S-09-740-359-7	; US-09-894-711-18 9 US-09-736-511-6 9 US-09-740-359-5 10 US-60-844-711-5	11 0S-09-858-9358-5 14 0S-10-028-410-3 9 0S-09-280-030-63 10 1 09-947-563-4 0 00-00-13-663-1	9 US 09 7 70 511 112 10 US 09 94 0 711 12 9 US 09 94 711 12 9 US 09 74 0 35 9 10	10 US-09-894-711-10 14 II 10-066-009A-3 10 G9-947-563-5 9 UN 09-205-658-125
191 191 191 217 163	191 229 246 190	138 52 147 147	124 144 144	3 17 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1	125444	125 50 96 96 110
55.05 56.03 50.13 50.13 50.13	47.8 46.8 37.8	37.0 36.9 35.9 9.35	35.7 35.7 35.7	2 8 8 8 8 8 8 8 8 8 8 8 8 8 8 8 8 8 8 8	2 8 8 8 8 8 8 9 9 9 9 9 9 9 9 9 9 9 9 9	34.0 34.0 9.0 9.0
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ALIGNMENTS

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Sequence 7, Application US/10054873
Publication No. US20020164712A1
GENERAL INFORMATION:
GENERAL INFORMATION:
TILLE OF INVENTION: Chimeric Protein Containing an Intramolecular Chaperone-Like Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER: IBM PC Compatible
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION UMBER: US/10/054,873
FILING DATE: 22-3an-2002
CLASSIFICATION: <UNKNOWN>
                                                                                                                                                                                                                     CORRESPONDENCE ADDRESS:
CORRESPONDENCE ADDRESS:
ADDRESSE: Townsend and Commend and Crew LLP
STREET: Two Enhancedory Center, Fighth Floor
CITY: San Fractisco
STATE: California
COUNTRY: USA
ZIP: 94111-3834
COMPUTER RADABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NAME: Mycroft, Frank J
REGISTRATION NUMBER: 46,946
REFERENCE/DOCKET NUMBER: 020167-000130US
INFORMATION FOR SEQ ID NO: 7:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRIOR APPLICATION DATA:
APPLICATION NUMBER: WO PCT/CN98/00052
FILING DATE: 31-MAR-1998
APPLICATION NUMBER: US 09/423,100
FILING DATE: 11-DEC-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LENGTH: 150 amino acids TYPE: amino acid
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US-10-054-873-7
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61 TPSNREETQQKSNLELLRISLLIJOSWLEPVQLGTGPRFVNQHLCGSHLVEALYLVGGER 120
                                                                      1 MFPTIPLSRLFDNAMLRAHRLHQLAFDTYQEFEEAYIPKEQKYSFLQNPQTSLSFSESIP 60
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                                                                                                                                                                                                                                                                                                                                                                                                                       Intramolecular Chaperone-Like Sequence
1 MFPTIPLSRLFUNAMLRAHRLHQLAFUTYQEFEEAYIPKEQKYSFLQNP---
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OPERATING SYSTEM: PC-FOS/MS-IXIS
SOFTWARE: PatentIn Release #1.0, Version #1.30
                                                                                                                                                                                                                                                                                                  Sequence 2, Application US/10054873
Publication No. US20020164712A1
GENERAL INFORMATION:
APPLICATT: Gan, Zhong Ru
TITLE OF INVENTION: Chimeric Protein Containing an
                                                                                                                                                                                                                                                                                                                                                                                                                                                              CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Crew LLP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STREET: Two Embarcadero Center, Eighth Floor
CITY: San Francisco
STATE: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    REFERENCE/DOCKET NUMBER: 020167-000130US INFORMATION FOR SEQ 1D NO: 2: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match 59.0%; Score 470; DB 14; Best Local Similarity 100.0%; Pred. No. 1.5e-44; Matches 92; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICATION NUMBER: W. PCT/CN98/00052
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               61 TPSNREETQQKSNLELI : SLLLIQSWLEPVQ 92
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                                                                                                                                        121 GEFYTPKTRGIVEGCCTSLCSLYGLENYCN 150
111111111111111111111111111
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APPLICATION NUMBER: US/10/054.873
FILING DATE: 22-Jan-1002
CLASSIFICATION: <00km, 400
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MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 2:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
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; Sequence 23, Application US/09984010
; Publication No. US20030104578A1
; GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LENGTH: 92 amino acids
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FILING DATE: 31-MAR APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FILING DATE: 11-DEC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRIOR APPLICATION DATA:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ZIP: 94111-3834
                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                             NUMBER OF
                                                                                                                                                                                                                                                                                 US-10-054-873-2
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                                                                                                                                                                                                                                                           1 MFPTIPLSRLFDNAMLRAHRLHQLAFDTYQEFEEAYIPKFGKYSFLQNPQTSLSFSESIP 60
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TITLE OF INVENTION: Chimeric Protein Containing an Intramolecular Chaperone-Like Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match 69.7%; Score 555.5; DB 14; Length 107; Best Local Similarity 71.3%; Pred. No. 5.9e-54; Matches 107; Conservative 0; Mismatches 0; Indels 43;
                                                                                                                                      Length 150;
                                                                                                                                                                                    Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFIWARE: Patentin Release #1.0, Version #1.30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, Eighth Floor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NAME: Mycroft, Frank J
REGISTRATION NUMBER: 46,946
REFERENCE/DOCKET NUMBER: 020167-000130US
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
                                                                                                                                   100.0%; Score 797; DB 14; 100.0%; Pred. No. 1.4e-80;
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APPLICATION NUMBER: WO PCT/CN98/00052
FILING DATE: 31-MAR-1998
APPLICATION NUMBER: US 09/423.100
FILING DATE: 11-DEC-2000
                                                                                                                                                                                                                                                                                                                                                                                                                  121 GFFYTPKTRGIVEQCCTSICSLYQLENYCN 150
                                                                                                                                                                                                                                                                                                                                                                                                                                        0; Mismatches
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APPLICATION NUMBER: US/10/054,873
FILING DATE: 22-Jan-2002
CLASSIFICATION: CURROWN>
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HOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 6:
US-10-054-873-6
                     TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 7:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ZIP: 94111-3834
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 6, Application US/10054873
Publication No. US2002016471241
GENERAL INFORMATION:
APPLICANT: Gan, Zhong Ru
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LENGTH: 107 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TYPE: amino acid
STRANDEDNESS: <Unknown>
  STRANDEDNESS: <Unknown>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CITY: San Francisco
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STATE: California
                                                                                                                                                            Best Local Similarity 100.
Matches 150; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COUNTRY: USA
                                                                                          US-10-054-873-7
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                                                                                                                                        Query Match
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                                                                                                                   ADDRESSEE: FINNEGAN, HENDERSON, FARABOW, GARRETT & DUNNER, ILLP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 FPTIPLSRLFDNAMLRAHRLHQLAFDTYQEFEEAYIPKEQKYSFLQNPQTSLCFSESIPT
APPLICANT: Ballance, David James
IITLE OF INVENTION: RECOMBINANT FUSION PROTEINS TO GROWTH HORMONE
AND SERUM ALBUMIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       16; Gaps
                                                                                                                                                                                                                                                                                        COMPUTER: TELPUPY OF TABLE OPERATING SYSTEM: PC-DOS/MS-DOS SOFEMARE: PALENTIN Release #1.0, Version #1.30 (EPO) CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/984,010 FILING DATE: 21-May-2002 PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 09/091,873 FILING DATE: 25-JUN-1998 APPLICATION NUMBER: US 09/091,873 FILING DATE: 19-DEC-1996 INFORMATION FOR SEQ ID NO: 2::
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Ouery Match 57.8%; Score 461; 58.11; Length 191; Best Local Similarity 70.3%; Pred. No. 3.9e-43; Matches 102; Conservative 7; Mismatches 20; Indels 16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: James A. Wells
APPLICANT: James A. Wells
APPLICANT: Brian C. Cunningham
ITILE OF INVENTION: GROWTH HORMONE VARIANTS
FILE REFERENCE: 669.12-US-C7
CURRENT APPLICATION NUMBER: US/10/153,207
CURRENT FILING DATE: 2002-05-22
PRIOR PPLICATION NUMBER: 08/479,884
PRIOR FILING DATE: 1995-06-07
PRIOR PILING DATE: 1994-02-02
PRIOR PILING DATE: 1994-02-02
PRIOR PPLICATION NUMBER: 07/960,227
PRIOR PPLICATION NUMBER: 07/962,227
PRIOR PPLICATION NUMBER: 07/960,227
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                                                                                                                                       STREET: 1300 I Street, NW CITY: Washington
                                                                                                                                                                                                                             ZIP: 20005-3315
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STRANDEDNESS: <Unknown>
TOPOLOGY: linear
MOLECULE TYPE: protein
HYPOTHETICAL: NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ; Sequence 1, Application US/10153207; Publication No. US20030153003A1; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LENGIH: 191 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE CHARACTERISTICS:
                                                                                             CORRESPONDENCE ADDRESS
                                                                    NUMBER OF SEQUENCES:
                                                                                                                                                                                                            COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ANTI-SENSE: NO
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US-10-153-207-1
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61 PSNREETQQKSNLELLRISLLLIQSWLEPVQF-LRSVFANSLVYGASDSNVYDLIKDLEE 119
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 1, Application US/1040'377
Publication Wo. US/20030162949A1
GENERAL INFORMATION
APPLICANT: COX 111, George N
APPLICANT: COX 111, George N
TITLE OF INVENTION: Derivatives of Growth Hormone and Related Proteins
TITLE OF INVENTION: Derivatives of Growth Hormone and Related Proteins
TITLE OF INVENTION: Derivatives of Growth Hormone and Related Proteins
CURRENT APPLICATION NUMBER: US/10/400,377
CURRENT FILING DATE: 2000-01-14
PRIOR FILING DATE: 1997-01-14
PRIOR FILING DATE: 1997-01-14
PRIOR FILING DATE: 1997-01-14
                                                                                                                                                                                                                                                                                                                                                                                                                      2 FPTIPLSRLFDNAMLRABRLHQLAFOTYOFFEEAYIPKEQKYSFFJUNPQTSLSFSESIPT 61
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                                                                                                                                                                                                                                                                                     Score 461; DB 12;
Pred. No. 3.9e 43;
7; Mismatches 20;
                                                                                                           ersion 4.0
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PRIOR FILING DATE: 1989-10-26
PRIOR APPLICATION NUMBER: 07/254,611
PRIOR FILING DATE: 1988-10-28
NUMBER OF SEQ ID NOS: 20
SOFTWARE: FASLSEV for Windows : rsion
SEQ ID NO 1
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Best Local Similarity 70.33
Matches 102, Conservative
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US-10-153-207-1
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Sequence 1, Application US/10298148
Sequence 1, Application US/203011284A1
SEGNETAL INFORMATION:
APPLICANT: COX III, George N
APPLICANT: Bolder Biotechnology, Inc.
TITLE OF INVENTION: Derivatives of Growth Hormone and Related Perveins
FILE REFREENCE: 4152-1-PUS
CURRENT APPLICATION NUMBER: US/09/462,94:
PRIOR APPLICATION NUMBER: US/09/462,94:
PRIOR FILING DATE: 2000-11-1.5
PRIOR PLICATION NUMBER: 60/052,516
PRIOR FILING DATE: 1997-07-14
NUMBER OF SEQ ID NOS: 41
SOFTWARE: PATENTIN VET. 2.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 FPTIPLSRLFDNAMLRAHRLHQLAFDTYQEFEEAYIPKEQKYSFLQNPQISLCFSESIPT 60
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Pred. No. 3.9e-43;
7; Mismatches 20; Indels 16; Gaps
APPLICANT: Cox III, George N
APPLICANT: Bolder Biotechnology, Inc.
ITILE OF INVENTION: Derivatives of Growth Hormone and Related Proteins
FILE REFERENCE: 4152-1-FUS
CURRENT APPLICATION NUMBER: US/10/400,708
CURRENT FILING DATE: 2003-03-26
PRIOR APPLICATION NUMBER: US/9/462,941
PRIOR APPLICATION NUMBER: 60/052,516
PRIOR APPLICATION NUMBER: 60/052,516
PRIOR FILING DATE: 1997-07-14
NUMBER OF SEQ ID NOS: 41
SOFTWARE: Patentin Ver. 2.0
                                                                                                                                                                                                                                                                                                                                                                                                  Query Match 57.8%; Score 461; DB 12; Length 191; Best Local Similarity 70.3%; Pred. No. 3.9e-43; Matches 102; Conservative 7; Mismatches 20; Indels 16;
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70.3%;
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Best Local Similarity 70.39
Matches 102; Conservative
                                                                                                                                                                                                                                                                                                               ; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-400-708-1
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APPLICANT: Kordyum, Vitaliy A.
APPLICANT: Chernykh, Svitlana I.
APPLICANT: Chernykh, Svitlana I.
APPLICANT: Chernykh, Svitlana I.
APPLICANT: Vozianov, Oleksandr
ITLE OF INVENTION: PHAGE-DEPENDENT SUPER PRODUCTION OF
ITLE OF INVENTION: PHAGE-DO6A
ITLE OF INVENTION: BIOLOGICALLY ACTIVE PROTEIN AND PEPTIDES
FILE REFERENCE: PHAGE.006A
ICURENT PRILIG DATE: 2001-08-15
PRIOR FILING DATE: 2001-08-15
PRIOR FILING DATE: 1999-05-25
NUMBER OF SEQ ID NOS: 11
SOFTWARE: FASESEQ for Windows Version 4.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       57.8%; Score 461; DB 12; Length 214; 70.3%; Pred. No. 4.5e-43; tive 7; Mismatches 20; Indels 19
                                                                   APPLICANT: James A. Wells
APPLICANT: Brian C. Cunningham
TITLE REFERENCE: 659.12-US-C7
CURRENT APPLICATION: GROWTH HORMONE VARIANTS
FILL REFERENCE: 659.12-US-C7
CURRENT APPLICATION NUMBER: US/10/15,207
CORRENT FILING DATE: 1995-06-07
PRIOR APPLICATION NUMBER: 08/479,884
PRIOR FILING DATE: 1995-06-07
PRIOR FILING DATE: 1995-06-07
PRIOR APPLICATION NUMBER: 07/960,227
PRIOR APPLICATION NUMBER: 07/960,227
PRIOR APPLICATION NUMBER: 07/86,227
PRIOR APPLICATION NUMBER: 07/86,227
PRIOR APPLICATION NUMBER: 07/86,227
PRIOR APPLICATION NUMBER: 07/428,066
PRIOR APPLICATION NUMBER: 07/428,066
PRIOR FILING DATE: 1989-10-26
PRIOR APPLICATION NUMBER: 07/264,611
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SOFTWARE: FastSEQ for Windows Version 4.0
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Patent No. US20020090678A1
Sequence 6, Application US/10153207
Publication No. US20030153003A1
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Matches 102; Conservative
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ORGANISM: Homo Sapiens
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; ORGANISM: Homo sapiens
US-09-929-918-9
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LENGTH: 217
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TYPE: PRT
ORGANISM: Homo sapiens
US-09-853-688-2
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APPLICANT: Hoshlkuni, Nachiko
APPLICANT: Hoshlkuni, Nachiko
APPLICANT: Hoshlkuni, Nachiko
APPLICANT: Hoshlyuki
APPLICANT: Hosho, Toshlyuki
APPLICANT: Kondo, Masaaki
TITLE OF INVENTION: DRAS ENCODING NEW FUSION PROTEINS AND PROCESSES FOR
TITLE OF INVENTION: DRAS
FILE REFERENCE: 382.1026
CURRENT APPLICATION NUMBER: US/09/280,030A
CURRENT FILING DATE: 1999-03-26
EARLIER APPLICATION NUMBER: JP10-87339/1998
EARLIER APPLICATION NUMBER: JP10-87339/1998
SOFWMARE: PARLICATION NUMBER: JP10-87339/1998
SOFWMARE: Patentin Ver. 2.0
SOFWMARE: Patentin Ver. 2.0
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                                                                                                                                                                                                            62 PSNREETQQKSNLELLRISLLLIQSWLEPVQLGTGPRFVNQHLCGS------HLVE 111
                                                                                                                   27 FPIIPLSRLFDNAMLRAHRLHQLAFDTYQEFEEAYIPKEQKYSFLQNPQTSLCFSESIPI 86
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                2 FPTIPLSRLFDNAMLRAHRLHQLAFDTYQEFERAYIPKEQKYSFLUNPQTSLSFSESIPT 61
                                                                                             2 FPTIPLSRLFDNAMLRAHRLHQLAFDTYQEFEEAYIPKEQKYSFLQNPQTSLSFSESIPT
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APPLICANT: FROCTER, ANNIE M.
APPLICANT: GREGORY, JOHN
APPLICANT: MILLAR, DAVID S.
TITLE OF INVENTION: METHOD FOR DETECTING GROWTH HORMONE VARIATIONS IN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   OTHER INFORMATION: Description of Artificial Sequence: Designated is OTHER INFORMATION: an amino acid sequence of MWPsp-MWPmp20-TEV-G-GH
Query Match 57.8%; Score 461; DB 9; Length 217; Best Local Similarity 70.3%; Pred. No. 4.6e-43; Matches 102; Conservative 7; Mismatches 20; Indels 16;
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Best Local Similarity 70.3%; Pred. No. 5.46-43;
Matches 102; Conservative 7; Mismatches 20; Indels
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. Sequence 66, Application US/09280030A
. Patent No. US20010021515A1
. GENERAL INFORMATION:
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; Patent No. US20020081605A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TYPE: PRT ORGANISM: Artificial Sequence
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US-09-853-688-2
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GENERAL INFORMATION:
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: HOUSTON, Lou, L.
APPLICANT: HOUSTON, Lou, L.
APPLICANT: HOUSTON, Lou, L.
APPLICANT: HAWLEY, Stephen
APPLICANT: HAWLEY, Stephen
APPLICANT: GLYNN, Jacquelinc, M.
APPLICANT: GLYNN, Jacquelinc, M.
APPLICANT: GLYNN, Jacquelinc, M.
APPLICANT: GLYNN, Jacquelinc, M.
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE TRANSPORT OF BIOLOGICALLY ACT
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE TRANSPORT OF BIOLOGICALLY ACT
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE BEFREACH OF SECOND OF SECOND APPLICATION NUMBER: US 50/24/248/3
FRIOR APPLICATION NUMBER: US 50/24/248/3
FRIOR APPLICATION NUMBER: US 50/24/8/3
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Indels
TITLE OF INVENTION: HUMANS, THE VARIATIONS AND THEIR USES FILE REFERENCE: WGANB CURRENT APPLICATION NUMBER: US/U9/853,688 CURRENT PILING DATE: 2001-05-14 WINDER OF SEQ ID NOS: 66 SOFTWARE PARENT PILING DATE: 2010 NOS: 65 SOFTWARE PARENTIN VET. 2.1 SEQ ID NO 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           57.1%; Score 455; DB 12; I
69.7%; Pred. No. 2.1e-42;
tive 7; Mismatches 21;
                                                                                                                                                                                                                                                                                                                                                                                                             Score 455; DB 9;
Pred, No. 2.le-42;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 4, Application US/099697480 Publication No. US20030161809Al GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                          57.18:
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Best Local Similarity 69.7%
Matches 101; Conservative
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Matches 101; Conservative
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APPLICANT: COOPER. DAVID N.
APPLICANT: COOPER. DAVID N.
APPLICANT: GREGORY, ANNIE M.
APPLICANT: GREGORY, JOHN
APPLICANT: MILLAR, DAVID S.
IITLE OF INVENTION: HUMANS, THE VARIATIONS AND THEIR USES
FILE REFERENCE: WCM78
CURRENT APPLICATION NUMBER: US/09/853,688
CURRENT FILING DATE: 2001-05-14
NUMBER OF SEQ 1D NOS: 66
                                                                                                                                                                      GENERAL INFORMATION:
APPLICANT: KIEFFER, TIMOTHY J.
APPLICANT: CHEUNC, ANTHONY J.
APPLICANT: CHEUNC, ANTHONY INTERPRETATION: CHEUNC, ANTHONY INTERPRETATION: CHEOREMETHODS FOR REGULATED PROTEIN TITLE OF INVENTION: EXPRESSION IN GUT FILLE REFERENCE: 029996/027 # 9721
CURRENT APPLICATION NUMBER: US/09/804,409A
CURRENT FILING DATE: 2001-03-12
NUMBER OF SEQ ID NOS: 18
SOFTWARE: PETENTIN VEF. 2.1
SEC ID NO 16.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   57.0%; Score 454; DB 10; Length 217; 69.7%; Pred. No. 2.8e-42; tive 7; Mismatches 21; Indels 1:
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Pred. No. 1.3e-41;
7: Mismatches 22; Indels
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146 GIQTLMGRLEDG---SPRIGQIFKQ 167
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                     112 ALYLVCG -- ERGFFYTPKTRGIVEQ 134
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US-09-804-409A-16
Sequence 16, Application US/09804409A
; Patent No. US20020155100Al
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Patent No. US20020081605A1
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69.0%;
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SEQ ID NO 4
LENGTH: 217
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Best Local Similarity 69.09
Matches 100; Conservative
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Matches 101; Conservative
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US-09-853-688-4
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US-09-853-688-4
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GenCore version 5.1.6 Copyright (c) 1993 - 2003 Compugen Ltd.

OM protein - protein search, using sw model

September 16, 2003, 12:36:15; Search time 17.5097 Seconds (without alignments) 823.845 Million cell updates/sec Run on:

DS-09-423-100-7
797
I MFPIPLSRLFDNAMLRAHR.....IVEQCCTSICSLYQLENYCN 150 Fitie: Perfect score:

Scoring table: Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5

Total number of hits satisfying chosen parameters:

283308 seqs, 96168682 residues

Searched:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 160% Listing first 45 summaries

PIR_76:*
1: pirl:*
2: pir2:*
3: pir3:*
4: pir4:* Database:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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Query Match		57.7	53.5	53.5	51.1	50.8		49.7	47.8	47.8	45.1	39.0	38.6	38.5	38.2	38.0	38.0	37.8	37.8	37.8	37.8	37.6	37.3	37.1	36.3	36.3	36.3	36.3	34.9
Score	461	460	426.5	426.5	407.5	405	366	396	381	381	359.5	310.5	307.5	306.5	304.5	302.5	302.5	301.5	301.5	301.5	301.5	299.5	297.5	295.5	289.5	289.5	289.5	289.5	278.5
Result No.		7	m	4	2	9	7	80	σ	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	52	56	27	28	53

insulin precursor	insulin precursor	somatotropin precu	epidermal growth f	insulin sperm wh	insulin - finback	insulin · elephant	insulin precursor	insulin precursor	insulin - hamster	insulin precursor	insulin - Egyptian	somatotropin . gre	insulin precursor	insulin precursor	insulin precursor
INRB	B42179	A60509	PC7082	J. WHP	ILWHF	INEL	300178	A42179	INHY	IPHU	INMSSP	A60625	A59151	ipBo	148166
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110	110	216	96	51	51	51	110	110	51	110	51	191	51	105	110
34.8	34.8	34.6	34.5	34.3	34.3	34.3	34.3	34.1	34.1	33.9	33.7	33.7	33.6	33.4	33.3
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AI.1GNMENTS

RESULT 1
STHU
somatotropin 1 precursor [validated] · human
N;Alternate names: growth hormone 1; hGH-N; pituitary somatotropin
N; Contains: growth hormone 5K peptide; somatotropin 1, long form; somatotropin 1, shc
C;Species: Homo sapiens (man)
C.Date: 24-Apr-1984 *sequence_revision 10-Feb-1995 *text_change 08-Dec-2000
C.Accession: A93731; A32435; A93694; A94247; A90051; A93397; A93778; A91764; A90217;
R; DeNoto, F.M.; Moore, D.D.; Goodman, H.M.
Nucleic Acids Res. 9, 3719-3730, 1981
A; Title: Human growth hormone DNA sequence and mRNA structure: possible alternative s
A; Reference number: A93731; MUID:82014939; PMID:6269091
A; Accession: A93731
A; Molecule type: DNA
A; Residues: 1-217 < DEN>
A;Cross·references: GB:V0C520
A;Note: the 20K short form somat: pin lacks residues 58-72 (32-45 in the active hor
R;Chen, E.Y.; Liao, Y.C.; Smith,; Barrera-Saldana, H.A.; Gelinas, R.E.; Seeburg,
A, Title: The human growth hormon. Gus: nucleotide sequence, biology, and evolution
A-Reference number: 832435. MITT 8. 617277. DMID: 2744760

Ž OE A32435; A;Reference number: A;Accession: A32435

A Molecule type: DNA A,Rossidues: 1-217 CCHE2 A,Crossidues: 1-217 CCHE2 A,Crossidues: 1-217 CCHE2 R,Roskan, W.: Rongent, E. Nucleic Arids Res. 7, 405-326, 1479 A,Fille: Molecular cloning and icievilde sequence of the human growth hormone struct A,Reference number: A93694; Multi-80034477; PMID:386281

A: Molecule type: mRNA
A: Residues: 1.217 - ROS2
A: Residues: 1.217 - ROS2
A: Residues: 1.217 - ROS2
A: Cross references: GB: V00519
A: Rosidues: 1.217 - ROS2
A: Cross references: GB: V00519
A: Martial, J. J. A., Hallewell, R. A.: Baxter, J. D.: Goodman, H. M.
Science 205. 602-607, 1979
A; Title: Human growth hormone: complementary DNA cloning and expression in bacteria.
A; Reference number: A94247
A; Molecule type: mRNA
A; Residues: 1.217 - CMAR.
A; Residues: 1.217 - CMAR.
A; Molecule type: mRNA
A; Residues: 1.217 - CMAR.
A; Title: Human pituitary growth hormone. XIX. The primary structure of the hormone.
A; Reference number: A90048: MUID: 69289202; PMID: 5810834
A; Contents: annotation
A; Reference number: A90048: MUID: 72143935; PMID: 5144027
A; Reference number: A90051: MUID: 72143935; PMID: 5144027
A; Reference number: A90051
A; Molecule type: protein

1

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C:Species: Macaca mulatta (rhesus macaque)
C:Date: 31-May-1996 *Sequence_revision 31-May-1996 *text_change 16-Jul-1999
C:Accession: 16/410; *Sequence_revision 31-May-1996 *text_change 16-Jul-1999
C:Accession: 16/410; *Ad5094 *M.; Fisher. J.M.; Fowler, P.D.
R:Golos, T.G.; Durning, M.; Fisher. J.M.; Fowler, P.D.
A:Tile: Cloning of four growth hormone/chorionic somatomammotropin:related complemen A:Reference number: 153267; MUID:44.208724; PMID:84.04617
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is transcribed only in sometetrophic cells of is the 22K long form.
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A:Introns: 4/1: 57/3: 97/3: 152/3
C:Superfamily: prolaction
C:Su
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A.Status: translated from GR/EMBL, :BJ
A.Molecule type: mRNA
A.Residues: 1-217 < RES-
A.Cross-references: GB.LIb5.6. NI., 1241114; PIGNI:AAA18842.;; PIB.u224115
A.Cross-references: GB.LIb5.6. NI., 1241114; PIGNI:AAA18842.;; PIB.u224115
A.Cross-references: GB.LIb5.6. NI., 1241114; PIGNI:AAA18842.;; PIB.u224115
A.Tille: The primary structure of monkey pituitary growth hormone.
A.Reference number: A05094; MUD:86129460; PMID:3080959
A.Accession: A05094
A.Molecule type: protein
A.Residues: 27-99; 'Q',101-178,'D', 180-217 < LIC>
A.Note: the monkey species is not identified in the reference
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          man and monkey
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A; Contents: annotation; identification of source organism
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  57.7%; Score 460; DB 2; 98.9%; 'ed. No. 9.4e-38; iive C Mismatches 1
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A;Cross-references: GDB:119982; GMIM:139250
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      112 ALYLVCG -- ERGFFYTPKTRGIVEG 134
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          146 GIQTI,MGRLEDG --- SPRIGUIFKQ 167
                     C.Comment: The gene for this horm
C.Comment: About 90% of somatotro
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Best Local Similarity 70.3%
Matches 102; Conservative
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Best Local Similarity 98.9
Matches 90; Conservative
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                                                                                                                    C;Genetics:
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A. Medicule type: protein
A. Medicules: 27-21, 6418-
A. Modecules: 27-21, 6418-
A. Modecules: 27-21, 6418-
A. Modecules: 27-21, 6418-
B. Mall, H.D.; Hogan, M.L.; Sauer, R.; Rosenblum. 1.Y.; Greenwood, F.C.
B. Mall, H.D.; Hogan, M.L.; Sauer, R.; Rosenblum. 1.Y.; Greenwood, F.C.
A. Title: Sequences of pituitary and placental lactogenic and growth hormones: evolution
A. Rocession: A93778; MUID:71153968; PMID:5279528
A. Modecule type: protein
A. Modecule type: protein
A. Modecule: Type: protein
A. Modecule: A. 
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A:Tritle: Human growth hormone peptide 1-3: isolation from piluitary diands.
A;Reference number: A61466
A;Accession: A61466
A;Accession: A61466
A;Molecule type: protein
A;Residues: 27-69 < SIN>
A;Note: growth hormone 5K peptide has insulin potentiating activity; its physiological parameter of the aspartimide structure in a previously-reported peptide.
A;Rebson, V.M.J.; Rae, 1.D.; NG, F.
Biol. Chem. Hoppe-Seyler 371, 423-431, 1990
A;Title: Identification of the aspartimide structure in a previously-reported peptide.
A;Reference number: S09685; MUID:90334745; PMID:2378679
A;Reference number: S09685; MUID:90334745; PMID:2378679
A;Reference number: A1736, MUID:90394745; PMID:1549776
A;Reference number: A41728; MUID:92196577; PMID:1549776
A;Contents: annotation; X:ray crystallography, 2, 8 angstroms
A;Note: the structure of the complex with growth hormone receptor is described
B;Contents: annotation; X:ray crystallography, 2, 8 angstroms
A;Note: the structure of the complex with growth hormone receptor is described
B;Contents: annotation; X:ray crystallography, 2, 8 angstroms
A;Note: the structure of the complex with growth hormone receptor is described
B;Contents: annotation; X:ray crystallography, 2, 8 angstroms
A;Note: the structure of the complex with growth hormone receptor is described
B;Contents: annotation; X:ray crystallography, 2, 8 angstroms
A;Reference number: A1126; MUID:913793; PMID:3912261
A;Reference number: A1126; MUID:913793; PMID:3912261
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A;Status: preliminary; translated from GB/EWBL/DDBJ
A;Molecule type: mRMA
A;Molecule type: mRMA
A;Residues: 1-26 <RBS>
A;Cross-references: GB:M14398; NID:g183158; PIDN:AAA52554.1; PID:g183159
A;Residues: 27-94:96-217 <LIC>
R;Niall, H.D.
Nature New Biol. 230, 90-91, 1971

A;Title: Revised primary structure for human growth hormone. A;Reference number: A93397; WUID:71139765; PMID:5279046
A;Accession: A93397
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C.Accession: 167409
R.Golos, T.G.; Durning, M.; Fisher, J.M.; Fowler, P.D.
Endocrinology, 133, 1744-1752, 1993
A.Title: Cloning of four growth hormone/chorionic somatomammotropin-related complemen A:Reference number: 153267; MUD:94008724; PMID:8404617
                                                                                                                                                                                                                                                                                                                                                                                                                                                           A;Title: Two distinct species of human growth hormone-variant mRNA in the human place A;Reference number: A92725; MUID:88243769; PMID:3379057 A;Accession: A28072
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             61
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                                                                                                                                                                                                                             somatotropin 2 precursor, splice form 2 - human
N.Alternale names: growth hormone variant-2; placental somatotropin form 2
C.Species: Homo sapiens (man)
C.Species: 30-Sep-1989 *sequence_revision 10-Feb-1995 *text_change 02-Sep-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            27 FPITITISHLEDNAMLRARRLYQLAYDTYQEFEEAYILKEQKYSFLQNPQTSLCFSESIPT
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A.Molecule type: mRNA
A.Residues: 1-217 cRES
A.Stossreferences: GB:L16554; NID:q293112; PIDN:AAA18841.1; PID:g293113
C.Superfamily: prolactin
                                  63 SNREETQQKSNLELLRISLLLIQSWLEPVQLGTGPRFVNQHLCGSHLVEALYLV 116
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F;27-256/Product: somatotropin 2 splice form 2 *status predicted <MAT>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A;Molecule type: mRNA
A;Residues: 1.256 <COO>
A;Note: an alternative splice junction for intron 4 is used
C;Genetics:
A;Gene: GDB:GH2
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71.9%; Pred. No. 1.4e-32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match 53.5%; Score 426.5; DB 1; Best Local Similarity 78.1%; Pred. No. 2.2e-34; Matches 89; Conservative 4; Mismatches 10;
                                                                                                                                                                                                                                                                                                                                                                                             R.Cooke, N.E.; Ray, J.; Emery, J.G.; Liebhaber, S.A.
J. Biol. Chem. 263, 9001-9006, 1988
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A;Map position: 17q22-17q24
A:Introns: 4/1: 57/3: 97/3: 152/3
C:Superfamily: prolactin
C:Keywords: already splicing; hormone: placenta
F:1-26/Domain: signal sequence *status predicted <S1
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   62 PSNREETQQKSNLELLRISLLLIQSWLEPVQL-
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                                                                                                                                                 Simulation of precursor - human
Nictoral 2 precursor - human 2 proveth hormone variant; hGH-V; placental somatotrop
C:Species: Homo sapiens (man)
C:Species: Homo sapiens (man)
C:Species: Homo sapiens (man)
C:Accession: D32435: B26072; A01511: 152104; A60711
R:Chen, E.Y.: Lido, V.C.: Smith, D.H.: Barrera-Saldana, H.A.; Gelinas, R.E.: Sceburg, P.
Genomics 4, 479-497, 1989
A;Title: The human growth hormone locus: nucleotide sequence, biology, and evolution.
A;Accession: D32435
A;Molecule type: DNA
A;Residues: 1-217 COHE>
A;Cross-references: GR:J03071; NID:g183148; PIDN:AA52552.1; PID:g183152
A;Cross-references: GR:J03071; NID:g183148; PIDN:AA52552.1; PID:g183152
A;Cross-reference on distinct species of human growth hormone-variant mRNA in the human placente
A;Recession: B28072
A;Reference number: A92725; MUID:88243769; PMID:3379057
A;Accession: B28072
A;Accession: B28072
A;Accession: B28072
A;Accession: A01511
A;Wolecule type: DNA
A;Residues: 1-217 csco>
B;Gebburg, P.H.
A;Molecule type: DNA
A;Residues: 1-34, Py 36-317 csco>
B;Accession: A01511
A;Wolecule type: DNA
A;Residues: 1-34, Py 36-317 csco>
B;Gebburg, P.H.
A;Molecule type: DNA
A;Residues: 1-34, Py 36-317 csco>
B;Hout, A.;Scippo, M.L.; Frankene, F.; Hennen, G.
Arch. Int. Physiol. Barchim, 96, 63-67, 1988
A;Title: Gloning and nucleotide sequence of placental hGH-V cDNA.
A;Reserence number: 152104; MUID:89024984; PMID:246050
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A:Status: preliminary: translated from GB/EMB: DDBJ
A:Molecule type: mRNA
A:References: GB:M38451: N10:g183179; PIDN:AAA35891.1; PID:q183180
R:Prankenne, F.: Scippo, M.L.: Van Beeumen, J.: Igout, A.; Hennen, G.
J. Clin. Endocrinol. Metab. 71, 15-18, 1990
A:Title: Identification of piacental human growth hormone as the arowth hormone A:Reference number: A60711; MUID:90317018; PMID:2196278
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A; Introns: 4/1; 57/3; 97/3; 152/3

C; Superfamily: prolactin
C; Keywords: alternative splicing; glycoprotein; hormone; placenta
C; Keywords: alternative splicing; glycoprotein; hormone; placenta
F; 1-26/Domain: signal sequence #status predicted <SIG>
F; 17-21/Product: somatotropin 2, long splice form #status predicted <SOL>
F; 27-57, 73-21/Product: somatotropin 2, short splice form #status predicted <SOS>
F; 91-191, 208-215/Disulfide bonds: #status predicted
F; 166/Binding site: carbohydrate (Asn) (covalent) #status predicted
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A:Molecule type: protein
A:Residues: 27-44;46-57 <FRA>
A:Rxperimental source: tissue placenta
A:Note: partial glycosylation was demonstrated by lectin binding C;Comment: This gene is expressed by the placenta.
C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             10; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           53.5%; Score 426.5; DB 1 78.1%; Pred. No. 1.8e-34; iive 4; Mismatches 10
   PSNREETQQKSNLELLRISLLLIQSWLEPVO 117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A;Gene: GDB:GH2
A;Cross-references: GDB:119983; OMIM:139240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Conservative
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es 89; Conserv
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qq

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Choriomammotropin A precursor [validated] - human
NiAlternate names: chorionic somatomammotropin ]; placental lactuages
Cispecies: Homo sapiens (man)
Cispecies: Homo sapiens (man)
Cispecies: Javocr.1981 #sequence_revision 23-oct.1981 #text_change uB bec-2000
Cispecies: Javocr.2000
Cispecies: Javocr.2000
Cispecies: Javocr.2000
A; Article: The human growth hormone locus: nucleotide sequence, biology, and evolution.
A; Accession: Cistais
A; Molecule type: DNA
A; Residues: Javocr.2007
A; Molecule type: DNA
A; Residues: Javocr.2007
A; Riddes: Javocr.2007
A; Riddes: Javocr.2007
A; Riddes: Javocr.2007
A; Reference number: Ag4422
A;Title: Cloning of four growth hormone/chorionic somatomammotropin related complemen A;Reference number: 153267; MUID:94008724; PMID:8404617 A;Accession: 153267 MUID:94008724; PMID:8404617 A;Accession: 153267 A;Accession: 153
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A;Title: Construction and analysis of recombinant DNA for human chorionic somatomammo
A;Reference number: A93192; MUID:78071761; PMID:593368
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A:Moleculc type: DNA
A:Residues: 50-217 <cshr>
A:Experimental source: placenta
A:Experimental source: placenta
R:Li, C.H.: Dixon, J.S.: Chung, D.
Arch. Biochem. Biophys. 155, 95-110, 1973
Arch. Biochem. Sources of human chorionic somatomanmotropin.
A:Title: A.Title: A.Molosource of human chorionic somatomanmotropin.
A:Reference number: A90054: MUID:73201971; PMID:4712450
A:Accession: A90054
                                                                                                                                                                                                                                                                                                                                                                                                                                                         49.7%; Score 396; DB 2; Length 217; B2.2%; Pred. No. 1.8e-31; tive 11; Mismatches 5; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   63 SNREETQQKSNLELLRISLLLIQSWLEPVQ 92
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Best Local Similarity 82.2
Matches 74; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A; Accession: A93192
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                                                                                                                                                     Nilternate names: growth hormone (Species: Macaca mulatta (rhesus macaque) (Spate: 31-May-1996 #sequence_revision 31-May-1996 #text_change 16.Jul-:999 (Stacession: 16641) (Station: M.; Fisher, J.M.; Fowler, P.D. (Station: Durning, M.; Fisher, J.M.; Fowler, P.D. (Station: Fisher, J.M.; Fowler, P.D. (Station: Fisher, MulD:94008724; PMID:8404617 (Station: Fisher) (Station:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Cispecies: Macaca mulatta (rhesus macaque (fragment)
Cispecies: Macaca mulatta (rhesus macaque)
Cispecies: Macaca mulatta (risper, J.M.; Fowler, P.D.
Ciscolog, 13, 1744-1752, 1993
A: Title: Cloning of four growth hormone/chorionic somatomarmotropin-related complementat
A: Reference number: 153267; M:JID:94008724; PMID:84046;7
A: Accession: 167408
A: Residue; preliminary; translated from GB/EMBL/DDBJ
A: Molecule type: mRNA
A: Residues: 1-212 ckEs>
A: Residues: 1-212 ckEs>
A: Cross-references: GB:L16553; NID:9293110; PIDN:AAA18840.1; PID:929*(1):
C: Superfamily: prolactin
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        6.1
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C;Species: Macaca mulatta (rhesus macaque)
C;Date: 31-May-1996 *sequence_revision 31-May-1996 *text_change 16-Jul-1999
C;Accession: 153267
R;Golos, T.G.; Durning, M.; Fisher, J.M.; Fowler, P.D.
Endocrinology 133, 1744-1752, 1993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   2 FPTIPLSRLFDNAMLRAHRLHQLAFDTYQEFEEAYIPKEQKYSFLQNPQTSLSFSESIPT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         18; Indels 14;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Ouery Match 50.8%; Score 405; DB 2; Length 217; Best Local Sir larity 67.7%; Pred. No. 2.4e-32; Matches 86; Conservative 9; Mismatches 18; Indels 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Match 49.7%; Score 396; DB 2; Length 212; Local Similarity 82.2%; Pred. No. 1.8e-31; les 74; Conservative 11; Mismatches 5; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                63 SNREETQOKSNLELLRISLLLIQSWLEPVQ 92
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        140 LKKLEEG 146
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Matches
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Contract and and

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choriomammotropin precursor (allele hCS-3) - human
C.Specios: Homo sapiens (man)
C.Date: 30-Jun-1968 Fsequence_revision 30-Jun-1988 #text_change 28-Jul-1995
C.Accession: A26449
R.HILT. H.: Kimelman, J.: Birnbaum, M.J.: Chen, E.Y.: Seeburg, P.H.: Eberhardt, P.L.,
DNA 6, 59-70, 1967
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ONA 6, 59-70, 1987
A:Title: The human growth hormone gene locus: structure, evolution, and allelic varia
A;Reference number: A26449; MUID:87161235; PMID:3030680
A:Accession: A26449.
                                                                                                                                                                                                                                                                                                                                                                                                                                  C.Accession: 32435
R:Chen, E.Y.; Liao, Y.C.; Smith, D.H.; Barrera-Saldana, H.A.; Gelinas, R.E.; Seeburg, Genomics 4, 479-497, 1989
A.Title: The human growth hormone locus; nucleotide sequence, biology, and evolution A:Reference number: A32435; MUID:89307277; PMID:2744760
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       4 TIPLSRLFUNAMIRAHRLHULAFDIYQEFEEAYIPKEQKYSFLQNPGTSLSFSESIPTPS 63
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                                                                                                                                                                                                                                                                                                                                                         C.Species: Homo sapiens (man)
C.Date: 29-Dec-1989 *Sequence_revision 29-Dec-1989 *text_change 16-Jul-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  29 TVPLSRLFDHAMLQAHRAHQLAIDTYQEFEETYIPKDQKYSFLHDSQTSFCFSDSIPTPS
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A:Residues: 1-215 <HIR>
C:Superfamily: prolactin
F:1-26/Domain: signal sequence *status predicted <SIG>
F:27-215/Product: choriomammolropin, hCS-3 allele *status predicted <MAT>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A;Cross-references: GB:J03071; NID:g183148; PIDN:AAA52553.1; PID:g183153
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80
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Pred. No. 5.4e-30;
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Pred. No. 7e-28;
                                                                                                                                                                                                                                                                                                                   N;Alternate names: chorionic somatomammotropin 2
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NREETQQKSNLELLRISLLI.1QSWLEPVQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A;Cross·references: GDB:119813; OMIM:118820
A;Map position: 17q22-17q24
C;Superfamily: prolactin
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80.5%;
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Best Local Similarity 82.0
Matches 73; Conservative
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Best Local Similarity 80.5:
Matches 70; Conservative
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A:Molecule type: DNA
A:Residues: 1-217 <CHE>
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Auture New Biol. 233, 59-61, 1971
Astitle. Amino-acid sequence of human placental lactogen
A. Reference number: A93401; MUID:72016313; PMID:5286363
A. Contents: amnotation
R. Sherwood, L.M.: Handwerger, S.; McLaurin, W.D.; Lanner, M.
R. Sherwood, L.M.: Handwerger, S.; McLaurin, W.D.; Lanner, M.
R. Reference number: A93405
A. Reference number: A93405
A. Contents: annotation
R. Schneider, A.B.: Kowalski, K.; Russell, J.; Sherwood, L.M.
B. Bool, Chem. 254, 3782-3787, 1979
A. Title: Identification of the interchain disulfide bonds of dimeric human placental lad A: Reference number: A92251; MUID:79173081; PMID:438159
A. Reference number: A. Baxter, J.D.; Bell, G.I.; Eberhardt, N.L.
B. Bool, Chem. 259, 13131-13138, 1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A.Molecule type: protein
A.Residues: 27-46 <NIC>
A.Note: choriomammotropin apparently copurified with placental catechol-O-methyltransfer
                                                                                                                                                                                                                                                                                             A.Molecule type: protein
A.Residues: 27-217 <NIA>
A.Residues: 27-217 <NIA>
A.Residues: 27-217 <NIA>
A.Residues: 27-217 <NIA>
B. Experimental Source: placenta
B. Nic A Bhaird, N.: Tipton, K.F.
Biochem. Soc. Trans. 19, 20S, 1991
A.Title: Catechol-O-methyltransferase from human placenta: purification and some propert
A.Reference number: A61283; MUID:91244006; PMID:2037148
A.Accession: A61283
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 <del>,</del>
                                                                                                                                                     in Prolactin and Carcinogenesis, Proc. Fourth Tenovus Workshop Prolactin, Griffiths, K.,
A;Title: The chemistry of the human lactogenic hormones.
A;Reference number: A94427
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A:Residues: 1-217 <RES>
A:Cross-references: GB:KO2401; NID:g181120; PIDN:AAA52115.1; PID:g181121
A:Cross-references: GB:KO2401; NID:g181120; PIDN:AAA52115.1; PID:g181121
Trans. Assoc. Am. Physicians 90, 109-116, 1977
A:Title: Nucleotide sequence of a human gene coding for a polypeptide :comone. A:Reference number: IS9658: MUID:78160787; PMID:611657
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A;Residues: 160-217 <RE2>
A;Gross-references: GB:M25118; NID:9181124; PIDN:AAA35721.1; PID:9181125
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A; Introns: 4/1; 5/7; 97/3; 152/3
C; Superfamily: prolactin
C; Superfamily: prolactin
C; Keywords: hormone; placenta
F; 1-26/Domain: signal sequence fistatus experimental <SIG>F; 1-26/Tobrain: experimental <MAI>F; 19-191/Disulfide bonds: fix monomeric form) **status experimental
F; 208-215/Disulfide bonds: (in monomeric form) **status experimental
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Pred. No. 5.4e-30;
----haa 8; Indels
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les 73; Conservation
                                                                            A; Experimental source: placenta
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Cjarcession: B21911
Ribnzer, D.L.H.: Talaman'es, F.
J. Blol. Chem. 260, 3574-4559, 1985
A.Fittle: Nucleotide sequence of mouse prolactin and growth hormone mRNAs and expression A;Reference number: A92548; MUID:87261358; PMID:2991252
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R:Roliver, L.: Hartree, A.S.
Biochem. J. 109, 19-24, 1968
A:Title: Amino acid sequences around the cystine residues in horse growth hormone. A:Reference number: A90240: MUID:KH:R68190; PMID:4875100
A:Accession: A90240
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A.Molecule type: mRNA
A.Molecule type: D10
A.Molecule type: D10
C.Superfamily: prolactin
A.Molecule
C.Superfamily: PIDN:CAA26650.1; PID:q51068
C.Superfamily: PID:q51069
C.Superfamily: PID:q
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C:Species: Mus musculus (house mo. .)
C:Date: 30:Sep-1987 #sequence_revision 30:Sep-1987 #text_change 28:May-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Rizakin, M.M.; Poskus, E.; Dellacha, J.M.; Paladini, A.C.; Santume, J.A. FEBS Lett. 25, 77-82, 1972
A.Title: Amino acid sequences and the cystine residues in equine grow A; Reference number: A91383
A.Accession: A91383
           A:Molecule type: protein
A:Residues: 1-190 <2RA.
R:Zakin, M.M.; Poskus, E.; Dellacha, J.M.; Paladini, A.C.; Santome, J.A.
FEBS Lett. 34, 353-355, 1973
A:Title: The amino acid sequence of equine growth hormone.
A:Reference number: A91395: MUID:7:220362; PMID:4747849
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C:Kcywords: hormone: pituitary
F;52-163,180-188/Disulfide bonds: #status experimental
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A:Residues: 176-190 <01.1>
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A; Residues: 1-190 <2A2>
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G;Species: Equus caballus (domestic horse)
C;Date: 13-Jul-1981 #sequence_revision 13-Jul-1981 #text_change 23-Aug-1996
R;Zakin, M. M.; Poskus, E.; Langton, A.A.; Ferrara, P.; Santome, J.A.; Dellacha, J.M.; Palit, J. Pept, Primary structure of equine 97owth hormone.
A;Title: Primary structure of equine 97owth hormone.
A;Reference number: A91772; MUID:77005410; PMID:965151
N;Alternate names: growth hormone c:Species: Mesocricetus auratus (golden hamster) c;Species: Mesocricetus auratus (golden hamster) c;Species: Mesocricetus auratus (golden hamster) c;Date: 1920-1991 #sequence_revision 18-Nov-1994 #text_change 21-Jul-2000 c;Accession: B49159 #sequence_revision 18-Nov-1994 #text_change 21-Jul-2000 c;Accession: B49159 #southard, J.N.; Sanchez-Jimenez, F.; Campbell, G.T.; Talamantes, F. andocrinology 129, 2965-2971, 1991 A:Title: Sequence and expression of hamster prolactin and growth hormone messenger RNAS. A:Reference number: A49159; MUID:92063850; PMID:1954881 A:Accession: B49159 A:Acce
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C;Species: Balaenoptera borealis (sei whale)
C;Species: Balaenoptera borealis (sei whale)
C;Bate: 07-May-1993 *sequence_revision 07-May-1993 *text_change 07-May-1999
C;Accession: PN0140
R;Yudaev, N.A.; Pankov, Y.A.; Bulatov, A.A.; Osipova, T.A.
Biokhimiia 47, 1059-1069, 1982
A;Title: Amino acid sequence of seiwhale somatotropin:
A;Reference number: PN0140; MUID:83000569; PMID:7115813
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A;Note: sequence extracted from NCBI backbone (NCBIN:66299, NCBIP:66300)
C;Superfamily: prolactin
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A,Residues: 1-190 <YUD>
A,Note: article in Russian with English abstract
C,Superfamily: plactin
C,Keywords: growth factor; hormone
F;52-163,180-188/Disulfide bonds: #status predicted
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Search completed: September 16, 2003, 12:40:36 Job time : 18:5097 secs

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GenCore version ( 1.6
Copyright (c) 1993 + 2003 Compugen Ltd.
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September 16, 2003, 12:33:30; Search time 11.6732 Seconds (without alignments) 604.293 Million cell updates/sec Run on:

Title: Perfect score: Sequence:

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127863 seqs, 47026705 residues BLOSUM62 Gapop 10.0 , Gapext 0.5 Searched:

Scoring table:

127863 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

SwissProt_41:* Database:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	Description	P01241 homo sapien	P58756 pan troglod	~	P58343 saimiri bol	_	Q99mb3 callithrix	P01242 home sapien	Q07370 macaca mula		-	P33092 balaenopter	-		Q99mb2 nycticebus		P46407 oryctolagus	P01244 rattus norv		•			_				062754 trichosurus	P01246 bos taurus	_	P01247 ovis aries	018938 bubalus bub	P22077 meleagris g	P30407 cercopithec	P01311 oryctolagus
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bos taurus	P01317	INS_BOVIN	~	105	33.4	266.5	44
chelonia my	P34005	SOMA_CHEMY	7	191	33.7	268.5	43
acomys cahi	P01324	I NS_ACOCA	~	51	33.7	268.5	42
homo sapien	P01308	INS_HUMAN	~	110	33.9	270	4,
pan troglod	P30410	INS_PANTR	٦	110	34.1	272	40
crocodylus	P55755	SOMA_CRONO	٦	190	34.2	272.5	39
macaca fasc	P30406	INS_MACFA	-	110	34.3	273.5	38
eiephas max	P01316	INS_ELEMA	٦,	51	34.3	273.5	37
balaenopter	P01312	INS_BALPH	_	51	34.3	273.5	36
struthio ca	09pwd3	SOMA_STRCA	~	217	34.4	274.5	35
gallus gall	P08998	SOMA_CHICK	٦	216	34.6	275.5	34

ALIGNMENTS

PO1241: 014405; Q16631: 09HB21; Q9UMJ 21-JUL-1996 [Rel. 21, Created) 01-MAR-1992 [Rel. 21, Last sequence u 15-SEP-2003 [Rel. 22, Last squence u 15-SEP-2003 (Rel. 42, Last annotation Somactotropin precursor (Growth hormon hormone of Growth hormone 1). Homoo sapiens (Human). Eukaryota: Metazoa; Chordata: Craniat Mammalia: Eutheria; Primates; Catarrh NCB1_Tax1D-9606: [1] SEQUENCE FROM N.A. (ISOFORM 1). MOLECULAT Cloning and nucler.ide seq hormone structural gene.; MOLECULAT Cloning and nucler.ide seq hormone structural gene.; MOLECULAT Cloning and nucler.ide seq hormone structural gene.; MOLECULAT CAIGS RES. [335-320(1979). SEQUENCE FROM N.A. (ISOFORM 1). MEDLINE-7920329; Pubmed-37496. Martial J.A., Hallewell R.A., Baxter "Human growth hormone complementary bacteria."; SCIENCE FROM N.A. (ISOFORM 1). MEDLINE-83182010; Pubmed-7169009; SEQUENCE FROM N.A. (ISOFORM 1). "The human growth hormone gene family recent divergence and predict a new pone DNA 1:239-249(1982). [4] SEQUENCE FROM N.A. MEDLINE-83302777; Pubmed-274 760; Chen E.Y. Liao Y.C., Smith J.H., Bar Gelinas R.E., Seeburg P.H.; "The human growth hormone locus: nucl evolution."; "A novel gene expressed in human pitu		SUMA HUMAN STANDARD; TRI; Z17 AA.
11-00-1986 (Rel. 10, Created) 01-WAR-1992 (Rel. 10, Created) 01-WAR-1992 (Rel. 10, Created) 15-SEP-2003 (Rel. 12, Last sequence update) Somactorophy precursor (Growth hormone) (GH) (GH-N) (Pituliary hormone) (Growth hormone 1). GH) Homo sapiens (Human). EUKATYOGE, MELAZOA: CROTGATA: Craniata: Vertebrata: Euteleostom Mammalia: Eutheria: Primates: Catarrhini: Hominidae: Homo. MCBL_TAXID-9606. [1] SEQUENCE FROW N.A. (ISOFORM 1). WOLCHIE-60034477; PubMed-586281; ROSKAM W., ROUGEDE T. 1305-320(1979). SEQUENCE FROM N.A. (ISOFORM 1). MUCLEIC Acids Res. 7.305-320(1979). SEQUENCE FROM N.A. (ISOFORM 1). MUCLEIC Acids Res. 7.305-320(1979). SEQUENCE FROM N.A. (ISOFORM 1). MUCLEIC Acids Res. 7.305-320(1979). SEQUENCE FROM N.A. (ISOFORM 1). MULLINE-3203293; PubMed-37496; MACTIAL J.A., Hallewell R.A., Baxter J.D., Goodman H.M.; MUMBAIN GROWTH HORMONE: COMPLEMENTARY DNA CLORING and expression becteria. SCHEME SEQUENCE FROM N.A. (ISOFORM 1). MUCLEIC Acids Res. 9:3719-3730(1981). SEQUENCE FROM N.A. (ISOFORM 1). MEDLINE-83182010; PubMed-274 760; MEDLINE-83182010; PubMed-274 760; Chen E.Y., Liao Y.C., Smith O.H., Barrera-Saldana H.A., Gelinas R.E., Seeburg P.H., The human growth hormone locus: nucleotide sequence, biology, evolution. The human growth hormone locus: nucleotide sequence, biology, evolution. The human growth hormone locus: nucleotide sequence, biology, evolution. The human growth hormone locus: nucleotide sequence, biology, evolution. The human growth hormone locus: nucleotide sequence, biology, evolution. The human growth hormone locus: nucleotide sequence, biology, evolution. The human growth hormone locus: nucleotide sequence, biology, evolution. The human growth hormone locus: nucleotide sequence, biology, evolution. The human growth hormone locus: nucleotide sequence, biology, evolution. The human growth hormone locus: nucleotide sequence, biology, evolution. The human growth hormone locus: nucleotide evolution. The human growth hormone locus: nucleotide evolution. The human growth hormone	Q I	P01241: Q14405: Q16631: Q9HB21: Q9UMJ7: Q9UNL5:
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01-0cT-1994 (Rel. 20, Last sequence update)
01-0cT-1994 (Rel. 41, Last annotation update)
Somatotropin precursor (Growth hormone) (GH) (GH-N) (Pitultary growth
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Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleosiomi;
Mammalia, Eutheria, Primates, Calarrhini, Cercopithecidae;
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PROSTIE; PS00266; SOMATOTROPIN_1: 1.
PROSTIE; PS00338; SOMATOTROPIN_2: 1.
Hormone; Pitultary; Signal.
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                                                                           4
                                                                                                                                                                                                                     62 PSNREETQQKSNLELLRISLLLIQSWLEPVQLGTGPRFVNQHLCGS-----HLVE 111
                                                                                                                                                                                                                                               2 FPTIPLSRLFDNAMLRAHRLHQLAFDTYQEFEEAYIPKEQKYSFLQNPQTSLSFSESIPT 61
                                                                                                                                                 27 FPIIPLSRLFDNAMLRAHRLHQLAFDTYQEFEEAYIPKEQKYSFLQNPQISLCFSESIPT 86
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      28-FEB-2003 (Rel. 41, Created)
28-FEB-2003 (Rel. 41, Last sequence update)
29-FEB-2003 (Rel. 41, Last annotation update)
Somatotropin precursor (Growth hormone) (GH) (GH-N) (Pituitary growth
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Pan troglodytes (Chimpanzee).
Eukaryota; Metazoa: Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Pan.
                                                                        16:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   tissues (By Similarity).
--- SUBCELLOLAR LOCATION: Secreted.
--- SIMILARITY: BELONGS TO THE SOMATOTROPIN/PROLACTIN FAMILY.
                       Length 217;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 217;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        20; Indels
                                                                        20; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SOMATOTROPIN.
BY SIMILARITY.
BY SIMILARITY.
FEA295EDE0518674 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ; DB 1;
4.6e-38;
                       57.8%; Score 461; DB 1;
70.3%; Pred. No. 4.6e-38;
iive 7; Mismatches 20;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      217 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     BY SIMILARITY.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    57.8%; Score 461; 70.3%; Pred. No. 4
                                                                                                                                                                                                                                                                                                                  112 ALYLVCG -- ERGFFYTPKTRGIVEQ 134
                                                                                                                                                                                                                                                                                                                                                               146 GIQTLMGRLEDG --- SPRTGQIFKQ 167
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EMBL; AF374232; AAL72284.1; -.
InterPro; IPR001400; Somatotropin.
Pfam; PF00103; hormone; 1.
PRINTS; PR00836; SOMATOTROPIN.
PROSTTE; PS00266; SOMATOTROPIN.
PROSITE; PS00338; SOMATOTROPIN.2; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        24843 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        hormone) (Growth hormone 1).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Hormone; Pituitary; Signal
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Best Local Similarity 70.33
Matches 102; Conservative
                          Ouery Match
Best Local Similarity 70.33
Matches 102; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STANDARD;
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79
208
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P58756:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SIGNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                          RESULT 2
SOMA_PANTR
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2 FPTIPLSRLFDNAMLRAHRLHQLAFDTYQEFEEAYIPKEQKYSFLQNPQTSLSFSESIPT
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24913 MW;

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                                                     2 FPTIPLSRLFDNAMLRAHRLHQLAFDTYQEFEEAYIPKEQKYSFI,ONPQTSLSFSESIPT 61
                                                                  27 FPTIPLSRLLDNAMLRAHRLHQLAFDTYQEFEEAYIPKEQKYSFLQNPQTSLCFSESIPT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     2 FPTIPLSRLFDNAMLRAHRLHQLAFDTYQEFEEAYIPKEQKYSFLQNPQTSLSFSESIPT
                                                                                                                                                                                                                                                                                                    Salmiri boliviensis boliviensis (Bolivian squirrel monkey).
Eukaryota: Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Platyrrhini; Cebidae; Cebinae; Saimiri.
                            Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        -1. SIMILARITY: BELONGS TO THE SOMATOTROPIN/PROLACTIN FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           54.8%; Score 437; DB 1; Length 217; 91.3%; Pred. No. le-35;
Length 217;
                         1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           3; Indels
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BY SIMILARITY.
BY SIMILARITY.
9515289992C529F7 CRC64;
57.7%; Score 460; DB 1; 98.9%; Pred. No. 5.8e-38; ive 0; Mismatches 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Pred. No. 1e-35;
5; Mismatches
                                                                                                                                                                                                                                  28-FEB-2003 (Rel. 41, Created)
28-FEB-2003 (Rel. 41, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Somatotropin precursor (Growth hormone).
                                                                                                                           62 PSNREETQQKSNLELLRISLLLIQSWLEPVQL 93
                                                                                                                                                                                                        217 AA
                                                                                                            62 PSNREETQQKSNLELLRISLLLIQSWLEPVQ 92
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             BY SIMILARITY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PROSITE; PS00266; SOMATOTROPIN_1; 1. PROSITE; PS00338; SOMATOTROPIN_2; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Secreted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EMBL; AF339060; AAK62287.1; ·.
InterPro; IPR001400; Somatotropin.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Pfam; PF00103; hormone; 1.
PRINTS: PR00836; SOMATOTROPIN.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 tissues (By similarity) subcellular location: 5
                            90; Conservative
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                                                                                                                                                                                                          STANDARD;
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Matches 84; Conserv
             Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                NCBI_TaxID-39432,
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DISULFID
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    Query Match
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This SWISS-PROT entry is cop; right. It is produced through a collaboration between the SWiss institute ( Bioinformatics and the EMBL outstation the European Bioinformatics Littute. There are no restrictions on its most by non-profit institutions as long as its content is in no way modified and this statement not removed. Usage by and for commercial entities requires a license ement (See http://www.isb-sib.ch/announce/or send an email to license...sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Submitted (APR-2001) to the EMBL/GenBank/DDBJ databases.
-!- FUNCTION: Plays an important role in growth control. Its major role in stimulating body growth is to stimulate the liver and other tissues to secrete IGF-1. It stimulates both the differentiation and proliferation of myoblasts. It also stimulates amino acid uptake and protein synthesis in muscle and other
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           2 FPTIPLSRLFUNAMLRAHKLHQLAFUTYQEFEEAYIPKEQKYSFLQNPQTSLSFSESIPT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
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28 -FEB-2003 (Rel. 41, Last annotation update)
Growth hormone variant precursor (GH-V) (Placenta-specific growth hormone) (Growth hormone 2).
                                                                                                                                                                                                                                                                                                                Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Pan.
NCBI_TaxID+9598,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Pred. No. 1.8e-35;
4; Mismatches 9; Indels 11;
                                                                                                                                                                                                                                                                                                                                                                                                                           PLOURINGE FROM N.A.

Revol A., Esquivel D., Santiago D., Barrera-Saldana H.;

**Independent duplication of the growth hormone gene in three **

**Independent duplication of the growth hormone gene in three **

**Independent duplication of the growth hormone gene in three **

**Independent duplication of the growth hormone gene in three **

**Independent duplication of the growth hormone gene in three **

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**Independent duplication of the growth hormone gene in three **

**Independent duplication of the growth hormone general duplication of the growth hormone 
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-:- IISSUE SPECIFICITY: Expressed in the placenta.
-:- SIMILARITY: BELONGS TO THE SCMATOTROPIN/PROLACTIN FAMILY.
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GROWTH HORMONE VARIANT
BY SIMILARITY.
BY SIMILARITY.
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(Rel. 41, Last sequence update)
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78.9%; Pred. No. 1.8
                                 217
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Pfam: PF00103; hormone: 1. PF051TE; PS00266; SOMATOTROPIN_1; 1. PROSITE; PS00338; SOMATOTROPIN_2: 1.
                                    PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EMBL; AF374233; AAL72285.1;
InterPro; IPR001400; Somatotropin.
                                                                                                28-FEB-2003 (Rel. 41, Created)
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                                                                                                                                                                                                                                                                                        troglodytes (Chimpanzee).
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Nes 90; Conservative
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                                 STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      217
191
215
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217 AA;
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28-FEB-2003
                                 SOM2_PANTR
P58757;
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Q9GMB3;
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MEDLINE-83182010; PubMed-7169009;
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                                                                                                                                                                                                                evolution.
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 This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                     2 FPTIPLSRLFDNAMLRAHRLHQLAFDTYQEFEEAYIPKEQKYSFLQNPQTSLSFSFSIPT 61
                                                                  It also stimulates
                                                                                                                                                                                                                                                                                                                                                                                           U; Caps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            P01242; P09587;
21-JUL-1986 (Rel. 01, Created)
28-FEB-2003 (Rel. 41, Last anotation update)
15-SEP-2003 (Rel. 42, Last anotation update)
Growth hormone variant precursor (GH-V) (Placenta-specific growth
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                       Callithrix jacchus (Common marmoset).
Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Platyrrhini; Callitrichidae;
                                                                                                                                                                                                                                                                                                                                                                           Length 217;
                                                                                                                                                                                                                                                                                                                                                                  54.28; Score 432; DB 1; Length 217
91.28; Pred. No. 3.2e-35; Pred. No. 3.2e-35; Indels
                                                                                                                                                                                                                                                                                                                                 SOMATOTROPIN.
BY SIMILARITY.
BY SIMILARITY.
E102151A12CE6192 CRC64;
 28-FEB-2003 (Rel. 41, Last annotation update) Somatotropin precursor (Growth hormone).
                                                                                                                                                                                                                                                                                                                                                                                                                                                      217 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                             62 PSNREETQQKSNLELLRISLLLLQSWLEPVQ 92
                                                                                                                                                                                                                                                                                                                          BY SIMILARITY.
                                                                                                                                                                                                                                                                                       Pfam; PF0013; hormone: 1.
PROSITE; PS00266; SOMATOTROPIN_1; 1.
PROSITE; PS00338; SOMATOTROPIN_2: 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRT;
                                                                                                                                                                                                                                                                                nterPro; IPR001400; Somatotropin.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A. (ISOFORM 1).
                                                                                                                                                                                                                                                                 EMBL; AJ297563; CAC03481.1; -.
                                                                                                                                                                                                                                                                                                                                                           24959 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         hormone) (Growth hormone 2).
                                                                                                                                                                                                                                                                                                                   Hormone; Pituitary; Signal
                                                                                                                                                                                                                                                                                                                                                                                   Local Similarity 91.2
es 83; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STANDARD;
                                                                                                                                                                                                                                                                                                                                         191
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Homo saplens (Human)
                                                                                                                                                                                                                                                                                                                                         79 1
208 2
217 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NCBI_TaxID=9606;
                                                           NCBI_TaxID=9483;
                                                    Callithrix.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SOM2_HUMAN
                                                                                                                                                                                                                                                                                                                                         DISULFID
DISULFID
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                            Query Match
                                                                                                                                                                                                                                                                                                                                                                                            Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RESULT 7
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Attacher R.D. Collins F.S. Wagner L., Shenmen C.M., Schuler G.D., Alschuler S.C. Wagner L., Shenmen C.M., Schuler G.D., Alschuler S.F., Zeeberg B., I Jetow K.H., Schaefer C.F., Bhat N.K., Alschul S.F., Zeeberg B., I Jetow K.H., Schaefer C.F., Bhat N.K., Hopkins R.F., Jordan H., Moore I., Max S.I., Wang J., Hsieh F., Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L., Schaefer M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E., Brownstein M.J., Usdin T.B., Toshlyuki S., Carninci P., Priange C., A Brownstein M.J., Usdin T.B., McFrian K.J., Malek J.A., Gunarathe P.H., Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J., A Richards S., Morley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W., Villalon D.K., Wuzny D.M., Sodergren F.J., Lu X., Gibbs R.A., Andran A., Rotting M. Madan A., Rotting M. Scher E.D., Dickson M.C., Shevchenko Y., Bouffard G.G., Abtracting M. Madan A., Yourd A.C., Shevchenko Y., Bouffard G.G., Abtracting M. Madan A., Young A.C., Shevchenko Y., Bouffard G.G., Abtracting M. Schein J.E., Jones S.J.M., Marra M.A., Schein J.E., Schein S.G., Schein J.E., Schein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                "Growth hormone heterogeneity in human pituitary and plasma.";
Horm. Res. 51 Suppl. 1.2-6(1999).
-i- FUNCTION: Plays an important role in growth control. Its major
role in stimulating body growth is to stimulate the liver and
other tissues to secrete IGF-1. It stimulates both the
differentiation and proliferation of myoblasts. It also stimulates
amino acid uptake and protein synthesis in muscle and other
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               -:- SUBUNIT: Monomer, dimer, trimer, tetramer and pentamer, disulfide-
linked or non-covalently associated, in homopolymeric and
heteropolymeric combinations. Can also form a complex either with
GHBP or with the alpha2-macroglobulin complex.
-:- SUBCELLUIAR LOCATION: Secreted.
-:- ALTERNATIVE PRODUCTS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    The human growth hormone ocus: nucleotide sequence, biology, and
                                                                                                                                                                                                                                                                                                                                                                    Cooke N.E., Ray J., Emery J.J., Liebhaber S.A.; Two distinct species of human growth hormone-variant mRNA in the human placenta predict the expression of novel growth hormone
"The human growth hormone gene family: nucleotide sequences recent divergence and predict a new polypeptide hormone."; ONA 1:239-249(1982).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Igout A., Scippo M.L., Frankenne F., Hennen G.; "Cloning and nucleotide sequence of placental hGH-V cDNA.": Arch. Int. Physiol. Biochim. 96:63-67(1988).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
MEDLINES-89307277: PubMed=27.4760;
Chen E.Y., Liao Y.C., Smith L.H., Barrera-Saldana H.A.,
Gelinas R.E., Seeburg P.H.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Event-Alternative splicing; Named isoforms-2; Name-1; Synonyms-GH-V1; Isold-P01242-1; Sequence-Displayed; Name-2; Synonyms-GH-V2;
                                                                                                                                                                                                                                                                SEQUENCE FROM N.A. (ISOFORM: 1 AND 2).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Biol. Chem. 263:9001-9006(1988)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TISSUE=Placenta;
MEDLINE=22388257; PubMed=12477932;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDLINE-99321812; Pubmed-10393484;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A. (ISOFORM 1).
MEDLINE-89024984; Pubmed-2460050:
                                                                                                                                                                                                                                                                                                                        MEDLINE-88243769; PubMed-33 057;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Genomics 4:479-497(1989).
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は、「からから、「からから、「これ」では、「これ」では、「ないない」では、「ないないない」では、「これ」では、「

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Cercopithecinae, Macaca.
                                                                 SEQUENCE FROM N.A.
                                                                                                                                               SEQUENCE FROM N.A.
                    NCBI_TaxID=9544;
                                                                                                                                                                                                                                                                                                                                                                                                                          tissues.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CONFLICT
CONFLICT
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
                                                                                   Golos
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PLL_HUMAN
    q
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                                                                                                  This SWISS-PROT entry is copyright. It is produced through a collaboration between the SWISS institute of Bloinformatics and the FWBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        2 FPTIPLSRLFONAMURAHRUHQLAFOTYQEFEEAYIPKEQKYSFLQNPQTSLSFSESIPT 61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LASRDWGEKHC "LESSQALIQENSPYSSFPLVNPPGLSLQ
PGGEGGKWMNE" REQCPSAWPLLLFLHFAEAGRWQPPDWA
DLOSYLQV ( 1 isoform 2).
FTIG-VSPV ( 1 isoform 2).
R -> W (IN dbSNP:5389).
/FTIG-VAR_014591.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     N-LINKED (GLCNAC. . .) (POTENTIAL).
RLEDGSPRTGQIFNQSYSKFDTKSHNDDALLKNYGLLYCFR
KDMDKVETFLRIVQCRSVEGSCGF -> VRVAPGIPNPGAP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 426.5; DB 1; Length 217;
Pred. No. 1.1e+34;
4; Mismatches 10; Indels 11; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               62 PSNREETQQKSNLELLRISLLLIQSWLEPVQL------GTGPRFVNQHL 104
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SOM2_MACMU STANDARD: PRI; 217 AA. 007370: Q28494; Clasted) Linov-1997 (Rel. 35, Created) 01-NOV-1997 (Rel. 35, Last sequence update) 28-FEB-2003 (Rel. 41, Last annotation update) Growth hormone variant precursor (GH-V) (Placenta-specific growth
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Eukaryota; Metazoa; Chordata; Cranlata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Cercopithecidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Pfam. PF00103; hormone; 1.
PROSITE; PS00266; SOMATOTROPIN_1; 1.
PROSITE; PS00388; SOMATOTROPIN_2; 1.
Hormone; Placenta; Signal: Glycoprotein; Alternative splicing;
IsoId=P01242-2: Sequence=VSP_006203;
NOCE=NO experimental confirmation available;
-! TISSUE SPECIFICITY: Expressed in the placenta.
-! SIMILARITY: BELONGS TO THE SOMATOTROPIN/PROLACTIN FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        -> I (IN REF. 2).
789324698E822F96 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GROWTH HORMONE VARIANT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          BY SIMILARITY
BY SIMILARITY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MIM; 139240; -.
GO; GO:0005180; F:peptide hormone; TAS.
InterPro; IPR001400; Somatotropin.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Macaca mulatta (Rhesus macaque).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 24999 MM:
                                                                                                                                                                                                                                                                                        EMBL, J03756; AAB59547.1; -. EMBL, J03756; AAB59548.1; -. EEMBL, M38451; AAA35891.1; -. EMBL, J03071; AAA52552.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     53.5%;
78.1%;
                                                                                                                                                                                                                                                                      EMBL; K00470; AAA98619.1; -.
                                                                                                                                                                                                                                                                                                                                                                       BC020760; AAH20760.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               hormone) (Growth hormone 2)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Local Similarity 78.1 es 89; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    26
217
191
215
215
217
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MIM; 139240;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        109 :
217 AA;
                                                                                                                                                                                                                                                                                                                                                                                           PIR; A28072; STHUV2.
PIR; D32435; STHUV.
HSSP; P01241; 1A22.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    90
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DISULFID
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SIGNAL
                                                                                                                                                                                                                                                                                                                                                       EMBL;
EMBL;
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Matches
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  SOLUTION TO THE TENEFIT TO THE PROPERTY OF THE TENEFIT TO THE TENEFIT TH
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              62 PSNREETQQKSNLELLRISLLLIQSWLEPVQLGTGPRFVNQHLCGSHLVEA-----LY 114
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                                                                                                                2 FPTIPLSRLFDNAMLRAHRLHQLAFDTYQEFEEAYIPKEQKYSFLQNPQTSLSFSESIPT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  19; Indels 14;
                                                                                                                                                                                                                                                                                                                                                  -:- SUBCELLULAR LOCATION: Secreted (By similarity).
-:- IISSUE SPECIFICITY: Expressed in the placenta.
-:- SIMILARITY: BELONGS TO THE SOMATOTROPIN/PROLACTIN FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 217;
Golos T.G.;
Submitted (JAN-1994) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   8DB116CBC24EA090 CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              5.4e-32;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       50.1%; Score 399; DB 66.9%; Pred. No. 5.4e ive 9; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EMBL; U02293; AAA03391.1; -.
EMBL: L16555; AAA20180.1; -.
PIR: 167411. 167411.
HSSP: P012411. HGU.
InterPro; IPR001400; Somatotropin.
Pfam: PP00103; hormone: 1.
PRINTS: PR00836; SOMATOTROPIN.
PROSITE: PS00366; SOMATOTROPIN.1: 1.
PROSITE: PS00338; SOMATOTROPIN.2: 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRT;
                                                                            TISSUE-Placenta;
MEDLINE-94008724; PubMed-8404617;
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P01243;
21-JUL-1986 (Rel. 01, Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   25221 MW:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Local Similarity 66.9 es 85; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            140 LKKLEEG 146
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57 2
57 1
152 1
217 AA:
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TILILITIELITET AND BURNER BURN
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TSSUERCE-Placentd, and Uterus;

A Klausner R.D., Collins F.S., Wagner L., Schemen C.M., Schuler G.D.,

Klausner R.D., Collins F.S., Wagner L., Scheefer C.F., Bhat N.K.,

A Altschul S.F., Zeeberg B., Buctow K.H., Scheefer C.F., Bhat N.K.,

A Altschul S.F., Zeeberg B., Buctow K.H., Scheefer C.F., Bhat N.K.,

A Altschul S.F., Jordan H., Moore T., Max. Rubin G.M., Hong L.,

B Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,

B Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,

B Brownsteln M.J., Usdin T.B., Toshlyuki S., Carninci P., Prange C.,

R Raha S.S., Loguellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,

B Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,

R Rhohards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

R Willalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,

R Hilting M., Madan A., Young A.C., Shevehenko Y., Bouffard G.G.,

B Hakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,

R Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,

R Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,

Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.,

R Generation and initial analysis of more than 15,000 full-length

M Drock Nath Least C.DN Schwuts S.J.M., Marra M.A.,

R Drock Nath Least C.DN Schwuts S.J.M., Marra M.A.,

R Drock Nath L. Schein J.E., School, JROON, JONEY R.D.,

R Drock Nath L. Schein J.E., School, JROON, JONEY R.D.,

R Drock Nath L. Schein J.E., School, JROON, JONEY R.D.,

R Drock Nath L. Schein J.E., School, JROON, JONEY R.D.,

R Drock Nath L. Schein J.E. School, JROON, JONEY R.D.,

R Drock Nath L. Schein J.E. School, JROON, JONEY R.D.,

R Drock Nath L. Schein J.E. School, JROON, JONEY R.D.,

R Drock Nath L. Schein J.E. School, JROON, JONEY R.D.,

R Drock Nath L. Schein J.E. School, JROON, JONEY R.D.,

R Drock Nath L. Schein J.E. School, JROON, JONEY R.D.,

R Drock R.D., McEwarth R.D., JROON, JONEY R.D.,

R Drock R.D., McEwarth R.D., JROON, JONEY R.D.,

R Drock R.D., JROO
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"Analysis of a major human chorionic somatomammotropin gene. Evidence for two functional promoter elements.";
J. Biol. Chem. 259:13131-13138(1984).
SEQUENCE FROM N.A. (GENE CSH2).
HILL H., Kimchman J., Birnbaum M.J., Chen E.Y., Seeburg P.H.,
Eberhardt N.L., Barta A.;
The human growth hormone gene locus: structure, evolution, and
allelic variations.";
01-APR-1998 (Rel. 07, Last sequence update)
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Lactogen precursor (Choriomanmotropin) (Chorionic somatomammotropin)
CSH1 AND CSH2.
Homo sapiens (Human)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDLINE-89307277; PubMed-2744760;
Chen E.Y., Lido Y.C., Smith D.H., Barrera-Saidana H.A., Gelinas R.E.
Seeburg P.H.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       "The human growth hormone locus: nucleotide sequence, biology, and evolution.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Barrera-Saldana H.A., Seeburg P.H., Saunders G.F.;
"Two Structurally different genes produce the same secreted human
of accordal partonan bytemens."
                                                                                                                                                                                            Eukaryota; Metazoa: Chordata: Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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MEDLINE-78071761; PubMed-593368;
Shine J., Seeburg P.H., Martial J.A., Baxter J.D., Goodman H.M.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Seeburg P.H.; "The human growth hormone gene family: nucleotide sequences show recent divergence and predict a new polypeptide hormone."; DNA 1:239-249(1982)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A. (GENES CSH1 AND CSH2).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       placental lactogen hormone.":
J. Biol. Chem. 258:3787-3793(1983).
                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A. (GENE CSH1).
MEDLINE-85030426; PubMed-6208192;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SECUENCE FROM N.A.
MEDLINE-83160916; PubMed=6300056;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Genomics 4:479-497(1989)
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                                                                                                                                                                                                                                                                          NCBI_TaxID-9606;
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                                                                                       Construction and analysis of recombinant DNA for human chorionic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                IN A DIMER).
                                                                                                                                                somatomammotropin.";
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Nature New Biol. 235:64-64(1972).
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INTERCHAIN (WITH C-208
P -> A (IN CSH2).
/FIId-VAR_007166.
                                                                                                                                                                                                                         MEDLINE-72016313; PubMed-5286363; Sherwood L.M., Handwerger S., McLaurin W.D., Lanner "Amino-acid sequence of human placental lactogen."; Nature New Biol. 233:59-61(1971).
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MISSING (IN REF. 9).
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                                                                                                      MEDLINE-73201971; PubMed-4712450;
Li C.H., Dixon J.S., Chung D.,
Lino acid sequence of human chorionic s
Arch. Blochem. Blophys, 155:95-110(1973).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              or send in email to license@isb-sib.ch).
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PROSITE; PS00266; SOMATOTROPIN_1; 1.
PROSITE; PS00338; SOMATOTROPIN_2: 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MIM; 150200; -. GO; GO:0007565; P:pregnancy; TAS. InterPro; IPR001400; Somatotropin.
                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDLIN -79173081; Pubmed-438159;
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EMBL: J00289; AAA98747.1; ...
EMBL: K02401; AAA52115.1; ...
EMBL: M15894; AAA52116.1; ...
EMBL: J03071; AAA52551.1; ...
EMBL: J030718; AAA98621.1; ...
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                                                                                                                                                                                                                                                                                                                                                                                                                        INTERCHAIN DISULFIDE BONDS
                          somatomammotropin.";
Nature 270:494-499(1977).
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Genew: HGNC:2441; CSH2.
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PIR, C32435; LCHUC.
HSSP; P01241; 1A22.
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Mammalia, Eutheria, Cetartiodactyla, Cetacea; Mysticeti;
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-i- SIMILARITY: BELONGS TO THE SOMATOTROPIN/PROLACTIN FAMILY
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HY SIMILARITY,
, 09FBFF6DB14A75D6 CRC64;
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Yudaev N.A., Pankov Y.A., Hulatov A.A., Osipova T.A.;
"Amino acid sequence of seiwhale somatotropin.";
Blokhimiia 47:1059-1069(1982).
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                                                                                                                                                                                                                                                                                                                        01-0CT-11)3 (Rel. 27, Created)
01-0CT-1993 (Rel. 27, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
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                                                                                                               14; Mismatches
                                                                                 62 PSNREETQQKSNLELLRISLLLIQSWLEPVQ
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HSSP: P01241; 1AXI.
InterPro: IPR01400; Somator-opin.
Pfam: PF00103; hormone: 1.
PROSITE: PS00266: SOMATOR PUN-1: 1.
PROSITE: PS00338; SOMATOR PUN-2: 1.
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Matches 61; Conservative
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P33092;
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                                                                                                                                                                                           4 TIPLSRLFDNAMLRAHRLHQLAFDTYQEFEEAYIPKKOKYSFLQNPQTSLSFSFSIPTPS 63
                                                                                                                                                                                                                     29 IVPLSRLEDHAMLQAHRAHQLAIDTYQEFEETYIPRDQKYSFLHDSQTSFCFSDSIFTPS 88
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                                                                                                                                         Gaps
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"Sequence and expression of hamster prolactin and growth hormone
massenger RNAs."
Endocrinology 129:2965-2971(1991).

-I- FUNCTION: Plays an important role in growth control. Its major
role in stimulating body growth is to stimulate the liver and
other tissues to secrete IGF-I. It stimulates both the
differentiation and proliferation of myoblasts. It also stimulate
amino acid uptake and protein synthesis in muscle and other
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Cricetinae,
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O
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-1- SIMILARITY: BELONGS TO THE SOMATOTROPIN/PROLACTIN FAMILY.
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                                                                                 Length 217;
                                                                              Score 381; DB 1; Lungth 21
Pred. No. 3.2e-30;
8: Mismatches 8; Indels
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SOMATOTROPIN.
BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
W; 3B69CE32AB6F1166 CRC64;
     SDD -> BBS (IN REF. 9).
235B0DC7A713F431 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   39.0%; Score 310.5; DB 1 67.0%; Pred. No. 2.5e-23;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           01-0CT-1994 (Rel. 30, Created)
01-0CT-1994 (Rel. 30, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
39.0%; Score 310.5; lest Local Similarity 67.0%; Pred. No. 2.5e
Matches 61; Conservative 13; Mismatches
                                                                                                                                                                                                                                                                                                                                 64 NREETOQKSNLELLRISLLLIQSWLEPVQ 92
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Somatotropin precursor (Growth hormone)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Mesocricetus auratus (Golden hamster).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Pfam; PF00103; hormone; 1.
PROSITE; PS00266; SOMATOTROPIN_1: 1.
PROSITE; PS00338; SOMATOTROPIN_2: 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
MEDLINE-92063850; PubMed-1954881;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1SSP; P01246; 1BST.
InterPro; 1PR001400; Somatotropin.
     136 S
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                                                                                 47.8%;
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                                                       Query Match
Best Local Similarity 82.vv
Best Local 3; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STANDARD;
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189
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     134 1
217 AA;
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216 AA;
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     CONFLICT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Biochem. J. 109:19-24(1968).
-!- FUNCTION: Plays an important role in growth control. Its major role in stimulating body growth is to stimulate the liver and other tissues to secrete IGF-1. It stimulates both the differentiation and proliferation of myoblasts. It also stimulates amino a:id uptake and protein synthesis in muscie and other
                                                                                                                                                                                                                                                                       PRELIMINARY SEQUENCE OF 27-216.
MEDLINE-74020362; PubMed-4747849;
MEDLINE-74020362; PubMed-4747849;
MEDLINE-74020362; PubMed-4747849;
MEDLINE-74020362; PubMed-4747849;
MEDLINE-74020362; Partome J.A.;
FEBS Lett. 34:353-355(1973).
                                                                                                                                                                                                                                                                                                                                                                Zakin M.M., Poskus E., Dellacha J.M., Paladini A.C., Santome J.A.; *Amino acid sequences around the cystine residues in equine growth
                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDLINE-68368390; PubMed-4876100;
Oliver L., Hartree A.S.;
"Amino acid sequences around the cystine residues in horse growth
                       Equus caballus (Horse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Perissodactyla; Equidae; Equus.
                                                                                                                                                                                           MEDLINE-77005410; PubMed-965151;
Zakin M.M., Poskus E., Langton A.A., Ferrara P., Santome J.A.,
Dellacha J.M., Paladini A.C.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 216;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SUBCELLULAR LOCATION: Secreted.
SIMILARITY: BELONGS TO THE SOMATOTROPIN/PROLACTIN FAMILY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    24423 MW; 37AB3173834D11AC CRC64;
                                                                                                    TISSUE-Pituitary;
MEDLINE-94266171; PubMed-8206392;
Ascacio-Martinez J.A., Barrera-Saldana H.A.;
"Sequence of a cDNA encoding horse growth hormone.";
Gene 143:299-300(1994).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           38.5%; Score 306.5; DB 1;
65.2%; Pred. No. 6.2e-23;
Live 14; Mismatches 17;
                                                                                                                                                                                                                                 "Primary structure of equine growth hormone.";
Int. J. Pept. Protein Res. 8:435-444(1976).
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Somatotropin precursor (Growth hormone)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Pfan; PF00103; hormone; 1.
PROSITE; PS00266; SOMATOTROPIN_1; 1.
PROSITE; PS00338; SOMATOTROPIN_2; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             InterPro; IPR001400; Somatotropin.
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                                                                                                                                                                                                                                                                                                                                                                                                      FEBS Lett. 25:77-82(1972).
                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE OF 202-216.
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206 2
216 AA;
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Best Local Similarity
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SEQUENCE OF 27-216.
                                                                                         SEQUENCE FROM N.A.
                                                               NCBI_TaxID=9796;
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DISULFID
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Gaps

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Indels

Conservative

90;

Matches

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This SWISS-PROT entry is considered through a collaboration between the Swiss Institut. If Bioinformatics and the EMB, outstation the European Bioinformatic. Itstitute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement. A not removed. Usage by and for commercial entities requires a license electric seed the system of the statement of some commercial or send an email to licensedishes).
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                        28 FPAMPLSSLFANAVLRAQHHHQLAADTYKEFERAYIPEGQRYS-1QNTQAAFCFSETIPA
2 FPTIPL/SRLFDNAMLRAHRLHQLAFDTYQEFEEAYIPKEQKYSFLQNPQTSLSFSESIPT
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                                                                                                                                                                                                                                                                                                                                                                                Galago senegalensis (Northern iesser bushbaby).
Eukaryota, Metazoa: Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia: Eutheria; Prima·os· Strepsirhini; Galagonidae; Galago.
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-i- SIMILARITY: BELONGS TO " E SOMATOTROPIN/PHOLACTIN FAMILY
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HY SIMILARITY.

BY SIMILARITY.

2FB61CD31136F005 CRC64;
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65.2%; Pred. No. 6.2e-23;
                                                                                                                                                                                                                                                                         28-FEB-2003 (Rel. 41, Created)
28-FEB-2003 (Rel. 41, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Somatotropin precursor (Growth hormone).
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                                                                                 62 PSNREETQQKSNLELLRISHLIQSWLEPVQL 93
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PROSITE, PS00266, SOMATOTRUPIN_1, 1.
PROSITE, PS00338; SOMATOTROPIN_2: 1.
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Pfam; PF00103; hormone:
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217
190
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                                                                                                                                                                                                                                                                  -: SUBCELLULAR LOCATION: Secreted.
-: SIMILARITY: BELONGS TO THE SOMATOTROPIN/PROLACTIN FAMILY.

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                                                                                                                                                                                  Gaps
                                                                                                                                                             Wallis O.C., Zhang Y.P., Wallis M.;
"Cloning and characterisation of the gene encoding slow loris growth
hormone.":
                                                                                       Nycticebus pygmaeus (Pygmy slow loris).
Eukaryota: Metazoa; Chordata; Craniata: Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Strepsirhini; Loridae; Nycticebus.
NycBI_TaxID=101278;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                  BY SIMILARITY.
SOMATOTROPIN.
BY SIMILARITY.
BY SIMILARITY.
A: 7FE90D77ES9085F6 CRC64;
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(Rel. 06, Last sequence update)
(Rel. 41, Last annotation update)
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28 FEB-2003 (Rel. 41, Last sequence update)
28 FEB-2003 (Rel. 41, Last annotation update)
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                    217 AA
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                                                                       Somatotropin precursor (Growth hormone).
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PROSITE; PSO0266; SOMATOTROPIN_1; 1.
PROSITE; PSO0338; SOMATOTROPIN_2; 1.
                                                                                                                                                                                                                                                                                                                                                                                                      InterPro; IPR001400; Somatotropin.
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79 190 BY
207 215 BY
217 AA; 24.395 MW;
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                    STANDARD;
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                                                                                                                                             SEQUENCE FROM N.A.
                                                                                                                                                       TISSUE-Liver;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            01-JAN-1988 (
01-JAN-1988 (
28-FEB-2003 (
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P06880;
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SOMA_MOUSE
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                                                                                                                                                                                         Linzer D.I.H., Talamantes F.:
"Nucleotide sequence of mouse prolactin and growth hormone mRNAs and expression of these mRNAs during pregnancy.":
J. Biol. Chem. 260:9574-9579(1985).
                                                        Sciurognathl; Muridae; Murinae; Mus
                          Craniata; Vertebrata; Euteleostomi;
                                                                                                                                                                                                                                                                                                                                                                                                                             1., Brockmann G., Schwerin M.:
ne-encoding gene and its promoter
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           amino acid uptake and protein synthesis in muscle and other
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               -1- SIMILARITY: BELONGS TO THE SOMATOTROPIN/PROLACTIN FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Ind. 1s
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Job time : 12.6732 secs
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                                                                                                                                                                       MEDI.INE-85261358; PubMed-2991252;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   216 AA: 24716 MW;
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PROSITE; PS00266; SOMATOTROPROSITE; PS00338; SOMATOTRO
Mus musculus (Mouse).
Eukaryota; Metazoa; Chordat.
Mammalia; Eutheria; Rodenti.
                                                                                                                                                                                                                                                                                                                                         SEGUENCE FROM N.A.
SIRAIN-F2TOU; IISSUE-LIVET;
MEDLINE-96194803; PubMed-8h
Das P., Meyer L., Seytert H
"Structure of the growth ho
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EMBL; X02891; CAA26650.1; ...
EMBL; Z46663; CAA86658.1; ...
PIR; B23911; STMS.
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112 ALYLVCG--ERGFFYTFKTRGIVEQ 134
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01447 homo sapien
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(without alignments)
1069.670 Million cell updates/sec
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GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.
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Maximum Match 100%
Listing first 45 summaries
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Q8WND9
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sp_unclassified:*
sp_uvrins:*
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Gapop 10.0 , Gapext 0.5
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sp_fungi:*
sp_human:*
sp_human:*
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sp_phage:*
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Maximum DB seq length: 200000000
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sp_mhc:*
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797
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ALIGNMENTS

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2 FPTIPLSRLFDNAMLRAHRLHQLAFDTYQEFEEAYIPKEQKYSFLQNPQTSLSFSESIPT 61
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                                                                                                                                                                                                    Ateles qeoffroyi (Black-handed spider monkey).
Enkaryota: Molazoa: Chordata: Chanata: Vertebrata: Enteleostomi:
Manmalia: Enterna: Prinatos: Platyrrindi: Orbidae: Ateliado: Ateles.
MOH: Taxio-9679;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   54.7%; Score 436; DB 6; Length 217;
66.9%; Pred. No. 1.4e-38;
tive 8; Mismatches 24; Indels 16; Gaps
                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
Revol A., Esquivel D., Santiago D., Barrera-Saldana H.:
Independent duplication of the growth hormone gene in three
Anthropoidean lineages.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Submitted (APR 2001) to the EMBL/GenBank/DDBJ databases EMBL, AF374234; AAL72286.1; -- InterPro; IPR001400; Somatotropin.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Piam; PF00103; hormone; 1.
PROSITE; PS00266; SOMATOTROPIN_1; 1.
PROSITE; PS00389; SOMATOTROPIN_2; 1.
SEQUENCE 217 AA; 24894 WW; 428829FF41EEAAE6 CRC64;
                                                  01-MAR-2002 (TrEMBLrel. 20, Created)
01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
217 AA
PRT;
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Best Local Similarity 66.9%
watches 97; Conservative
PRELIMINARY;
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SEQUENCE FROM N.A.
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Q07367
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TISSUE-Midpregnancy placenta;

MEDLINE-94008724; PubMed-840617;

Golos T.G., Durning M., Fisher J.M., Fowler P.D.;

"Cloning of four growth hormone/chorionic somatomanmotropin-related complementary deoxyribonucleic acids differentially expressed during pregnancy in the rhesus monkey placenta.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 13: Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                        TISSUE-Term placenta;

BEDINE-24:73313; pubmed-9709963;

Boquszewsi L C.L., Svensson P.A., Jansson T., Clark R.,

Carlsson L.M.S., Carlsson B.;

Cloning of two novel growth hormone transcripts expressed in human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Chorionic somatomamnotropin-3.
Macaca mulatta (Rhesus macaque)
Eukaryota: Metazoa, Chordata: Craniata: Vertebrata: Euteleostomi:
Mammalia; Eutheria: Primates: Catarrhini: Cercopithecidae:
                                                                                                                                                                                                                                                                                                             Eukaryota; Metazoa: Chordata; Craniata; Pertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini Hominidae; Homo.
NCBL_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   53.6%; Score 427.5; DB 4; Lenyth 245; 71.9%; Pred. No. 1.3e-37; ative 6; Mismatches 17; Indels 13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        14CC7F8CD75D91C8 CRC64;
                                                                                                                                                                                                 01-JAN-1998 (TrEMBLrel. 05, Last sequence update) 01-DEC-2001 (TrEMBLrel. 19, Last annotation update) Placental growth hormone isoform hGH-V3 precursor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              01-NOV-1996 (TrEMBLrel. 01, Created)
01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     J. Clin. Endocrinol. Metab. 83:2878-2885(1998)
EMBL: AF006061: AAB71829.1;
HSSP; P01241; 1A22.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       217 AA
                                                                                                                                  245 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     POTENTIAL
146 GIQTLMGRLEDG---SPQTGEIFRQ 167
                                                                                                                                                                                Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PROSITE; PS00266; SOMATOTROPIN_1: 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PKT;
                                                                                                                                  PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         InterPro; IPR001400; Somatotropin.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        27101 MW:
                                                                                                                                                                         01-JAN-1998 (TrEMBLrel. 05, 01-JAN-1998 (TrEMBLrel. 05, 01-DEC-2001 (TrEMBLrel. 19,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity 71.9%
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NCBI_TaxID+9544;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Pfam; PF00103; hormone;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             111 EALYLVCG 118
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EGIQTLIG 152
                                                                                                                                                                                                                                                                                          Homo sapiens (Human).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE 245 AA;
                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
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Q07369;
                                                                                                                                  014644
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                                                                                                                                                                                                                                                                                                                                                                                   87
                                                                                                                                                                                                                                                                                                                                                                28 PSVPLSRLFDNIMMQAHRLHQLAFDTYQEFEKTYIPKEKKHSLMGNPQASFCFSESIPTP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Golos T.G., Durning M., Fisher J.M., Fowler P.D.;
"Cloning of four growth hormone/chorronic somatomammotropin-related
"Cloning of four growth hormone/chorronic somatomammotropin-related
complementary decyribbonucleur enids differentially expressed during
pregnancy in the rhesus monkey placenta.";
Endocrinology 138:1744-1752(1993).
Endocrinology 138:1744-1752(1993).
ENBL: L16553; AAA18840.1; ''HAXI.
HSSP: PG1241; JAXI.
                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                        Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Cercopithecidae;
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                                                                                                                                                                                                                                    Length 217;
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01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
Somatotropin 2 precursor (Growth hormone 2) (Fragment).
Macaca mulatta (Rhesus macaque)
                                                                    DISCIPLIANCE TO THROUGH SOME TO THE PROBLET OF THE PROBLET PAR 24874 MW. FIEBGAFDBBAIB185 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  212 AA; 24525 KW: 278091106255E6F5 CRC64;
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007367;
01-NOV-1996 (TrEMBLrel. 01, Created)
01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-NAV-2003 (TrEMBLrel. 23, Last annotation update)
Chorionic somatomammotropin-1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        49.7%; Score 396; DB 6; Le
82.2%; Prod. No. 2.6e*34;
Mismatches 5;
                                                                                                                                                                                                                                    DB 6;
                                                                                                                                                                                                                                 51.1%; Score 407.5; DB 6
71.9%; Pred. No. 1.6e-35;
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Pfam: PF03163: hormone: 1.
PRGSITE: PS0338; SCHATCHENIN_C: 3.
NON_TER
SEQUENCE 212 AA; 245.25 NW. COMMON.
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Endocrinology 133:1744-1752(1993).
EMBL: L16554; AAA18841.1; -.
HSSP; P01241; 1AXI.
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                                                                                                                                                                                                                                                             Best Local Similarity 71.9%
Matches 82; Conservative
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es 74; Conserv
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HSSP; P01241; 1A22.
InterPro; IPR001400; Somatotropin.
Pfam; PF00103; hormone; 1.
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                    EMBL; BC022044; AAH22044.1; ... EMBL; BC035965; AAH35965.1; ...
  EMBL; J03071; AAA52553.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              69; Conservative
                                                                                                                                                                                                                                                            73; Conservative
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                                                                                                                                                                                                                    Query Match
Best Local Similarity
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Best Local Similarity
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QBWND9
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014643
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                                                                                                                                 3 PTIPLSRLFDNAMLRAHRLHQLAFDTYQEFEEAYIPKEQKYSFLQNPQTSLSFSESIPTP 62
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  28 PSVPLSRLFDHAMIQAHRLHQLAFDTYQEFEEAXIPKEKKHSLMENPQASFCFADSIPTP 87
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
Chorionic somatomammotropin CS-2 (Chorionic somatomammotropin hormone
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      14)
REQUENCE FROM N.A.
MEDLINE-89307277; PubMed-2744760;
Chen E.Y., Liao Y.C., Smith D.H., Barrera-Saldana H.A., Gelinas R.E.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        0; Gaps
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SEQUENCE FROM N.A.
MEDLINE-91102558; PubMed-1980158;
Whencak-Jones C.L., Phillips J.A. III.:
Hot spots for growth hormone gene deletions in homologous regions
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Chen E.Y., Liao Y.C., Smlun c..... Seeburg P.H.;
Seeburg P.H.;
"The human growth hormone locus: nucleotide sequence, biology, and
Macaca mulatta (Rhesus macaque).
Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Cercop:thecidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Eukaryota: Metazoa: Chordata; Craniata; Vertebrata; Euteleostomi
Mammalia; Eutheria: Primates; Catarrhin: Hominidae; Homo.
NCBL_TaxID-9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 217;
                                                                                                                                                                                                                                                                                                                                                                                                           49.7%; Score 396; DB 6; Length 21
82.2%; Pred. No. 2.7e-34;
No. 2.7e-34; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Strausberg R.;
Submitted (JUL-2002) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Submitted (JAN-2002) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           217 AA
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01-NOV-1996 (TrEMBLrel, 01, Last seq
01-MAR-2003 (TrEMBLrel, 23, Last anno
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               outside of Alu repeats.";
Science 250:1745-1748(1990)
                                                                                                                                                                                                                                                                                                                                                                                                                                                 Local Similarity 82.2% es 74; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRELIMINARY;
                                                          Cercopithecinae; Macaca
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Homo sapiens (Human)
                                                                                                                    SEQUENCE FROM N.A.
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                                                                             WCBI_TaxID=9544;
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                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
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Q14407;
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                                                                                                                                                                                                                                                                    2 FPTIPLSRLFDNAMLRAHRLHQLAFDTYQEFEEAYIPKEQKYSFLQNPQTSLSFSESIPT 61
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Mammalia; Eutheria; Primates; Piatyrrhini; Cebidae; Atelinae; Ateles.
NCBI_TaxID=9509;
                                                                                                                                                                                          Saps
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Revol A., Esquivel D., Santiago D., Marrera-Saldana H.;
"Independent duplication of the growth hormone gene in three
                                                                                                                                    Length 217;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       43.7%; Score 348; DB 6; Length 217;
75.8%; Pred. No. 3.7e-29;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          14; Indels
                                                                                                                                                                                    Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Anthropoidean lineages.".
Submitted (APR-2001) to the EMEGAGENBANK/DDBJ databases.
EMBL: AF374235; AAL72287.1;
PRINTS; PROGRAG; SOMATOTROPIN.
PROSITE; PSOUZ66; SOMATOTROPIN_1; 1.
FROSITE; PSOU388; SOMATOTROPIN_2; 1.
SEQUENCE 217 AA; 24994 MW; 39+AACDDB6B2E951 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Pfam: PF00103; hormone; 1.
PRINTS: PR00836; SOMAIOTROPIN.; 1.
PR0311E; PS00266; SUMAIOTROPIN.; 1.
SEQUENCE 217 AA: SSMATCHEFFIN.; 1.
SEQUENCE 217 AA: 25.293 MW: 741745A1875/053E CR064;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               01-MAR-2002 (TrEMBLre), 20, Created)
01-MAR-2002 (TrEMBLrel, 20, Last sequence update)
01-OCT-2002 (TrEMBLrel, 22, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     014643 PRELIMINARY; PRT; 202 AA. 014643. 01-JAN-1998 (TrEMBLrel. 05, Created) 01-JAN-1998 (TrEMBLrel. 05, Last sequence update) 01-JAN-1998 (TrEMBLrel. 21, Last annotation update) Placental growth hormone 20kDa isoform precursor.
                                                                                                  47.8%; Score 381; DB 4; Li
82.0%; Pred. No. 1.1e-32;
no. 1.1e-32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Ateles geoffroyi (Black-handed spider monkey).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  8; Mismatches
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Conservative
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                                                                                                                                                  Growth hormone precursor
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                                                                                          PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                 26
216
                                                                                                                                                                                                                                                                                                                                                                                                                                                         Best Local Similarity
Matches 60, Conserv
                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
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                                                                                                                                                                                                           NCB1_Tax1D-30637;
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                                                                                                                                                                                                 Nannospalax
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                                                                                                                                                                                                                                                                                                                             InterPro;
                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
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                                                                                         070615
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Q8M173
                                                                   RESULT 10
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Callithrix jacchus (Common marmoset).
Eukaryota: Metazca; Chordatu: Craniata: Vertebrata: Euteleostom::
Mammalia; Eutheria; Primates; Platyrrhini; Callitrickhdae: Carlithrix.
NCBI_TaxID=9483;
                                                                                                                                                                                                                                                                                                    26; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1; Gaps
                                                                 TISSUE-Term placenta;
MEDLINE-98373737; PubMed-9709963;
BOUSZEWSKI C.L., Svensson P.A., Jansson T., Clark R.,
Carlsson L.M.S., Carlsson B.;
"Cloning of two novel growth hormone transcripts expressed in human placenta.";
                                                                                                                                                                                                                                                                                                                                                                                      Wallis O.C., Wallis M.;
Characterisation of the GH gene cluster in a new-world monkey, the
marmoset (Callithiix jacchus).":
J. Mol. Endocrinol. 0:0-0(2002).
                                                                                                                                                                                                                                                                                                                                                                        62 PSNREETQQKSNLELLRISLLLIQSWLEPVQL------GTGPRFVNQHL 104
          Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DB 6; Length 217;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           POTENTIAL.
GROWTH HORMONE-LIKE PROTEIN 6.
5 SECF148798278F1A CRC64;
                                                                                                                                                                                                                                                                            Length 202;
                                                                                                                                                                                                                                                                           / Match 42.8%; Score 341; DB 4; Length 202
Local Similarity 65.8%; Pred. No. 1.9e-28;
nes 75; Conservative 4; Mismatches 9; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              40.5%; Score 322.5; DB 6; Lengtn & 64.7%; Pred. No. 2e-26; uismatches 22; Indels
                                                                                                                                                                                                                                             POTENTIAL.
38B64D011A9197C6 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Last sequence update)
Last annotation update)
                                                                                                                                   J. Clin. Endocrinol. Metab. 83:2878-2885(1998).
EMBL, RAF006060, AAB71828-1;
EMSP. PO1241: 1A22.
InterPro. IPR001400; Somatotropin.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Best Local Similarity 64.7%; Pred. No. 2e-26
Matches 66; Conservative 13; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                       217 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Growth hormone-like protein 6 precursor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           01-0CT-2002 (TrEMBLrel, 22, Created)
01-0CT-2002 (TrEMBLrel, 22, Last sequ
01-MAR-2003 (TrEMBLrel, 23, Last anno
                                                                                                                                                                                                          PROSITE; PS00266; SOMATOTROPIN_1; 1. PROSITE; PS00338; SOMATOTROPIN_2; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRINTS; PR00836; SOMATOTROPIN.
PROSITE; PS00338; SOMATOTROPIN_2; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRT:
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InterPro; IPR001400; Somatotropin.
Pfam; PF00103; hormone; 1.
                                                                                                                                                                                                                                             SIGNAL 1 26 PC
SEQUENCE 202 AA; 23128 MW;
                                                                                                                                                                                   Pfam; PF00103; hormone; 1.
PRINTS; PR00836; SOMATOTROPIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 25177 MW;
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Homo sapiens (Human)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SIĞNAL 1
CHAIN 27 2
SEQUENCE 217 AA;
                                                        SEQUENCE FROM N.A.
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                               NCBI_TaxID-9506;
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QBM174;
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2 FPTIPLSRLFDNAMLKAHRLMGMAFUTYQEFEEAYIPKEQKYSFLQNPQTSLSFSFPT 61
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Eukaryota; Metazoa: Chordata: Craniata; Vertebrata; Euteleostomi:
Mammalia: Eutheria: Cetartiodactyla; Cetacea; Odontoceti; Delphinidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Maniou Z., Wallis O.C., Wallis M.; "Cloning and characterisation of the GH gene from the common dolphin (Delphinus delphis)."; "Submitted (JUN-2002) to the EMBL/GenBank/DDBJ databases.
EMBL: AJ492191; CAD37292.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDLINE-99124645; PubMed-9920177;
Licupis A., Nevo E., Mallis K.;
Cloning and characterisation of the gene encoding mole rat (Spalax
Chenberdi) growth hormone.":
                                                                                                                                                                                                                                                                                                                                                                                                                                            Spalax Jeucodon ehrenberg (Ehrenberg's mole rat).
Eukaryota; Metazoa: Chordata: Craniata; Vertebrata; Euteleostomi;
Mammalia: Eutheria; Rodentia: Sciurognathi; Muridae; Spalacinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     38.5%; Score 306.5; DB 11; Length 216; 65.9%; Pred. No. le-24; Live 13; Mismatches 17; Indels 1;
                                    88 FHKEEMLGKSNVELLHISLLLISSWLEPMO-RLGSIFANSQL 128
63 SNREETQQKSNLELLRISLLIQSWLEPVQLGTGPRFVNQHL 104
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE 216 AA; 24627 MW; EFABBA523BA0ADFE CRC64;
                                                                                                                                                                                                                                                                                                    01-AUG-1998 (TrEMBLrel, 07, Created)
01-AUG-1998 (TrEMBLrel, 07, Last sequence update)
01-MAR-2003 (TrEMBLrel, 22, Last annotation update)
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01-0CT-2002 (TrEMBLrel. 22, Last sequence update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 86 PTGKEEAQQRSDMELLRESULLIUSWEGPVQ 116
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GROWTH HORMONE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PUTENTIAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Pfam: PF00103; hormone; 1.
PRINTS; PR0010836; SOMATOTROP:
PROSTIE; PS00266; SOMATOTROPIN_; 1
PROSTIE; PS00338; SOMATOTROPIN_; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRT;
                                                                                                                                                                                                                                          PRT;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ehrenbergi) growth hormone."
J. Moil. Endocrinol. 22:29-36
EMBL: AJO05819; CAA06716.1;
HSSP: P01241; lAXI.
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86 PICKEFAQORTDMHLLRFSLLLIQSWLGPVQ 116
                                                                                                                                                                                                                                                                                                     62 PSNREETQQKSNLELI,RISLLI,1QSWLEPVQ 92
                                                                                                                                                                                                                                                                                                                                                                                                    204 AA
                                                                EMBL. 034362; AAC99988.1;
HSSP: P01241: 1AXI.
InterPro; IPR001400: Somatotropin.
Pfam: PF00103; hormone; 1.
PR.NTS: PR00836; SOMATOTROPIN.
PROSITE; PS00256; SOMATOTROPIN.
PROSITE; PS00338: SOMATOTROPIN.
SEQUENCE 216 AA; 24682 MW. FC2A0604
SEQUENCE FROM N.A.
Nguyen T.N.K., Liebhaber S.
Mouse Growth Hormone Locus
Analyses.";
                                                                                                                                                                                           37.58:
63.78.
                                                                                                                                                                                           Query Match
Best Local Similarity 63.78
Matches 58; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                  PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Bovidae; Caprinae; Ovis.
NCBL_TaxID=9940;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
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SEQUENCE
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095205
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                                                                                                                                                                                           2 FPTIPLSRLFDNAMLRAHRLHQLAFDTYQEFEEAYIPKEQKYSFLQNPQISLSFSESIPT 61
                                                                                                                                                               1; Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Growth Announce: 23, Last unnotation update;
Growth Announce:
Mus musculus (Mouse).
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
[1]
                                                                                                                                                                                                                                                                                                                                                                                                           Growth hormone precursor.
Alluropoda melanoleuca (Giant panda).
Bukaryota: Merazoa: Chordata: Craniata: Vertebrata: Euteleostomi;
Mammalia: Eutheria: Carnivora; Fissiped ;; Ursidae; Ailuropoda.
                                                                                                                                     DB 6; Length 216;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             37.8%; Score 301.5; DB 6; Length 216; 64.8%; Pred, No. 3.40-24; ative 14; Mismatches 17; Indels 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TISSUE-Pituitary:
Liao M., Zhu M., Zhang A.;
Liao M., Zhu M., Zhang A.;
"Cloning and expression of cDNA encodin, growth hormone from Alluropoda melanoleuca.":
Submitted (AuG-2002) to the EMBL/GenBank/DDBJ databases.
EMBL, AF540936; AAN77228.1;
                                                                                                                                                                 Indels
                                                                                1 26 POTENTIAL.
27 216 GROWTH HORMONE.
216 AA: 24509 MW: 1EC467A84CCFEB02 CRC64;
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SEQUENCE 216 AA; 24383 MW; 44ECITEC44BCB056 CRC64;
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Last annotation update)
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01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
                                                                                                                                   / Match 37.8%; Score 301.5; DB 6; Local Similarity 64.8%; Pred. No. 3.4e-24; hes 59; Conservative 14; Mismatches 17;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PTGKDEAQQRSDVELLRFSLLLIQSWLGPVQ 116
                                                                                                                                                                                                                                             62 PSNREETQQKSNLELLRISLLLIQSWLEPVQ 92
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             Pfam: PF00103; hormone; 1.
PRINTS; PR0010836; SOMATOTROPIN.
PROSITE; PS00266; SOMATOTROPIN.; 1.
PROSITE; PS00338; SOMATOTROPIN...; 1.
 InterPro; IPR001400; Somatotropin
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Local Similarity 64.8% les 59; Conservative
                                                                                                                                                                                                                                                                                                                                            PRELIMINARY;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NCBI_TaxID=9646;
                                                                                                          SEQUENCE
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                                                                    Signal.
SIGNAL
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Q9R2C3
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Lacroix M.C., Devinoy E., 2 (vely J.L., Puissant C., Kann G.;
Lacroix M.C., Devinoy E., 2 (vely J.L., Puissant C., Kann G.;
Expression of the growth - imone gene in ovine placenta: detection
Endocrinology 137:4886-489, 996;
EMBL: U49065; Adv48679.1;
HSSP: 104002406; Somatotropin.
PROD.241; LAXI.
PROD.341; LAXI.
PROD.351; PROD.366; SOMATOTROPIN.
PROSITE; PSO0338; SOMATOTROPIN.
PROSITE; PSO0338; SOMATOTROPIN.
2 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   01-FEB-1997 (TrEMBLrel. 02, Created)
01-FEB-1997 (TrEMBLrel. 02, Last sequence update)
01-MFR-2003 (TrEMBLrel. 23, Last annotation update)
01-MFR-2003 (TrEMBLrel. 23, Last annotation update)
11-MFR-2003 (TrEMBLrel. 23, Last annotation update)
11-MFR-2003 (Shep)
11-MFR-2003 (Shep)
11-MFR-2003 (Chordata: Craniata; Vertebrata: Exteleostomi:
11-MFR-2003 (MFR-2003) 
Sucleotide Sequence and Phylogenetic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        "core 298.5; DB 11; Length 216;
"red, No. 7.2e-24;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 204;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             indels
                                                                                                                                                                    Submitted (AUG-1995) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        204 AA; 23462 MW: EBBB9451892635C6 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FC2A06DA02536B1B CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Mismatches 18;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DB 6;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ry Match 37.3%; Score 297.5; DB 6, t Local Similarity 64.8%; Pred. No. 8,6e-24; ches 59; Conservative 14; Mismatches 17,
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Q9JKM4 PRELIMINARY; PRT: 216 AA.
01-0CT-2000 (TrEMBLrel. 15, Created)
01-0CT-2000 (TrEMBLrel. 15, Last sequence update)
01-0CT-2000 (TrEMBLrel. 13, Last annotation update)
01-0CT-2000 (TrEMBLrel. 23, Last annotation update)
Growth hormone precursor.
Cavia porcellus (Guinea pig).
Cavia porcellus (Guinea pig).
Mammalia: Eutheria: Rodentia: Hystricognathi; Caviidae; Cavia.
MCBI_TaxID-10141:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match 37.3%; Score 297.5; DB 11; Length 216; Best Local Similarity 63.7%; Pred. No. 9.2e-24; Matches 58; Conservative 14; Mismatches 18; Indels 1;
                                                                                                                                                                                                                           SEQUENCE FROM N.A.
SEQUENCE FROM N.A.
SCOUENCE D.M., Fuller P.J., Herington A.C.;
"Cloning and sequence of guinea pig growth hormone (GH).";
Submitted (FEB-2000) to the EMBL/GenBank /DDBJ databases.
EMBL; AF233853; AAF36409.1;
HSSP; P01241; 1AXI.

        SIĞNAL
        1
        26
        POTENTIAL.

        CHAIN
        27
        216
        GROWTH HORMONE.

        SEQUENCE
        216
        AA;
        24822
        MW;
        45996BEI19B08DD3
        CRC64;

                                                                                                                                                                                                                                                                                                                                                                             Pfam: PF00103; Somatotropin. Pfam: PF00103; hormone: 1. PF00103; hormone: 1. PF001175; PF00836; SOMATOTROPIN. 1. PPROSITE; PS00266; SOMATOTROPIN. 1: 1. PPROSITE; PS00338; SOMATOTROPIN. 2: 1.
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2 FPTIPLSRLFDNAMLRAHRLHQLAFDTYQEFEEAYIPKEQKYSFLQNPQTSLSFSESIPT 61

g ò Search completed: September 16, 2003, 12:40:01 Job time : 37.1868 secs

1; Gaps

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